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(54) **METHODS AND COMPOSITIONS RELATED TO THIOESTERASE ENZYMES**

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(57) **ABSTRACT**

The present invention relates to novel mutant thioesterase enzymes and naturally-occurring equivalents thereof, compositions made from such enzymes and uses of thioesterase enzymes. In particular, the present invention provides mutant thioesterase enzymes that have altered properties, for example, altered substrate specificity, altered activity, altered selectivity, and/or altered proportional yields in the product mixtures. The present invention also provides polynucleotides encoding such mutant thioesterase enzymes, and vectors and host cells comprising such polynucleotides. The invention further provides for novel uses of thioesterases in the production of various fatty acid derivatives, which are useful as, or as components of, industrial chemicals and fuels.

9 Claims, 226 Drawing Sheets

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FIG. 1

Accession Numbers are from NCBI, GenBank, Release 159.0 as of March 2008
EC Numbers are from KEGG, Release 42.0 as of April 2007 (plus daily updates up to March 2008)

CATEGORY	GENE	NAME	ACCESSION	EC NUMBER	MODIFICATION	USE	ORGANISM
1. Fatty Acid Production Increase / Product Production Increase							
increase acyl-CoA							
reduce catabolism of derivatives and intermediates							
reduce feedback inhibition							
attenuate other pathways that consume fatty acids							
	accA	Acetyl-CoA carboxylase, subunit A (carboxyltransferase alpha)	AAC73296, NP_414727	6.4.1.2	Over-express	increase Malonyl-CoA production	*Escherichia coli, Lactococci*
	accB	Acetyl-CoA carboxylase, subunit B (BCCP: biotin carboxyl carrier protein)	NP_417721	6.4.1.2	Over-express	increase Malonyl-CoA production	*Escherichia coli, Lactococci*
	accC	Acetyl-CoA carboxylase, subunit C (biotin carboxylase)	NP_417722	6.4.1.2, 6.3.4.14	Over-express	increase Malonyl-CoA production	*Escherichia coli, Lactococci*
	accD	Acetyl-CoA carboxylase, subunit D (carboxyltransferase	NP_416819	6.4.1.2	Over-express	increase Malonyl-CoA production	*Escherichia coli, Lactococci*

FIG. 1 Cont.

		beta)					
	aceE	pyruvate dehydrogenase, subunit E1	NP_414656, AAC73226	1.2.4.1	Over-express	increase Acetyl-CoA production	*Escherichia coli*
	aceF	pyruvate dehydrogenase, subunit E2	NP_414657	2.3.1.12	Over-express	increase Acetyl-CoA production	*Escherichia coli*
	ackA	acetate kinase	AAC75356, NP_416799	2.7.2.1	Delete or reduce	increase Acetyl-CoA production	*Escherichia coli*
	ackB	acetate kinase AckB	BAB81430	2.7.2.1	Delete or reduce	increase Acetyl-CoA production	*Escherichia coli*
	acpP	acyl carrier protein	AAC74178	NONE	Over-express	increase Acetyl-CoA production	*Escherichia coli*
	fadD	acyl-CoA synthase	AP_002424	2.3.1.86, 6.2.1.3	Over-express	increase Fatty acid production	*Escherichia coli W3110*
	adhE	alcohol dehydrogenase	CAA47743	1.1.1.1, 1.2.1.10	Delete or reduce	increase Acetyl-CoA production	*Escherichia coli W3111*
	cer1	Aldehyde decarbonylase	BAA11024	4.1.99.5	Over-express	increase Acetyl-CoA production	*Arabidopsis thaliana*
	fabA	beta-hydroxydecanoyl thioester dehydrase	NP_415474	4.2.1.60	express	fatty acyl-CoA production	*E. coli K12*
	fabD	[acyl-carrier-protein] S-malonyltransferase	AAC74176	2.3.1.39	Over-express	increase Acetyl-CoA production	*E. coli K12*
	fabF	3-oxoacyl-[acyl-carrier-protein] synthase II	AAC74179	2.3.1.179	Delete or OverExpress	increase Acetyl-CoA production	*E. coli K12*
	fabG	3-oxoacyl-[acyl-carrier protein] reductase	AAC74177	1.1.1.100	Over-express	increase Acetyl-CoA production	*E. coli K12*

FIG. 1 Cont.

	fabH	3-oxoacyl-[acyl-carrier-protein] synthase III	AAC74175	2.3.1.180	Over-express	increase Acetyl-CoA production	*E. coli K12, lactococci*
	fabI	enoyl-[acyl-carrier-protein] reductase, NADH-dependent	NP_415804	1.3.1.9	express	fatty acyl-CoA production	*E. coli K12, lactococci*
	fabR	Transcriptional Repressor	NP_418398	NONE	Delete or reduce	modulate unsaturated fatty acid production	*E. coli K12*
	fabZ	(3R)-hydroxymyristol acyl carrier protein dehydratase	NP_414722	4.2.1.-			*E. coli K12*
	fadE	acyl-CoA dehydrogenase	AAC73325	1.3.99.3, 1.3.99.-	Delete or reduce	increase Acetyl-CoA production	
	acr1	Fatty Acyl-CoA reductase	YP_047869, AAC45217	1.2.1.42	Over-express	for fatty alcohol production	*Acinetobacter sp., i.e. calcoaceticus*
	GST, gshB	Glutathione synthase	P04425	6.3.2.3	Delete or reduce	increase Acyl-CoA	*E. coli K12*
	gpsA	biosynthetic sn-glycerol 3-phosphate dehydrogenase	AAC76632, NP_418065	EC: 1.1.1.94	Delete or reduce	increase Acetyl-CoA production	*E. coli K12*
	ldhA	lactate dehydrogenase	AAC74462, NP_415898	EC: 1.1.1.27, 1.1.1.28	Delete or reduce	increase Acetyl-CoA production	*E. coli K12*
	Lipase	Triglyceride Lipase	CAA89087, CAA98876	3.1.1.3	express	increase Fatty acid production	*Saccharomyces cerevisiae*
		Malonyl-CoA decarboxylase	AAA26500	4.1.1.9, 4.1.1.41	Over-express		*Saccharopolyspora erythraea*

FIG. 1 Cont.

	panD	aspartate 1-decarboxylase	BAB96708	4.1.1.11	Over-express	increase Acyl-CoA	*Escherichia coli W3110*
	panK a.k.a. coaA	pantothenate kinase	AAC76952	2.7.1.33	Over-express	increase Acetyl-CoA production	*E. coli*
	panK a.k.a. coaA, R106K	pantothenate kinase	AAC76952	2.7.1.33	Express, Over-express, R106K mutation	increase Acetyl-CoA production	*E. coli*
	pdh	Pyruvate dehydrogenase	BAB34380, AAC73226, NP_415392	1.2.4.1	Over-express	increase Acetyl-CoA production	
	pflB	formate acetyltransferase (pyruvate formate lyase)	AAC73989, P09373	EC: 2.3.1.54	Delete or reduce	increase Acetyl-CoA production	
	plsB	acyltransferase	AAC77011	2.3.1.15	D311E mutation	reduce limits on Acyl-CoA pool	*E. coli K12*
	poxB	pyruvate oxidase	AAC73958, NP_415392	1.2.2.2	Delete or reduce	increase Acetyl-CoA production	
	pta	phosphotransacetylase	AAC75357, NP_416800	2.3.1.8	Delete or reduce	increase Acetyl-CoA production	
	udhA	pyridine nucleotide transhydrogenase	CAA46822	1.6.1.1	Over-express	conversion NADH to NADPH or vice versa	
	fadB	fused 3-hydroxybutyryl-CoA epimerase/delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase/enoyl-CoA hydratase and 3-hydroxyacyl-CoA	AP_003956	4.2.1.17, 5.1.2.3, 5.3.3.8, 1.1.1.35	Delete or reduce	Block fatty acid degradation	*E. coli*

FIG. 1 Cont.

		dehydrogenase					
	fadJ	3-hydroxyacyl-CoA dehydrogenase; K01692 enoyl-CoA hydratase; K01782 3-hydroxybutyryl-CoA epimerase	AAC75401	1.1.1.35, 4.2.1.17, 5.1.2.3	Delete or reduce	Block fatty acid degradation	*E. coli*
	fadA	3-ketoacyl-CoA thiolase	BAE77458	2.3.1.16	Delete or reduce	Block fatty acid degradation	*E. coli*
	fadI	beta-ketoacyl-CoA thiolase	AAC75402	2.3.1.16	Delete or reduce	Block fatty acid degradation	*E. coli*
	YdiO	acyl-coA dehydrogenase	YP_852786	1.3.99.-	Delete or reduce	Block fatty acid degradation	*E. coli*
2. Structure Control							
2A. Chain Length Control							
2	tesA	thioesterase	P0ADA1	3.1.2.-, 3.1.1.5	Delete and/or express	C18 Chain Length	
	tesA without leader sequence	thioesterase	AAC73596, NP_415027	3.1.2.-, 3.1.1.5	express or overexpress	C18:1	*E.coli*
	tesA without leader sequence:L109P	thioesterase	P0ADA1	3.1.2.-, 3.1.1.5	Express and/or overexpress mutation L109P	<C18 Chain Length	*E. coli*

FIG. 1 Cont.

	fatB1 (umbellularia)	thioesterase	Q41635	3.1.2.14	express or overexpress	C12:0	*Umbellularia californica*
	fatB2 (umbellularia)DELETE umbelluria)	thioesterase	AAC49269	3.1.2.14	express or overexpress	C8:0 - C10:0	*Cuphea hookeriana*
	fatB3	thioesterase	AAC72881	3.1.2.14	express or overexpress	C14:0 - C16:0	*Cuphea hookeriana*
	fatB (cinnamonum)	thioesterase	Q39473	3.1.2.14	express or overexpress	C14:0	*Cinnamomum camphora*
	fatB[M141T]*	thioesterase	CAA85388	3.1.2.14	express or overexpress	C16:1	*Arabidopsis thaliana*
	fatA1 (Helianthus)	thioesterase	AAL79361	3.1.2.14	express or overexpress	*C18:1*	*Helianthus annuus*
	atfata (ARABIDOPSIS FATA ACYL-ACP THIOESTERASE)	thioesterase	NP_189147, NP_193041	3.1.2.14	express or overexpress	C18:1	*Arabidopsis thaliana*
	fatA	thioesterase	CAC39106	3.1.2.14	express or overexpress	C18:1	*Brassica juncea*
	fatA (cuphea)	thioesterase	AAC72883	3.1.2.14	express or overexpress	C18:1	*Cuphea hookeriana*
2B. Branching Control							
	attenuate FabH						

FIG. 1 Cont.

	express FabH from S. glaucescens or S. coelicolor and knock out endogenouse FabH						increase branched chain fatty acid derivatives	
	express FabH from B. subtilis and knock out endogenouse FabH							
	bdk - E3 - dihydroplipoyl dehyrodgenase subunit			EC 1.2.4.4				
	bkd - E1-alpha/beta subunit	decarboxylase subunits of branched-chain α-keto acid dehydrogenase complex		EC 1.2.4.4				
	bkd - E2 - dihydrolipoyl transacylase subunit			EC 1.2.4.4				
	bkdA1	branched-chain α-keto acid dehydrogenase a-subunit (E1a)	NP_628006	EC 1.2.4.4	express or Over-Express		make branched-chain acyl-CoA precursors	*Streptomyces coelicolor*
	bkdB1	branched-chain α-keto acid dehydrogenase a-	NP_628005	EC 1.2.4.4	express or Over-Express		make branched-chain acyl-CoA	*Streptomyces coelicolor*

FIG. 1 Cont.

		subunit (E1b)				precursors	
	bkdC1	dihydrolipoyl transacetylase (E2)	NP_628004	EC 2.3.1.168	express or Over-Express	make branched-chain acyl-CoA precursors	*Streptomyces coelicolor*
	bkdA2	branched-chain a-ketoacid dehydrogenase a-subunit (E1a)	NP_733618	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	*Streptomyces coelicolor*
	bkdB2	branched-chain a-ketoacid dehydrogenase b-subunit (E1b)	NP_628019	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	*Streptomyces coelicolor*
	bkdC2	dihydrolipoyl transacetylase (E2)	NP_628018	EC 2.3.1.168	express or Over-Express	make branched-chain acyl-CoA precursors	*Streptomyces coelicolor*
	bkdA	branched-chain a-ketoacid dehydrogenase a-subunit (E1a)	BAC72074	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	*Streptomyces avermitilis*
	bkdB	branched-chain a-ketoacid dehydrogenase b-subunit (E1b)	BAC72075	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	*Streptomyces avermitilis*
	bkdC	dihydrolipoyl transacetylase (E2)	BAC72076	EC 2.3.1.168	express or Over-Express	make branched-chain acyl-CoA precursors	*Streptomyces avermitilis*
	bkdF	branched-chain a-ketoacid dehydrogenase a-	BAC72088	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	*Streptomyces avermitilis*

FIG. 1 Cont.

		subunit (E1a)					
	bkdG	branched-chain a-ketoacid dehydrogenase b-subunit (E1b)	BAC72089	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	*Streptomyces avermitilis*
	bkdH	dihydrolipoyl transacetylase (E2)	BAC72090	EC 2.3.1.168	express or Over-Express	make branched-chain acyl-CoA precursors	*Streptomyces avermitilis*
	bkdAA	branched-chain a-ketoacid dehydrogenase a-subunit (E1a)	NP_390285	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	*Bacillus subtilis*
	bkdAB	branched-chain a-ketoacid dehydrogenase b-subunit (E1b)	NP_390284	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	*Bacillus subtilis*
	bkdB	dihydrolipoyl transacetylase (E2)	NP_390283	EC 2.3.1.168	express or Over-Express	make branched-chain acyl-CoA precursors	*Bacillus subtilis*
	bkdA1	branched-chain a-ketoacid dehydrogenase a-subunit (E1a)	AAA65614	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	*Pseudomonas putida*
	bkdA2	branched-chain a-ketoacid dehydrogenase b-subunit (E1b)	AAA65615	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	*Pseudomonas putida*
	bkdC	dihydrolipoyl transacetylase (E2)	AAA65617	EC 2.3.1.168	express or Over-Express	make branched-chain acyl-CoA	*Pseudomonas putida*

FIG. 1 Cont.

						precursors	
	lpd	dihydrolipoamide dehydrogenase (E3)	NP_414658	1.8.1.4	express or Over-Express	make branched-chain acyl-CoA precursors	*Escherichia coli*
	IlvE	branched-chain amino acid aminotransferase	YP_026247	2.6.1.42	express or Over-Express	make branched a-ketoacids	*Escherichia coli*
	IlvE	branched-chain amino acid aminotransferase	AAF34406	2.6.1.42	express or Over-Express	make branched a-ketoacids	*Lactococcus lactis*
	IlvE	branched-chain amino acid aminotransferase	NP_745648	2.6.1.42	express or Over-Express	make branched a-ketoacids	*Pseudomonas putida*
	IlvE	branched-chain amino acid aminotransferase	NP_629657	2.6.1.42	express or Over-Express	make branched a-ketoacids	*Streptomyces coelicolor*
	ccr	crotonyl-CoA reductase	NP_630556	1.6.5.5,1.1.1.1	express or Over-Express	Converting crotonyl-CoA to butyryl-CoA	*Streptomyces coelicolor*
	ccr	crotonyl-CoA reductase	AAD53915	1.6.5.5,1.1.1.1	express or Over-Express	Converting crotonyl-CoA to butyryl-CoA	*Streptomyces cinnamonensis*
	IcmA, isobutyryl-CoA mutase	isobutyryl-CoA mutase, subunit A	NP_629554	5.4.99.2	express or Over-Express	converting butyryl-CoA to isobutyryl-CoA	*Streptomyces coelicolor*
	IcmA, isobutyryl-CoA mutase	isobutyryl-CoA mutase, subunit A	AAC08713	5.4.99.2	express or Over-Express	converting butyryl-CoA to isobutyryl-CoA	*Streptomyces cinnamonensis*
	IcmB, isobutyryl-CoA mutase	isobutyryl-CoA mutase, subunit B	NP_630904	5.4.99.2	express or Over-Express	converting butyryl-CoA to isobutyryl-CoA	*Streptomyces coelicolor*

FIG. 1 Cont.

	lcmB, isobutyryl-CoA mutase	isobutyryl-CoA mutase, subunit B	CAB59633	5.4.99.2	express or Over-Express	converting butyryl-CoA to isobutyryl-CoA	*Streptomyces cinnamonensis*
	FabH, ACPs and fabF genes with specificity for branched chain acyl-CoAs						
	IlvE	branched-chain amino acid aminotransferase	CAC12788	EC2.6.1.42	over express	branched chain amino acid amino transferase	Staphylococcus camosus
	FabH1	beta-ketoacyl-ACP synthase III	NP_626634	2.3.1.180	express or Over-Express	initiation of branched-chain fatty acid biosynthesis	Streptomyces coelicolor
	ACP	acyl-carrier protein	NP_626635	NONE	express or Over-Express	initiation and elongation of branched-chain fatty acid biosynthesis	*Streptomyces coelicolor*
	FabF	beta-ketoacyl-ACP synthase II	NP_626636	2.3.1.179	express or Over-Express	elongation of branched-chain fatty acid biosynthesis	*Streptomyces coelicolor*
	FabH3	beta-ketoacyl-ACP synthase III	NP_823466	2.3.1.180	express or Over-Express	initiation of branched-chain fatty acid biosynthesis	*Streptomyces avermitilis*

FIG. 1 Cont.

	FabC3 (ACP)	acyl-carrier protein	NP_823467	NONE	express or Over-Express	initiation and elongation of branched-chain fatty acid biosynthesis	*Streptomyces avermitilis*
	FabF	beta-ketoacyl-ACP synthase II	NP_823468	2.3.1.179	express or Over-Express	elongation of branched-chain fatty acid biosynthesis	*Streptomyces avermitilis*
	FabH_A	beta-ketoacyl-ACP synthase III	NP_389015	2.3.1.180	express or Over-Express	initiation of branched-chain fatty acid biosynthesis	*Bacillus subtillis*
	FabH_B	beta-ketoacyl-ACP synthase III	NP_388898	2.3.1.180	express or Over-Express	initiation of branched-chain fatty acid biosynthesis	*Bacillus subtillis*
	ACP	acyl-carrier protein	NP_389474	NONE	express or Over-Express	initiation and elongation of branched-chain fatty acid biosynthesis	*Bacillus subtillis*
	FabF	beta-ketoacyl-ACP synthase II	NP_389016	2.3.1.179	express or Over-Express	elongation of branched-chain fatty acid biosynthesis	*Bacillus subtillis*
	SmalDRAFT_0818	beta-ketoacyl-ACP synthase III	ZP_01643059	2.3.1.180	express or Over-Express	initiation of branched-chain fatty acid biosynthesis	*Stenotrophomonas maltophilia*

FIG. 1 Cont.

	SmalDRAFT_0821	acyl-carrier protein	ZP_01643063	NONE	express or Over-Express	initiation and elongation of branched-chain fatty acid biosynthesis	*Stenotrophomonas maltophilia*
	SmalDRAFT_0822	beta-ketoacyl-ACP synthase II	ZP_01643064	2.3.1.179	express or Over-Express	elongation of branched-chain fatty acid biosynthesis	*Stenotrophomonas maltophilia*
	FabH	beta-ketoacyl-ACP synthase III	YP_123672	2.3.1.180	express or Over-Express	initiation of branched-chain fatty acid biosynthesis	*Legionella pneumophila*
	ACP	acyl-carrier protein	YP_123675	NONE	express or Over-Express	initiation and elongation of branched-chain fatty acid biosynthesis	*Legionella pneumophila*
	FabF	beta-ketoacyl-ACP synthase II	YP_123676	2.3.1.179	express or Over-Express	elongation of branched-chain fatty acid biosynthesis	*Legionella pneumophila*
	FabH	beta-ketoacyl-ACP synthase III	NP_415609	2.3.1.180	delete or reduce	initiation of branched-chain fatty acid biosynthesis	*Escherichia coli*
	FabF	beta-ketoacyl-ACP synthase II	NP_415613	2.3.1.179	delete or reduce	elongation of branched-chain fatty acid biosynthesis	*Escherichia coli*

FIG. 1 Cont.

To Produce Cyclic Fatty Acids							
AnsJ	dehydratase (putative)	not available	not available	express or Over-Express	cyclohexylcarbonyl-CoA boiosynthesis	*Streptomyces collinus*
AnsK	CoA ligase (putative)	not available	not available	express or Over-Express	cyclohexylcarbonyl-CoA boiosynthesis	*Streptomyces collinus*
AnsL	dehydrogenase (putative)	not available	not available	express or Over-Express	cyclohexylcarbonyl-CoA boiosynthesis	*Streptomyces collinus*
ChcA	enoyl-CoA reductase	U72144	EC 1.3.1.34	express or Over-Express	cyclohexylcarbonyl-CoA boiosynthesis	*Streptomyces collinus*
AnsM	oxidorecutase (putative)	not available	not available	express or Over-Express	cyclohexylcarbonyl-CoA boiosynthesis	*Streptomyces collinus*
PlmJ	dehydratase (putative)	AAQ84158	not available	express or Over-Express	cyclohexylcarbonyl-CoA boiosynthesis	*Streptomyces sp. HK803*
PlmK	CoA ligase (putative)	AAQ84158	not available	express or Over-Express	cyclohexylcarbonyl-CoA boiosynthesis	*Streptomyces sp. HK803*
PlmL	dehydrogenase (putative)	AAQ84159	not available	express or Over-Express	cyclohexylcarbonyl-CoA boiosynthesis	*Streptomyces sp. HK803*
ChcA	enoyl-CoA reductase	AAQ84160	EC 1.3.1.34	express or Over-Express	cyclohexylcarbonyl-CoA boiosynthesis	*Streptomyces sp. HK803*
PlmM	oxidorecutase (putative)	AAQ84161	not available	express or Over-Express	cyclohexylcarbonyl-CoA	*Streptomyces sp. HK803*

FIG. 1 Cont.

						boiosynthesis	
	ChcB	enoyl-CoA isomerase	AF268489	not available	express or Over-Express	cyclohexylcarbonyl-CoA boiosynthesis	*Streptomyces collinus*
	ChcB/CaiD	enoyl-CoA isomerase	NP_629292	4.2.1.-	express or Over-Express	cyclohexylcarbonyl-CoA boiosynthesis	*Streptomyces coelicolor*
	ChcB/CaiD	enoyl-CoA isomerase	NP_824296	4.2.1.-	express or Over-Express	cyclohexylcarbonyl-CoA boiosynthesis	*Streptomyces avermitilis*
2C. Saturation Level Control							
	Sfa	Suppressor of FabA	AAN79592, AAC44390	NONE	Over-express	increase monounsaturated fatty acids	*E.coli*
	also *see* FabA in sec. 1				express	produce unsaturated fatty acids	
	GnsA	suppressors of the secG null mutation	ABD18647.1	NONE	Over-express	increase unsaturated fatty acid esters	*E.coli*
	GnsB	suppressors of the secG null mutation	AAC74076.1	NONE	Over-express	increase unsaturated fatty acid esters	*E.coli*

FIG. 1 Cont.

	also *see* section 2A - items with :0 are unsaturated (no double bonds) and with :1 are saturated (1 double bond)						
	fabB	3-oxoacyl-[acyl-carrier-protein] synthase I	BAA16180	EC:2.3.1.41	overexpress	modulate unsaturated fatty acid production	*Escherichia coli*
	fabK	trans-2-enoyl-ACP reductase II	AAF98273	1.3.1.9	express	modulate unsaturated fatty acid production	*Streptococcus pneumoniae*
	fabL	enoyl-(acyl carrier protein) reductase	AAU39821	1.3.1.9	express	modulate unsaturated fatty acid production	*Bacillus licheniformis DSM 13*
	fabM	trans-2, cis-3-decenoyl-ACP isomerase	DAA05501	4.2.1.17	Over-express	modulate unsaturated fatty acid production	*Streptococcus mutans*
Fatty Aldehyde Output							
	thioesterase	*see* chain length control section			express	produce	
Export							

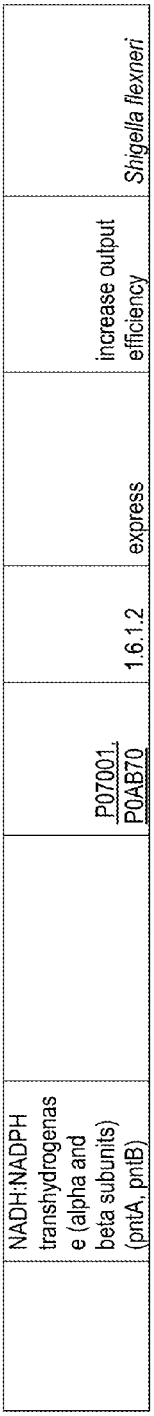
FIG. 1 Cont.

	Wax ester exporter (FATP family, Fatty Acid (long chain) Transport Protein)		NP_524723	NONE	express	export wax	*Drosophila melanogaster*
	ABC transport protein	putative alkane transporter	AAN73268	NONE	express	export products	*Rhodococcus erythropolis*
	CER5	wax transporter	At1g51500, AY734542, At3g21090, At1g51460	NONE	express	export products	*Arabidopsis thaliana*
	AtMRP5	Arabidopsis thaliana multidrug resistance-associated	NP_171908	NONE	express	export products	*Arabidopsis thaliana*
	AmiS2	ABC transporter AmiS2	JC5491	NONE	express	export products	*Rhodococcus sp.*
	AtPGP1	ARABIDOPSIS THALIANA P GLYCOPROTEIN1	NP_181228	NONE	express	export products	*Arabidopsis thaliana*
	AcrA	putative multidrug-efflux transport protein acrA	CAF23274	NONE	express	export products	*Candidatus Protochlamydia amoebophila UWE25*
	AcrB	probable multidrug-efflux transport protein, acrB	CAF23275	NONE	express	export products	*Candidatus Protochlamydia amoebophila UWE25*
	TolC	Outer membrane protein [Cell envelope	ABD59001	NONE	express	export products	*Francisella tularensis subsp.*

FIG. 1 Cont.

		biogenesis,					*novicida*
	AcrE	transmembrane protein affects septum formation and cell membrane permeability	YP_312213	NONE	express	export products	*Shigella sonnei Ss046*
	AcrF	Acriflavine resistance protein F	P24181	NONE	express	export products	*Escherichia coli*
	tll1618	multidrug efflux transporter	NP_682408.1	NONE	express	export products	*Thermosynechoc occus elongatus BP-1]*
	tll1619	multidrug efflux transporter	NP_682409.1	NONE	express	export products	*Thermosynechoc occus elongatus BP-1]*
	tll0139	multidrug efflux transporter	NP_680930.1	NONE	express	export products	*Thermosynechoc occus elongatus BP-1]*
5. Fermentation							
	replication checkpoint genes					increase output efficiency	
	umuD	DNA polymerase V, subunit	YP_310132	3.4.21.-	Over-express	increase output efficiency	*Shigella sonnei Ss046*
	umuC	DNA polymerase V, subunit	ABC42261	2.7.7.7	Over-express	increase output efficiency	*Escherichia coli*

FIG. 1 Cont.


NADH:NADPH transhydrogenase (alpha and beta subunits) (pntA, pntB)
P07001 P0AB70
1.6.1.2
express
increase output efficiency
Shigella flexneri

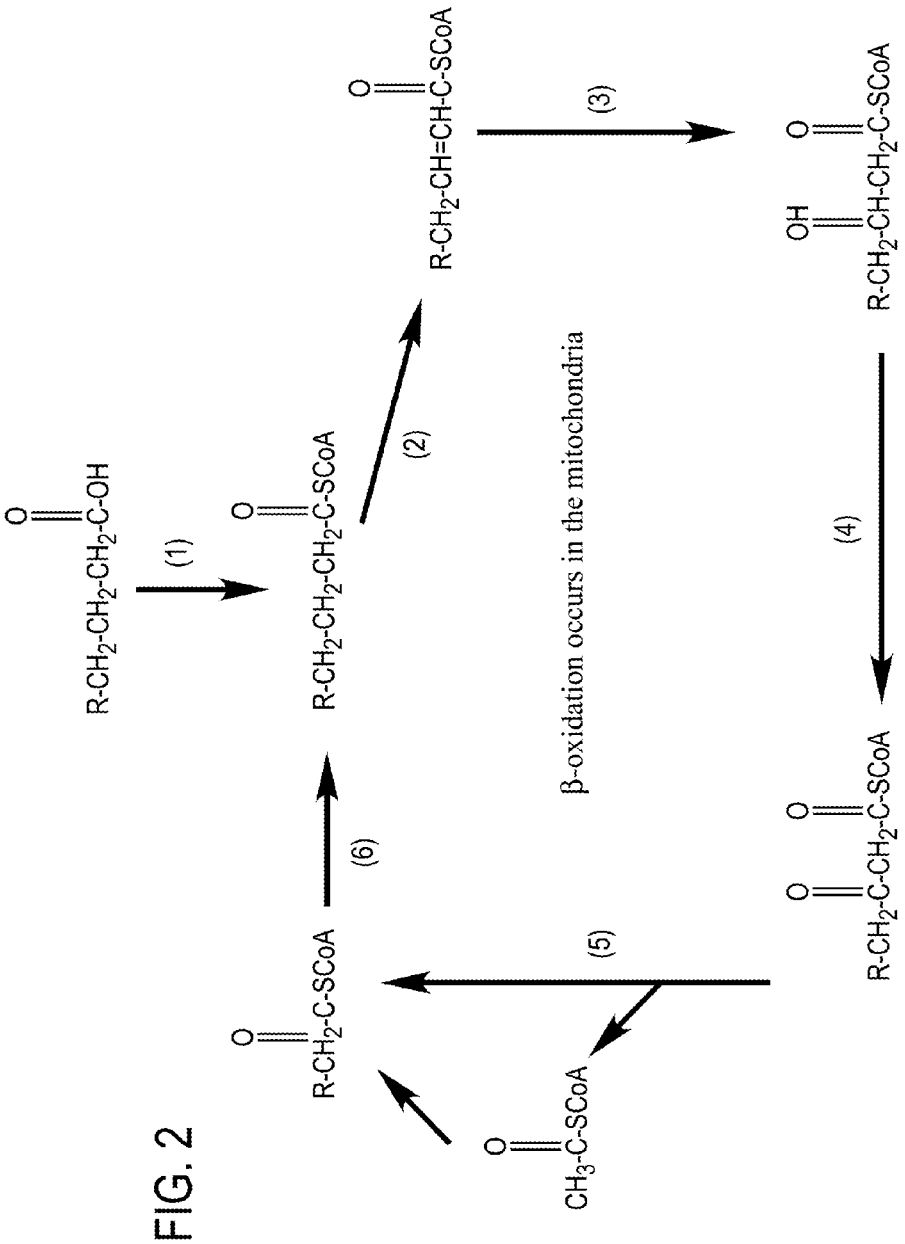

R-CH2-CH2-CH2-C-OH
(1)
R-CH2-CH2-CH2-C-SCoA
(2)
R-CH2-CH=CH-C-SCoA
(3)
OH
R-CH2-CH-CH2-C-SCoA
(4)
β-oxidation occurs in the mitochondria
R-CH2-C-CH2-C-SCoA
(5)
CH3-C-SCoA
(6)
R-CH2-C-SCoA

FIG. 2

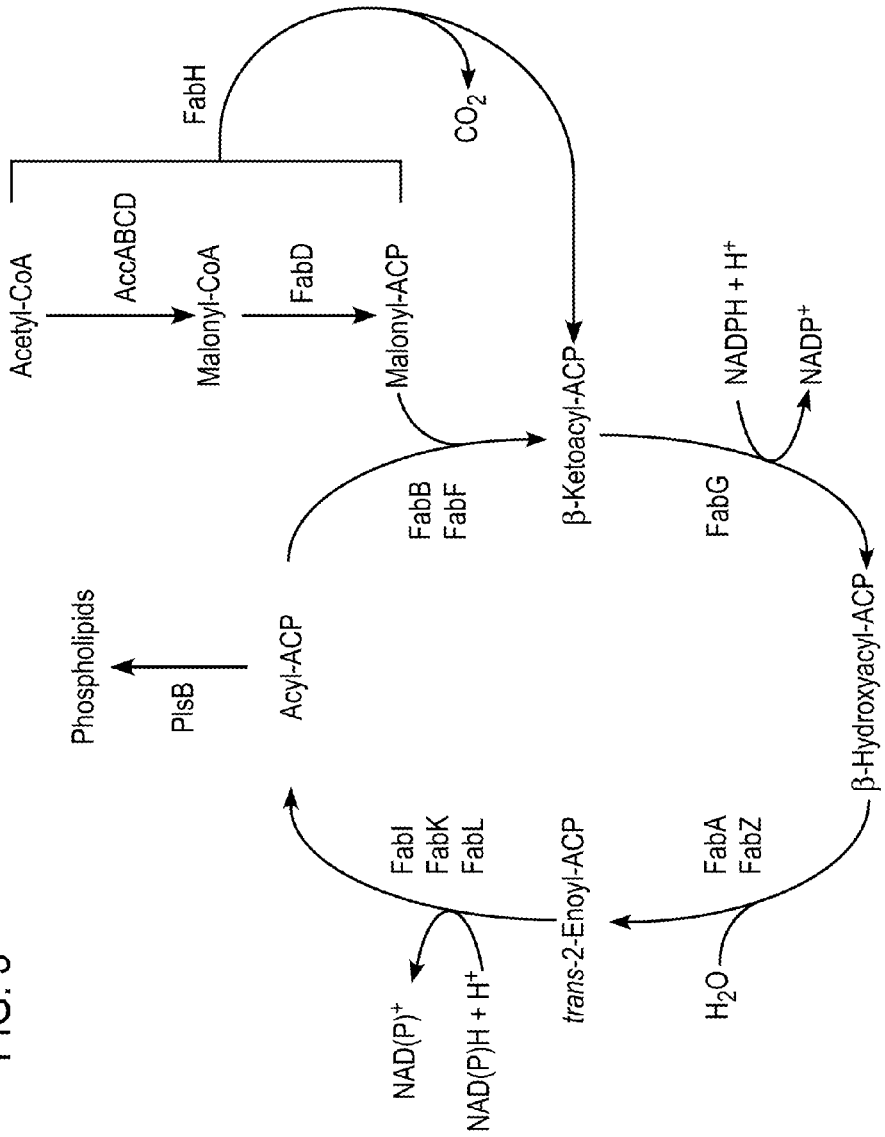
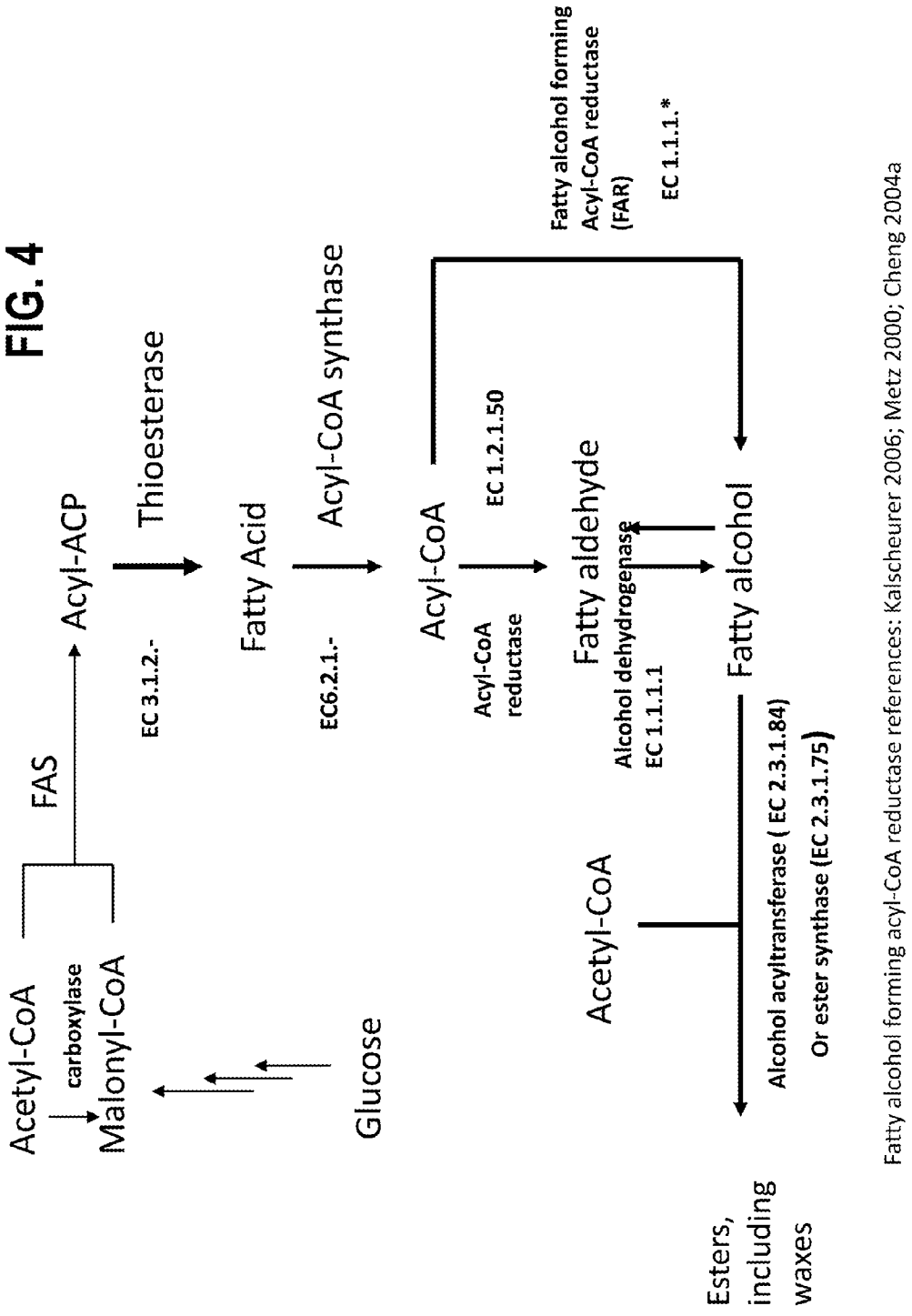

Acetyl-CoA
AccABCD
Malonyl-CoA
FabD
Malonyl-ACP
FabH
CO_2
FabB
FabF
β-Ketoacyl-ACP
FabG
NADPH + H^+
$NADP^+$
β-Hydroxyacyl-ACP
FabA
FabZ
trans-2-Enoyl-ACP
FabI
FabK
FabL
$NAD(P)^+$
$NAD(P)H + H^+$
H_2O
Acyl-ACP
PlsB
Phospholipids

FIG. 3

FIG. 4



Fatty alcohol forming acyl-CoA reductase references: Kalscheurer 2006; Metz 2000; Cheng 2004a

FIG. 5

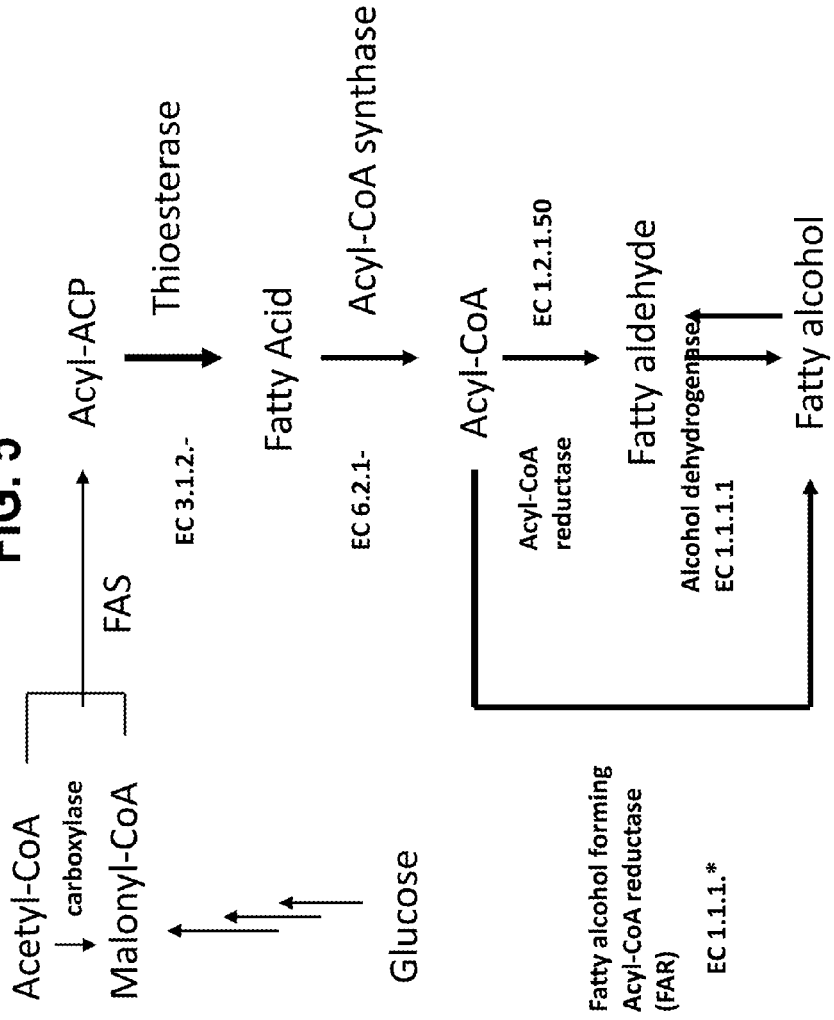

Acetyl-CoA
carboxylase
Malonyl-CoA
FAS
Acyl-ACP
EC 3.1.2.-
Thioesterase
Fatty Acid
EC 6.2.1-
Acyl-CoA synthase
Acyl-CoA
Acyl-CoA reductase
EC 1.2.1.50
Fatty aldehyde
Alcohol dehydrogenase
EC 1.1.1.1
Fatty alcohol
Glucose
Fatty alcohol forming Acyl-CoA reductase (FAR)
EC 1.1.1.*

FIG. 6

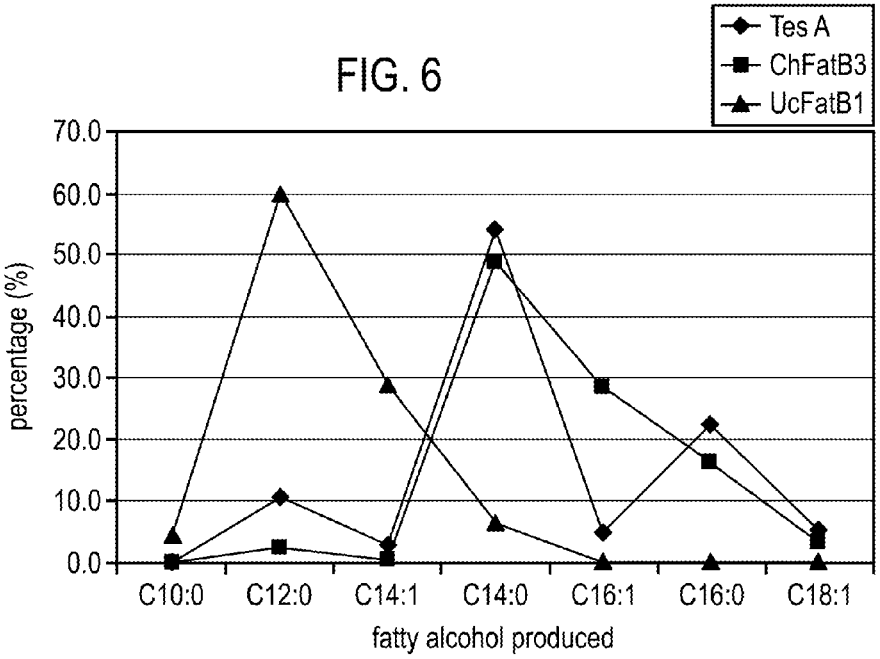

Tes A
ChFatB3
UcFatB1
70.0
60.0
50.0
40.0
30.0
20.0
10.0
0.0
percentage (%)
C10:0
C12:0
C14:1
C14:0
C16:1
C16:0
C18:1
fatty alcohol produced

FIG. 7

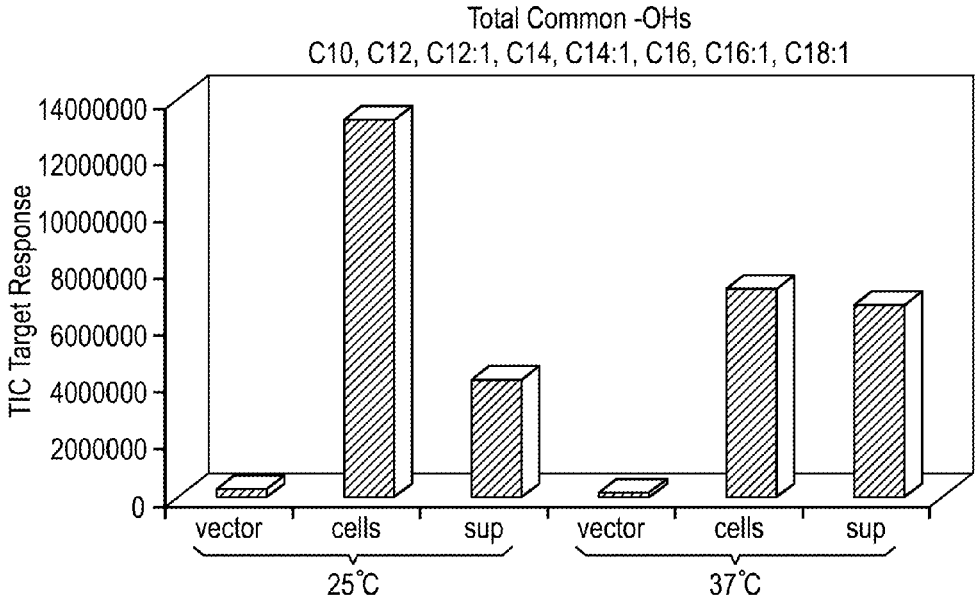

Total Common -OHs
C10, C12, C12:1, C14, C14:1, C16, C16:1, C18:1
14000000
12000000
10000000
8000000
6000000
4000000
2000000
0
TIC Target Response
vector
cells
sup
vector
cells
sup
25°C
37°C

FIG. 8A

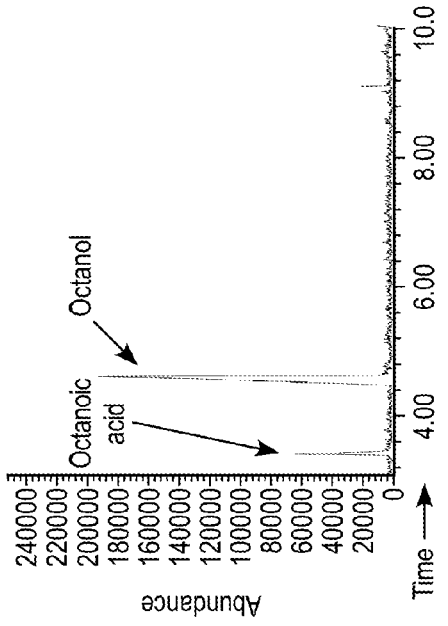


FIG. 8B

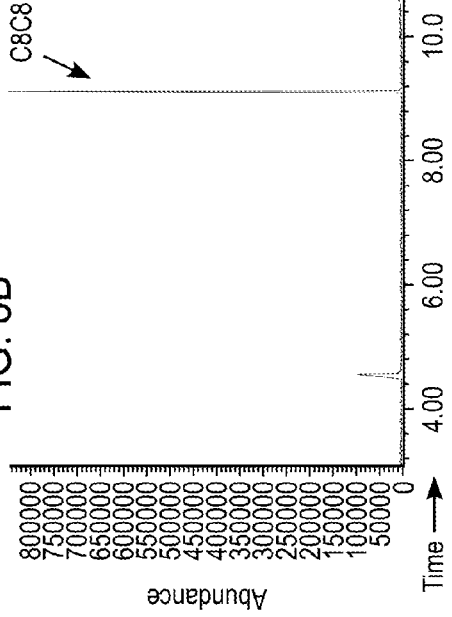


FIG. 8C

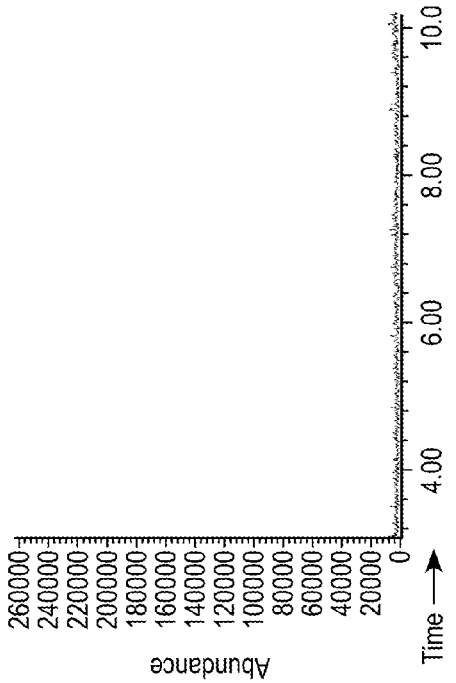
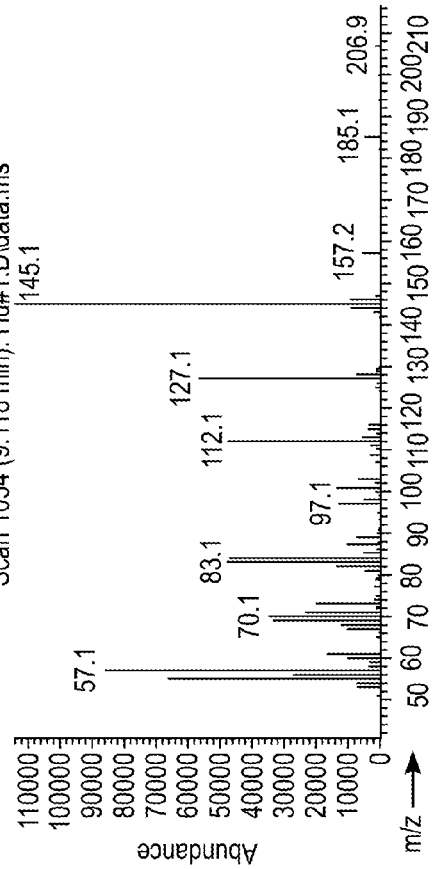


FIG. 8D



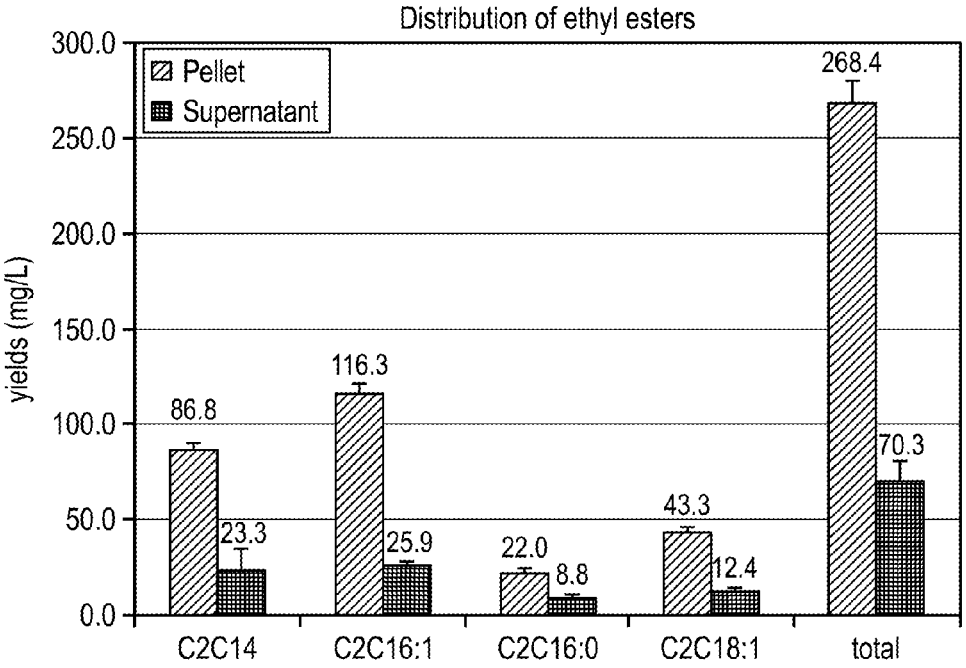
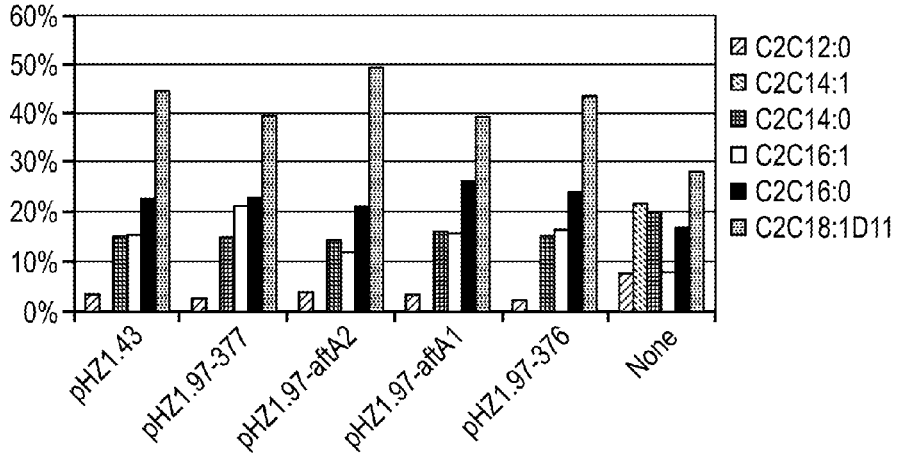

Distribution of ethyl esters
Pellet
Supernatant
yields (mg/L)
300.0
250.0
200.0
150.0
100.0
50.0
0.0
86.8
23.3
116.3
25.9
22.0
8.8
43.3
12.4
268.4
70.3
C2C14
C2C16:1
C2C16:0
C2C18:1
total

FIG. 9

FIG. 10


60%
50%
40%
30%
20%
10%
0%
C2C12:0
C2C14:1
C2C14:0
C2C16:1
C2C16:0
C2C18:1D11
pHZ1.43
pHZ1.97-377
pHZ1.97-aftA2
pHZ1.97-aftA1
pHZ1.97-376
None

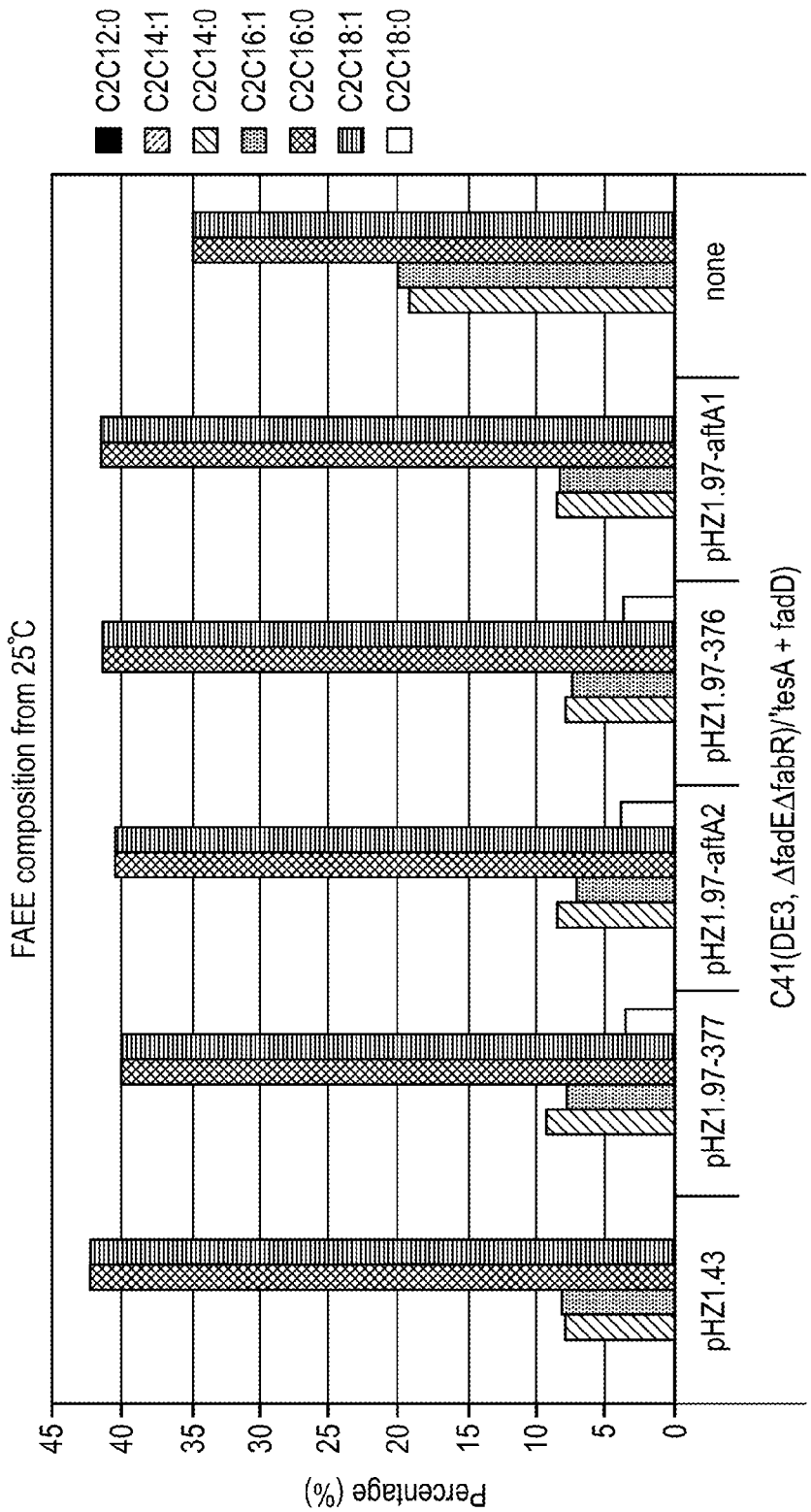

C2C12:0
C2C14:1
C2C14:0
C2C16:1
C2C16:0
C2C18:1
C2C18:0
FAEE composition from 25°C
Percentage (%)
45
40
35
30
25
20
15
10
5
0
pHZ1.43
pHZ1.97-377
pHZ1.97-aftA2
pHZ1.97-376
pHZ1.97-aftA1
none
C41(DE3, ΔfadEΔfabR)/'tesA + fadD)

FIG. 11

FIG. 12

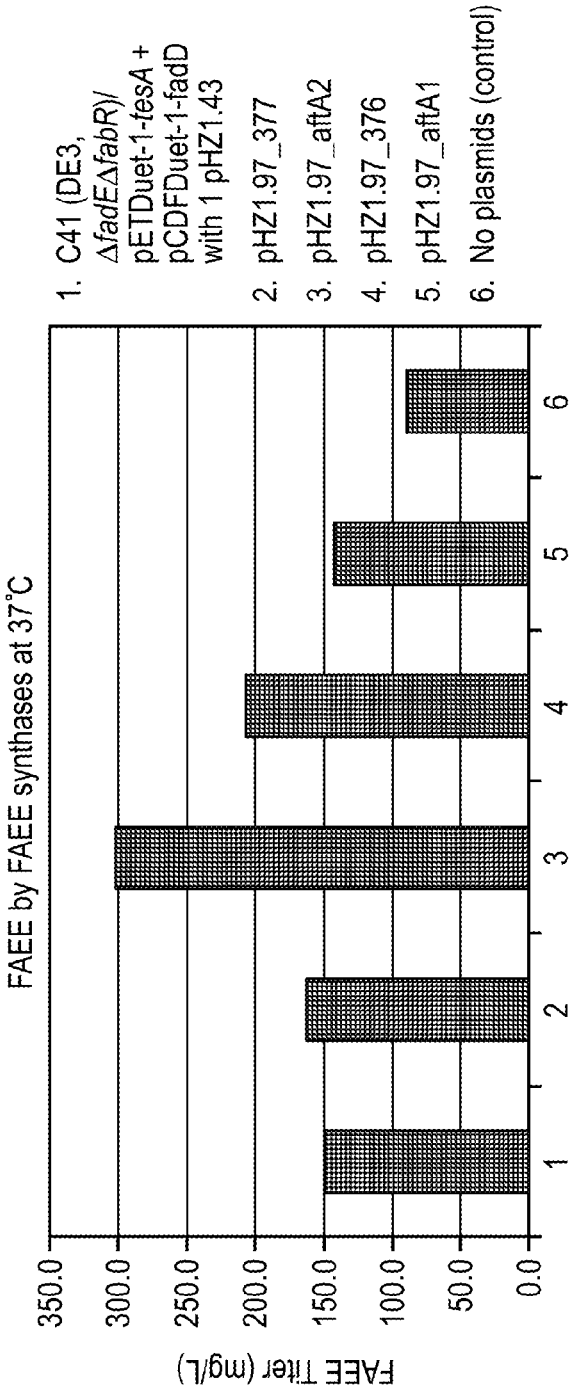
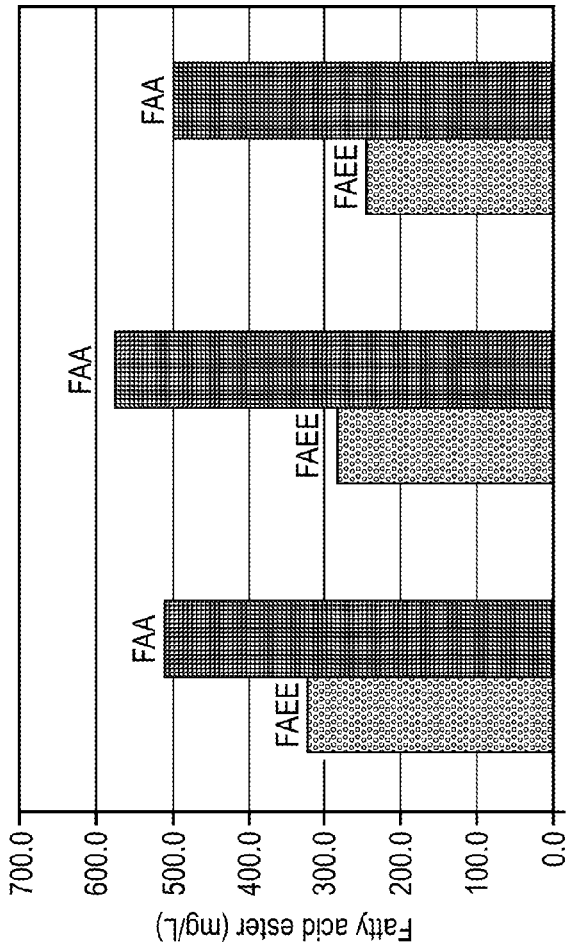
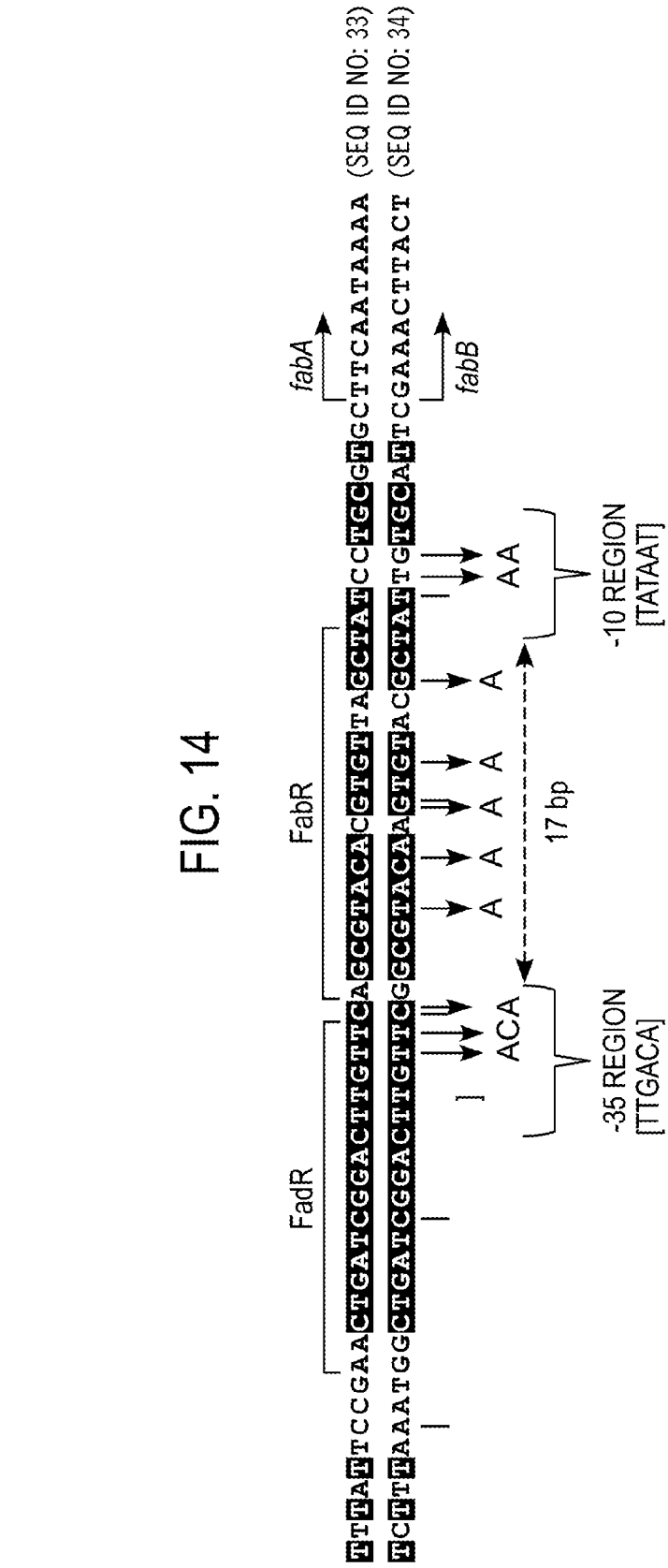

FAEE by FAEE synthases at 37°C
FAEE Titer (mg/L)
350.0
300.0
250.0
200.0
150.0
100.0
50.0
0.0
1
2
3
4
5
6
1. C41 (DE3, ΔfadEΔfabR)/ pETDuet-1-tesA + pCDFDuet-1-fadD with 1 pHZ1.43
2. pHZ1.97_377
3. pHZ1.97_aftA2
4. pHZ1.97_376
5. pHZ1.97_aftA1
6. No plasmids (control)

FIG. 13



Concentrations of free fatty acids (FFA) and fatty acid ethyl esters (FAEE) produced from three individual colonies of C41 (DE3, Δ*fadE*Δ*fabR*)/ pETDuet-1-*fesA* + pCDFDuet-1-fadD +pHZ1.97_atfA2 t

FIG. 14


fabA
fabB
FadR
FabR
TTTATTCCGAACTGATCGGACTTGTTCAGCGTACACGTGTTAGCTATCCTGCGTGCTTCAATAAAA (SEQ ID NO: 33)
TCTTTAAATGGCTGATCGGACTTGTTCGGCGTACAAGTGTACGCTATTGTGCATTCGAAACTTACT (SEQ ID NO: 34)
1
ACA
A A A A A
AA
17 bp
-35 REGION
[TTGACA]
-10 REGION
[TATAAT]

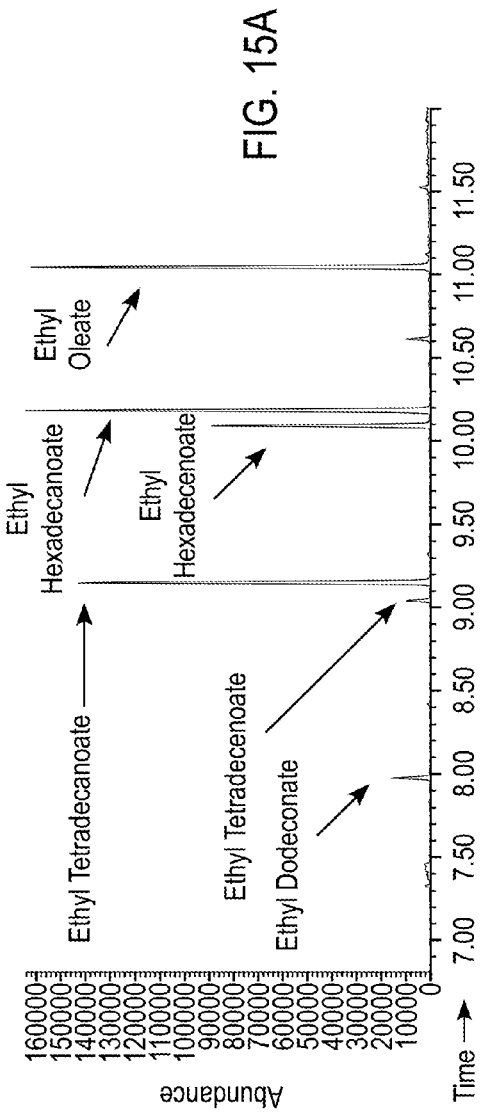


FIG. 15A

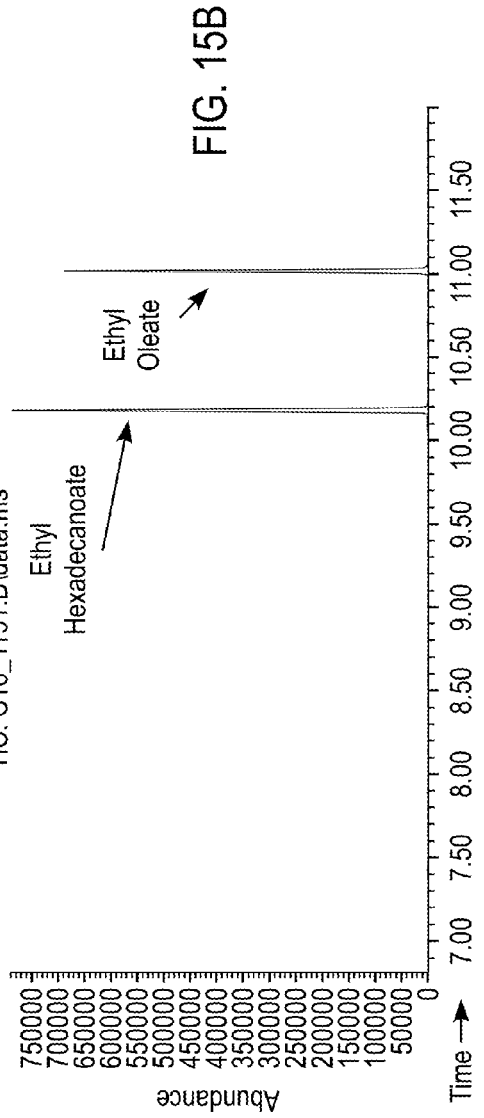


FIG. 15B

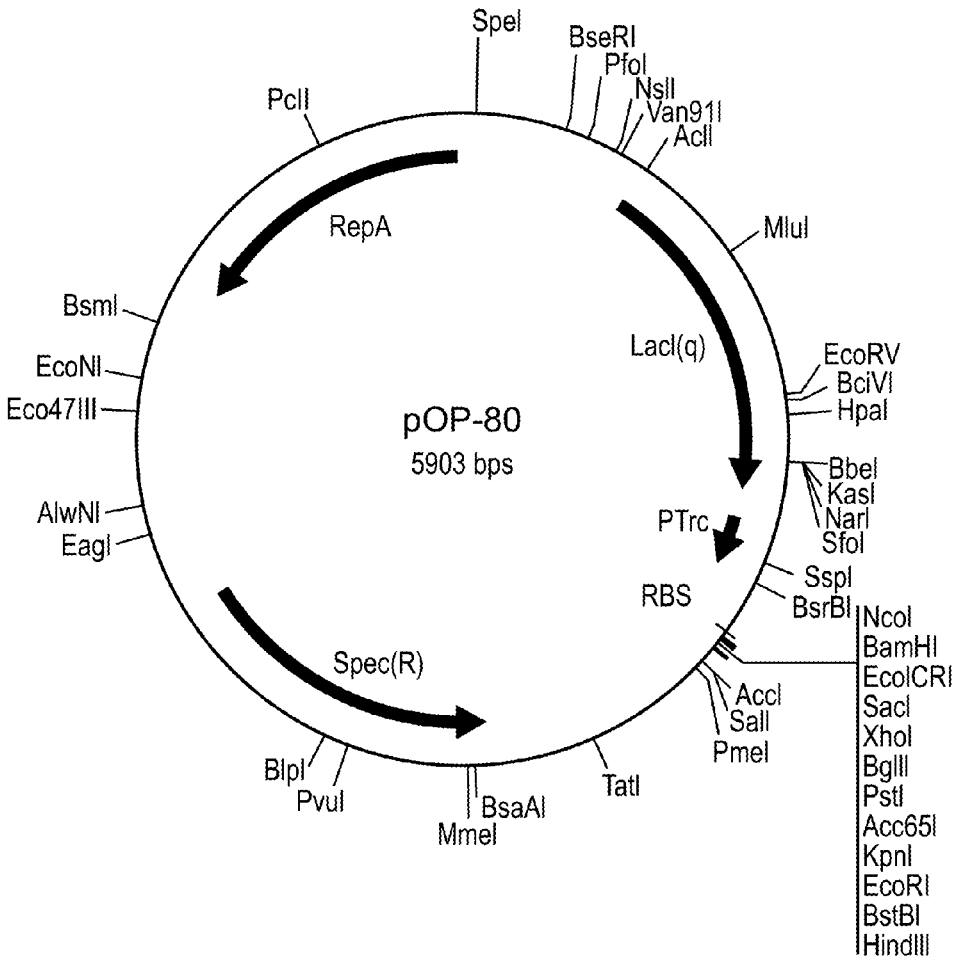

SpeI
BseRI
PfoI
NsiI
Van91I
AclI
PclI
MluI
RepA
BsmI
EcoNI
Eco47III
LacI(q)
EcoRV
BciVI
HpaI
pOP-80
5903 bps
BbeI
KasI
NarI
SfoI
AlwNI
EagI
PTrc
RBS
SspI
BsrBI
NcoI
BamHI
EcoICRI
SacI
XhoI
BglII
PstI
Acc65I
KpnI
EcoRI
BstBI
HindIII
Spec(R)
AccI
SalI
PmeI
BlpI
PvuI
BsaAI
MmeI
TatI

FIG. 16

FIG. 17

SEQ ID NO:1 - DNA SEQUENCE OF EXPRESSION VECTOR POP-80

CACTATACCA ATTGAGATGG GCTAGTCAAT GATAATTACT AGTCCTTTTC CTTTGAGTTG
TGGGTATCTG TAAATTCTGC TAGACCTTTG CTGGAAAACT TGTAAATTCT GCTAGACCCT
CTGTAAATTC CGCTAGACCT TTGTCTGTTT TTTTTGTTTA TATTCAAGTG GTTATAATTT
ATAGAATAAA GAAAGAATAA AAAAAGATAA AAAGAATAGA TCCCAGCCCT GTGTATAACT
CACTACTTTA GTCAGTTCCG CAGTATTACA AAAGGATGTC GCAAACGCTG TTTGCTCCTC
TACAAAACAG ACCTTAAAAC CCTAAAGGCG TCGGCATCCG CTTACAGACA AGCTGTGACC
GTCTCCGGGA GCTGCATGTG TCAGAGGTTT TCACCGTCAT CACCGAAACG CGCGAGGCAG
CAGATCAATT CGCGCGCGAA GGCGAAGCGG CATGCATTTA CGTTGACACC ATCGAATGGT
GCAAAACCTT TCGCGGTATG GCATGATAGC GCCCGGAAGA GAGTCAATTC AGGGTGGTGA
ATGTGAAACC AGTAACGTTA TACGATGTCG CAGAGTATGC CGGTGTCTCT TATCAGACCG
TTTCCCGCGT GGTGAACCAG GCCAGCCACG TTTCTGCGAA AACGCGGGAA AAAGTGGAAG
CGGCGATGGC GGAGCTGAAT TACATTCCCA ACCGCGTGGC ACAACAACTG GCGGGCAAAC
AGTCGTTGCT GATTGGCGTT GCCACCTCCA GTCTGGCCCT GCACGCGCCG TCGCAAATTG
TCGCGGCGAT TAAATCTCGC GCCGATCAAC TGGGTGCCAG CGTGGTGGTG TCGATGGTAG
AACGAAGCGG CGTCGAAGCC TGTAAAGCGG CGGTGCACAA TCTTCTCGCG CAACGCGTCA
GTGGGCTGAT CATTAACTAT CCGCTGGATG ACCAGGATGC CATTGCTGTG GAAGCTGCCT
GCACTAATGT TCCGGCGTTA TTTCTTGATG TCTCTGACCA GACACCCATC AACAGTATTA
TTTTCTCCCA TGAAGACGGT ACGCGACTGG GCGTGGAGCA TCTGGTCGCA TTGGGTCACC
AGCAAATCGC GCTGTTAGCG GGCCCATTAA GTTCTGTCTC GGCGCGTCTG CGTCTGGCTG
GCTGGCATAA ATATCTCACT CGCAATCAAA TTCAGCCGAT AGCGGAACGG GAAGGCGACT
GGAGTGCCAT GTCCGGTTTT CAACAAACCA TGCAAATGCT GAATGAGGGC ATCGTTCCCA
CTGCGATGCT GGTTGCCAAC GATCAGATGG CGCTGGGCGC AATGCGCGCC ATTACCGAGT
CCGGGCTGCG CGTTGGTGCG GATATCTCGG TAGTGGGATA CGACGATACC GAAGACAGCT
CATGTTATAT CCCGCCGTTA ACCACCATCA AACAGGATTT TCGCCTGCTG GGGCAAACCA
GCGTGGACCG CTTGCTGCAA CTCTCTCAGG GCCAGGCGGT GAAGGGCAAT CAGCTGTTGC

FIG. 17 Cont.

CCGTCTCACT GGTGAAAAGA AAAACCACCC TGGCCCCCAA TACGCAAACC GCCTCTCCCC
GCGCGTTGGC CGATTCATTA ATGCAGCTGG CACGACAGGT TTCCCGACTG GAAAGCGGGC
AGTGAGCGCA ACGCAATTAA TGTAAGTTAG CGCGAATTGA TCTGGTTTGA CAGCTTATCA
TCGACTGCAC GGTGCACCAA TGCTTCTGGC GTCAGGCAGC CATCGGAAGC TGTGGTATGG
CTGTGCAGGT CGTAAATCAC TGCATAATTC GTGTCGCTCA AGGCGCACTC CCGTTCTGGA
TAATGTTTTT TGCGCCGACA TCATAACGGT TCTGGCAAAT ATTCTGAAAT GAGCTGTTGA
CAATTAATCA TCCGGCTCGT ATAATGTGTG GAATTGTGAG CGGATAACAA TTTCACACAG
GAAACAGCGC CGCTGAGAAA AAGCGAAGCG GCACTGCTCT TTAACAATTT ATCAGACAAT
CTGTGTGGGC ACTCGACCGG AATTATCGAT TAACTTTATT ATTAAAAATT AAAGAGGTAT
ATATTAATGT ATCGATTAAA TAAGGAGGAA TAAACCATGG ATCCGAGCTC GAGATCTGCA
GCTGGTACCA TATGGGAATT CGAAGCTTGG GCCCGAACAA AAACTCATCT CAGAAGAGGA
TCTGAATAGC GCCGTCGACC ATCATCATCA TCATCATTGA GTTTAAACGG TCTCCAGCTT
GGCTGTTTTG GCGGATGAGA GAAGATTTTC AGCCTGATAC AGATTAAATC AGAACGCAGA
AGCGGTCTGA TAAAACAGAA TTTGCCTGGC GGCAGTAGCG CGGTGGTCCC ACCTGACCCC
ATGCCGAACT CAGAAGTGAA ACGCCGTAGC GCCGATGGTA GTGTGGGGTC TCCCCATGCG
AGAGTAGGGA ACTGCCAGGC ATCAAATAAA ACGAAAGGCT CAGTCGAAAG ACTGGGCCTT
TCGTTTTATC TGTTGTTTGT CGGTGAACGC TCTCCTGACG CCTGATGCGG TATTTTCTCC
TTACGCATCT GTGCGGTATT TCACACCGCA TATGGTGCAC TCTCAGTACA ATCTGCTCTG
ATGCCGCATA GTTAAGCCAG CCCCGACACC CGCCAACACC CGCTGACGAG CTTAGTAAAG
CCCTCGCTAG ATTTTAATGC GGATGTTGCG ATTACTTCGC CAACTATTGC GATAACAAGA
AAAAGCCAGC CTTTCATGAT ATATCTCCCA ATTTGTGTAG GGCTTATTAT GCACGCTTAA
AAATAATAAA AGCAGACTTG ACCTGATAGT TTGGCTGTGA GCAATTATGT GCTTAGTGCA
TCTAACGCTT GAGTTAAGCC GCGCCGCGAA GCGGCGTCGG CTTGAACGAA TTGTTAGACA
TTATTTGCCG ACTACCTTGG TGATCTCGCC TTTCACGTAG TGGACAAAAT CTTCCAACTG
ATCTGCGCGC GAGGCCAAGC GATCTTCTTC TTGTCCAAGA TAAGCCTGTC TAGCTTCAAG
TATGACGGGC TGATACTGGG CCGGCAGGCG CTCCATTGCC CAGTCGGCAG CGACATCCTT
CGGCGCGATT TTGCCCGGTTA CTGCGCTGTA CCAAAATGCGG GACAACGTAA GCACTACATT

FIG. 17 Cont.

TCGCTCATCG CCAGCCCAGT CGGGCGGCGA GTTCCATAGC GTTAAGGTTT CATTTAGCGC
CTCAAATAGA TCCTGTTCAG GAACCGGATC AAAGAGTTCC TCCGCCGCTG GACCTACCAA
GGCAACGCTA TGTTCTCTTG CTTTTGTCAG CAAGATAGCC AGATCAATGT CGATCGTGGC
TGGCTCGAAG ATACCTGCAA GAATGTCATT GCGCTGCCAT TCTCCAAATT GCAGTTCGCG
CTTAGCTGGA TAACGCCACG GAATGATGTC GTCGTGCACA ACAATGGTGA CTTCTACAGC
GCGGAGAATC TCGCTCTCTC CAGGGGAAGC CGAAGTTTCC AAAAGGTCGT TGATCAAAGC
TCGCCGCGTT GTTTCATCAA GCCTTACGGT CACCGTAACC AGCAAATCAA TATCACTGTG
TGGCTTCAGG CCGCCATCCA CTGCGGAGCC GTACAAATGT ACGGCCAGCA ACGTCGGTTC
GAGATGGCGC TCGATGACGC CAACTACCTC TGATAGTTGA GTCGATACTT CGGCGATCAC
CGCTTCCCTC ATGATGTTTA ACTTTGTTTT AGGGCGACTG CCCTGCTGCG TAACATCGTT
GCTGCTCCAT AACATCAAAC ATCGACCCAC GGCGTAACGC GCTTGCTGCT TGGATGCCCG
AGGCATAGAC TGTACCCCAA AAAAACAGTC ATAACAAGCC ATGAAAACCG CCACTGCGCC
GTTACCACCG CTGCGTTCGG TCAAGGTTCT GGACCAGTTG CGTGAGCGCA TACGCTACTT
GCATTACAGC TTACGAACCG AACAGGCTTA TGTCCACTGG GTTCGTGCCT TCATCCGTTT
CCACGGTGTG CGTCACCCGG CAACCTTGGG CAGCAGCGAA GTCGAGGCAT TTCTGTCCTG
GCTGGCGAAC GAGCGCAAGG TTTCGGTCTC CACGCATCGT CAGGCATTGG CGGCCTTGCT
GTTCTTCTAC GGCAAGGTGC TGTGCACGGA TCTGCCCTGG CTTCAGGAGA TCGGAAGACC
TCGGCCGTCG CGGCGCTTGC CGGTGGTGCT GACCCCGGAT GAAGTGGTTC GCATCCTCGG
TTTTCTGGAA GGCGAGCATC GTTTGTTCGC CCAGCTTCTG TATGGAACGG GCATGCGGAT
CAGTGAGGGT TTGCAACTGC GGGTCAAGGA TCTGGATTTC GATCACGGCA CGATCATCGT
GCGGGAGGGC AAGGGCTCCA AGGATCGGGC CTTGATGTTA CCCGAGAGCT TGGCACCCAG
CCTGCGCGAG CAGGGGAATT AATTCCCACG GGTTTTGCTG CCCGCAAACG GGCTGTTCTG
GTGTTGCTAG TTTGTTATCA GAATCGCAGA TCCGGCTTCA GCCGGTTTGC CGGCTGAAAG

FIG. 17 Cont.

CGCTATTTCT TCCAGAATTG CCATGATTTT TTCCCCACGG GAGGCGTCAC TGGCTCCCGT
GTTGTCGGCA GCTTTGATTC GATAAGCAGC ATCGCCTGTT TCAGGCTGTC TATGTGTGAC
TGTTGAGCTG TAACAAGTTG TCTCAGGTGT TCAATTTCAT GTTCTAGTTG CTTTGTTTTA
CTGGTTTCAC CTGTTCTATT AGGTGTTACA TGCTGTTCAT CTGTTACATT GTCGATCTGT
TCATGGTGAA CAGCTTTGAA TGCACCAAAA ACTCGTAAAA GCTCTGATGT ATCTATCTTT
TTTACACCGT TTTCATCTGT GCATATGGAC AGTTTTCCCT TTGATATGTA ACGGTGAACA
GTTGTTCTAC TTTTGTTTGT TAGTCTTGAT GCTTCACTGA TAGATACAAG AGCCATAAGA
ACCTCAGATC CTTCCGTATT TAGCCAGTAT GTTCTCTAGT GTGGTTCGTT GTTTTTGCGT
GAGCCATGAG AACGAACCAT TGAGATCATA CTTACTTTGC ATGTCACTCA AAAATTTTGC
CTCAAAACTG GTGAGCTGAA TTTTTGCAGT TAAAGCATCG TGTAGTGTTT TTCTTAGTCC
GTTATGTAGG TAGGAATCTG ATGTAATGGT TGTTGGTATT TTGTCACCAT TCATTTTTAT
CTGGTTGTTC TCAAGTTCGG TTACGAGATC CATTTGTCTA TCTAGTTCAA CTTGGAAAAT
CAACGTATCA GTCGGGCGGC CTCGCTTATC AACCACCAAT TTCATATTGC TGTAAGTGTT
TAAATCTTTA CTTATTGGTT TCAAAACCCA TTGGTTAAGC CTTTTAAACT CATGGTAGTT
ATTTTCAAGC ATTAACATGA ACTTAAATTC ATCAAGGCTA ATCTCTATAT TTGCCTTGTG
AGTTTTCTTT TGTGTTAGTT CTTTTAATAA CCACTCATAA ATCCTCATAG AGTATTTGTT
TTCAAAAGAC TTAACATGTT CCAGATTATA TTTTATGAAT TTTTTTAACT GGAAAAGATA
AGGCAATATC TCTTCACTAA AAACTAATTC TAATTTTTCG CTTGAGAACT TGGCATAGTT
TGTCCACTGG AAAATCTCAA AGCCTTTAAC CAAAGGATTC CTGATTTCCA CAGTTCTCGT
CATCAGCTCT CTGGTTGCTT TAGCTAATAC ACCATAAGCA TTTTCCCTAC TGATGTTCAT
CATCTGAGCG TATTGGTTAT AAGTGAACGA TACCGTCCGT TCTTTCCTTG TAGGGTTTTC
AATCGTGGGG TTGAGTAGTG CCACACAGCA TAAAATTAGC TTGGTTTCAT GCTCCGTTAA
GTCATAGCGA CTAATCGCTA GTTCATTTGC TTTGAAAACA ACTAATTCAG ACATACATCT
CAATTGGTCT AGGTGATTTT AAT

FIG. 18

SEQ ID NO:2- DNA sequence of *E.coli* codon-optimized gene *fadD35* from *Mycobacterium tuberculosis* HR7Rv

CC**ATG**GCAGC AGCGGAAGTG GTTGATCCAA ATCGTCTGAG CTATGATCGT GGCCCGAGCG CGCCGAGCCT
GTTGGAGAGC ACCATCGGTG CAAACCTGGC CGCTACGGCG GCCCGTTACG GCCACCGCGA GGCCCTGGTG
GACATGGTCG CACGCCGTCG CTTCAATTAT AGCGAGCTGC TGACGGATGT TCACCGTTTG GCTACGGGCC
TGGTGCGTGC TGGTATTGGC CCAGGCGACC GTGTGGGTAT TTGGGCGCCG AATCGTTGGG AGTGGGTTCT
GGTCCAGTAT GCAACGGCGG AGATTGGTGC GATCCTGGTT ACGATTAACC CGGCTTATCG CGTGCGTGAG
GTTGAATACG CGCTGCGTCA ATCTGGCGTC GCGATGGTCA TTGCGGTTGC GTCCTTCAAG GACGCTGATT
ACGCTGCGAT GCTGGCGGAG GTTGGTCCGC GTTGCCCGGA CCTGGCTGAC GTGATCCTGT TGGAAAGCGA
CCGTTGGGAC GCACTGGCAG GTGCCGAGCC GGATCTGCCG GCGCTGCAGC AGACCGCTGC CCGCCTGGAT
GGTTCCGATC CGGTTAACAT TCAATACACC AGCGGTACGA CCGCGTACCC GAAAGGTGTT ACGCTGAGCC
ACCGCAATAT CCTGAATAAC GGTTATTTGG TTGGTGAGCT GTTGGGTTAT ACGGCGCAGG ATCGTATTTG
CATCCCGGTG CCGTTCTACC ACTGCTTTGG TATGGTCATG GGCAACTTGG CGGCGACCTC CCACGGTGCG
GCGATGGTTA TTCCGGCGCC AGGTTTCGAC CCAGCGGCTA CGCTGCGCGC GGTGCAAGAT GAACGCTGTA
CGTCTCTGTA CGGCGTTCCG ACCATGTTTA TTGCAGAACT GGGTCTGCCG GATTTCACCG ATTACGAGCT
GGGTTCTTTG CGTACCGGCA TCATGGCAGG CGCAGCGTGT CCGGTTGAAG TCATGCGTAA AGTGATCAGC
CGTATGCACA TGCCGGGTGT CAGCATTTGC TACGGTATGA CCGAGACGAG CCCGGTGAGC ACCCAAACCC
GTGCGGACGA TAGCGTGGAC CGTCGTGTGG GCACCGTTGG CCGCGTCGGC CCGCACCTGG AAATTAAAGT
TGTTGACCCA GCGACCGGCG AAACCGTTCC GCGCGGTGTT GTTGGCGAAT TTTGCACGCG TGGCTACTCT
GTCATGGCGG GTTATTGGAA TGACCCGCAG AAAACGGCAG AGGTGATCGA CGCTGATGGT TGGATGCATA
CCGGTGACCT GGCGGAAATG GACCCGAGCG GTTACGTTCG TATTGCAGGC CGCATTAAAG ACCTGGTGGT
TCGTGGCGGT GAGAACATTA GCCCGCGTGA AATTGAGGAG CTGCTGCATA CCCATCCGGA CATCGTTGAT
GGTCACGTGA TCGGTGTTCC GGATGCGAAA TATGGCGAAG AGCTGATGGC AGTTGTGAAG CTGCGTAATG
ATGCGCCGGA GTTGACGATT GAACGCCTGC GTGAGTATTG CATGGGTCGC ATCGCACGCT TTAAAATCCC
GCGCTACTTG TGGATCGTTG ACGAGTTCCC GATGACCGTG ACCGGCAAGG TCCGTAAGGT CGAGATGCGT
CAGCAGGCAT TGGAATATCT GCGTGGTCAA CAG**TAA**GAAT TC

FIG. 19

SEQ ID NO:3-DNA sequence of *E.coli* codon-optimized gene *fadD1* from *Pseudomonas aeruginosa* PAO1

TC**ATG**ATCGA GAATTTTTGG AAGGACAAGT ATCCGGCAGG TATTGCAGCA GAAATTAATC CGGATCAGTA
TCCGAATATT CTGAGCGTCC TGAAGGAGAG CTGCCAACGT TTTGCGACCA AGCCGGCGTT TACGAACTTG
GGTAAGACCT TGACCTATGG TGAGCTGTAC AAACTGTCTG GCGACTTCGC AGCGTACCTG CAACAACATA
CCGATCTGAA ACCGGGTGAT CGTATTGCCG TTCAGCTGCC GAACGTTCTG CAGTACCCGA TCGTTGTCTT
CGGCGCAATG CGTGCGGGTC TGATCGTGGT GAACACGAAC CCGTTGTATA CGGCGCGTGA GTTGGAACAC
CAGTTTAATG ATAGCGGCGC AAAAGCGGTG GTTTGTTTGG CTAATATGGC CCACCTGGTT GAAGGTGTTT
TGCCGAAGAC CGGTGTTAAA CAGGTGATTG TCACCGAGGT GGGCGACATT CTGCCACCGC TGAAGCGTTT
CATTGTCAAT TTCGTCGTCA AACACATTAA GAAGATGGTC CCGGCCTATT CCCTGCCGCA GGCCACGAAG
TTGACCGATG CACTGGCCCG TGGTGCAGGC AAGAGCTTCC AAGAAGCGGC ACCGCAGGCA GACGACGTCG
CGGTGCTGCA GTACACCGGC GGTACCACGG GCGTCGCCAA GGGTGCGATG CTGACCCATC GTAACCTGGT
CGCTAACATG TTGCAGTGTA AAGCGCTGAT GGGTGCGAAC CTGAACGAGG GTTGCGAAAT CTTGATTGCC
CCGTTGCCGC TGTATCACAT TTATGCGTTT ACCTTCCACT GTATGGCTAT GATGCTGACG GGTAATCATA
ACATTCTGAT CACCAATCCG CGCGACCTGC CGAGCATGCT GAAGGACCTG GGTCAGTGGA AGTTCACGGG
TTTCGTGGGT CTGAATACGC TGTTCGTCGC GCTGTGCAAT AATGAGACCT TCCGTAAGCT GGACTTTAGC
GCACTGAAGC TGACCCTGAG CGGCGGCATG GCGCTGCAGC TGGCCACGGC GGAACGTTGG AAAGAGGTCA
CGGGCTGCGC TATTTGCGAG GGTTATGGTA TGACCGAAAC GGCCCCGGTG GTTTCCGTCA ACCCGTTTCA
GAACATTCAA GTTGGCACCA TCGGTATTCC GGTGCCAAGC ACCTTGTGTA AGGTTATTGG CGATGACGGT
CAAGAAGTTC CGCTGGGCGA GCGCGGTGAG TTGTGCGTCA AGGGTCCGCA GGTTATGAAG GGCTACTGGC
AGCGCCAGGA GGCAACGGAC GAGATTCTGG ACGCTGATGG TTGGTTGAAA ACCGGCGATA TTGCAATTAT
TCAAGAAGAC GGCTATATGC GCATTGTCGA TCGTAAGAAA GACATGATTT TGGTTAGCGG TTTCAACGTT
TACCCGAATG AATTGGAAGA TGTTTTGGCG ACCTTGCCGG GTGTGCTGCA ATGCGCAGCG ATCGGTATCC
CGGATGAAAA GAGCGGCGAG TCTATCAAGG TTTTCGTTGT TGTGAAGCCG GGTGCGACCC TGACCAAAGA
GCAGGTCATG CAGCATATGC ACGATAACCT GACCGGCTAC AAACGCCCGA AAGCAGTGGA GTTCCGTGAT
AGCCTGCCAA CGACCAATGT TGGCAAGATT TTGCGTCGTG AGCTGCGCGA TGAAGAGCTG AAAAAGGCAG
GCCAGAAG**TA A**GAATTC

FIG. 20

SEQ ID NO:4-the BsyhfLBspHIF primer based on the DNA sequence deposited at NCBI with the accession code NC_000964.

CATCATGAATCTTGTTTC

FIG. 21

SEQ ID NO:5-the BsyhfLEcoR primer based on the DNA sequence deposited at NCBI with the accession code NC_000964.

CGGAATTCTTATTGGGGCAAAATATC

FIG. 22

SEQ ID NO:6-DNA sequence of the *Bacillus subtilis yhfL* gene.

TC**ATG**AATCT TGTTTCAAAA TTGGAAGAAA CAGCATCTGA GAAGCCCGAC AGCATCGCAT GCAGGTTTAA
AGATCACATG ATGACGTATC AAGAGCTGAA TGAATATATT CAGCGATTTG CGGACGGCCT TCAGGAAGCC
GGTATGGAGA AAGGGGACCA TTTAGCTTTG CTGCTTGGCA ATTCGCCTGA TTTTATCATC GCGTTTTTTG
GCGCTTTAAA AGCTGGGATC GTAGTTGTTC CCATCAATCC GTTGTACACG CCGACAGAAA TTGGTTATAT
GCTGACAAAT GGCGATGTAA AGGCAATCGT GGGCGTTAGC CAGCTTTTGC CGCTTTATGA GAGCATGCAT
GAATCGCTGC CAAAGGTTGA GCTCGTCATT TTATGCCAGA CGGGGGAGGC CGAGCCGGAA GCTGCGGACC
CAGAGGTCAG GATGAAAATG ACAACGTTTG CAAAAATATT GCGGCCGACA TCTGCCGCTA AACAAAACCA
AGAACCTGTA CCTGATGATA CCGCGGTTAT TTTATATACG TCAGGAACGA CTGGAAAACC GAAAGGCGCG
ATGCTGACAC ATCAGAATTT GTACAGCAAT GCCAACGATG TCGCAGGCTA TTTGGGAATG GATGAGAGGG
ACAATGTGGT CTGCGCTCTT CCCATGTGTC ACGTGTTTTG TTTAACCGTC TGTATGAATG CACCGCTGAT
GAGCGGCGCA ACTGTATTGA TTGAGCCTCA ATTCAGTCCG GCATCTGTTT TTAAGCTTGT TAAGCAGCAG
CAGGCGACCA TTTTTGCCGG TGTGCCTACA ATGTATAACT ACTTGTTTCA GCATGAAAAC GGAAAGAAAG
ATGATTTTTC TTCGATCCGG CTGTGCATTT CGGGAGGCGC GTCCATGCCA GTCGCGTTGC TGACGGCGTT
TGAAGAAAAA TTCGGTGTTA CCATTTTGGA AGGCTACGGG CTCTCGGAAG CATCACCCGT CACGTGCTTT
AACCCGTTTG ACAGGGGCAG AAAGCCGGGC TCCATCGGGA CAAGTATCTT ACATGTCGAA AACAAGGTCG
TAGATCCGCT CGGACGCGAG CTGCCCGCTC ACCAGGTCGG CGAATTGATC GTGAAAGGCC CCAATGTGAT
GAAGGGCTAT TATAAAATGC CGATGGAAAC AGAGCATGCA TTAAAAGACG GGTGGCTTTA TACGGGGGAC
TTGGCAAGAC GGGATGAGGA CGGCTATTTT TACATTGTTG ACCGGAAAAA AGACATGATC ATTGTAGGAG
GATACAATGT GTATCCGCGG GAGGTGGAGG AGGTGCTGTA CAGCCATCCG GACGTCAAGG AGGCGGTTGT
CATCGGCGTG CCGGACCCCC AAAGCGGGGA AGCGGTAAAG GGATATGTGG TGCCGAAACG CTCTGGGGTA
ACAGAGGAGG ACATCATGCA GCACTGCGAA AAGCATCTGG CAAAATACAA GCGGCCTGCC GCCATTACGT
TTCTTGACGA TATTCCGAAA AATGCGACGG GGAAAATGCT CAGACGGGCA CTGAGAGATA TTTTGCCCCA
A**TAA**GAATTC

FIG. 23

SEQ ID NO:7-the Scfaa3pPciF primer designed based on the DNA sequence deposited at NCBI with the accession code NC_001141.

CGACATGTCCGAACAACAC

FIG. 24

SEQ ID NO:8 – the Scfaa3pPCII primer designed based on the DNA sequence deposited at NCBI with the accession code NC_001141.

GCAAGCTTCTAAGAATTTTCTTTG

FIG. 25

SEQ ID NO:9 - DNA sequence of the *faa3p* structural gene from *Saccharomyces cerevisiae.*

TC**ATG**AGTCT GGATCGTCCC TGGCTGCAGA GCTATCCGAA AGGCGTTCCC GCCGAAATCG ACGTCAACGA
ATTCCATTCG GTCGCCTCGG TCTTCGACGC TTCCGTCGCG AAATTCCGCG ACCGTCCCGC CTACTCCAGC
TTCGGCAAGG TCCTCACCTA TGGTGAGACG GACGCGCTGG TCACCCAGTT CGCCGCCTAC CTGCTGGGTG
AGCTCAAGCT CAAGAAGGGT GACCGCGTCG CCCTGATGAT GCCCAACTGC CTGCAGTACC CGGTGGCCAC
CTTCGGCGTG CTGCGCGCCG GCCTGACCGT GGTCAACGTC AACCCGCTGT ACACCGCGCG CGAACTCAAG
CACCAGCTGG TTGATGCCGG CGTCAGCGCC CTGGTGGTGG TCGACAACTT CGGCGACACC GTCGAACAGG
TCATCGCCGA TACACCGGTC AAGCACGTGG TCACCACCGG CCTGGGCGAC CTGCTCGGCG CCAAGGGCGC
GATCGTCAAC TTCGTGCTGA AGTACATCAA GAAGATGGTG CCCAACTACC ACATCAAGGG CGCCGTCCGC
TTCAAGCAGG CGCTCAAGCT GGGCAGCCGC CACGCGCTTC CGCCGGTCGA GATCGACCAC GACGACATTG
CCTTCCTGCA GTACACCGGC GGGACCACCG GCGTGGCCAA GGGTGCGATG CTGACCAACC GCAACCTGAT
CGCCAACATG CAGCAGGCGT CAGCGTGGCT GTCCACCTCC GGCATCGAGC CGGGCAAGGA AGTGATCATC
ACTGCCCTGC CGCTGTACCA CATCTTCGCA TTGACCGCGA ACGGCCTGGT CTTTATGAAG TTCGGTGGCT
GCAACCACCT GATCACCAAC CCACGCGACA TGAAGGGCTT CGTAAAGGAG CTCAAGGGCA CCCGCTTCAC
TGCCATCACC GGCGTCAACA CGCTGTTCAA CGGCCTGCTC AACACCCCGG GCTTCGACGA GATCGACTTC
TCTTCGGTCA AGTTCACCCT GGGCGGCGGC ATGGCGGTGC AACGTGCCGT GGCCGAACGC TGGAAGAAGG
TCACCGGCGT GACCCTGGTC GAAGCCTATG GCCTGACCGA GACCTCGCCC GCGGCCTGCA TCAATCCGCT
CACCCTGCCC GAGTACAACG GTGCCATCGG CCTGCCGATC CCGTCTACCG ATGCCTGCAT CAAGGACGAC
AACGGCAACA TCCTGGCGCT GGGCGAAGTG GGCGAGCTGT GCATCAAGGG CCCGCAGGTA ATGAAGGGCT
ACTGGCAGCG TCCGGAAGAA ACCGCCACCG CCATCGATGC GGACGGCTGG CTGCACACCG GCGACATGGC
GAAGATGGAC GAACAGGGCT TCTTCTACAT CGTCGACCGC AAGAAGGACA TGATCCTGGT GTCCGGCTTC
AACGTGTACC CGAATGAGGT CGAAGACGTC ATCGGGATGA TGCCGGGCGT GCTGGAAGTC GCCGCCGTCG
GTGTCCCGGA CGAAAAGTCC GGCGAAGTGG TCAAGGTCGT GATCGTGAAG AAGGACCCGA ACCTGACCGC
GGAAATGGTC AAGGAACATG CGCGGGCAAA CCTGACCGGT TACAAGCACC CCAGAATCGT AGAATTCCGA
AAGGAGCTGC CGAAGACCAA CGTCGGCAAG ATCCTCCGTC GCGAGCTGCG TGATACGCCC GCCCCG**TAA**G
AATTC

FIG. 26

SEQ ID NO:10 - the Smprk59BspF primer based on the DNA sequence deposited at NCBI with the accession code NZ_AAVZ01000044.

AGTCATGAGTCTGGATCG

FIG. 27

SEQ ID NO:11 - the Smprk59HindR primer based on the DNA sequence deposited at NCBI with the accession code NZ_AAVZ01000044.

GGAAGCTTACGGGGCGGGCG

FIG. 28

SEQ ID NO:12 - the primer PrkBsp

GCGAACGGCCTGGTCTTTATGAAGTTCGGTGG

FIG. 29

SEQ ID NO:13 - DNA sequence of the gene encoding the protein ZP_01644857 from *Stenotrophomonas maltophilia* R551-3.

TC**ATG**AGTCT GGATCGTCCC TGGCTGCAGA GCTATCCGAA AGGCGTTCCC GCCGAAATCG ACGTCAACGA
ATTCCATTCG GTCGCCTCGG TCTTCGACGC TTCCGTCGCG AAATTCCGCG ACCGTCCCGC CTACTCCAGC
TTCGGCAAGG TCCTCACCTA TGGTGAGACG GACGCGCTGG TCACCCAGTT CGCCGCCTAC CTGCTGGGTG
AGCTCAAGCT CAAGAAGGGT GACCGCGTCG CCCTGATGAT GCCCAACTGC CTGCAGTACC CGGTGGCCAC
CTTCGGCGTG CTGCGCGCCG GCCTGACCGT GGTCAACGTC AACCCGCTGT ACACCGCGCG CGAACTCAAG
CACCAGCTGG TTGATGCCGG CGTCAGCGCC CTGGTGGTGG TCGACAACTT CGGCGACACC GTCGAACAGG
TCATCGCCGA TACACCGGTC AAGCACGTGG TCACCACCGG CCTGGGCGAC CTGCTCGGCG CCAAGGGCGC
GATCGTCAAC TTCGTGCTGA AGTACATCAA GAAGATGGTG CCCAACTACC ACATCAAGGG CGCCGTCCGC
TTCAAGCAGG CGCTCAAGCT GGGCAGCCGC CACGCGCTTC CGCCGGTCGA GATCGACCAC GACGACATTG
CCTTCCTGCA GTACACCGGC GGGACCACCG GCGTGGCCAA GGGTGCGATG CTGACCAACC GCAACCTGAT
CGCCAACATG CAGCAGGCGT CAGCGTGGCT GTCCACCTCC GGCATCGAGC CGGGCAAGGA AGTGATCATC
ACTGCCCTGC CGCTGTACCA CATCTTCGCA TTGACCGCGA ACGGCCTGGT CTTTATGAAG TTCGGTGGCT
GCAACCACCT GATCACCAAC CCACGCGACA TGAAGGGCTT CGTAAAGGAG CTCAAGGGCA CCCGCTTCAC
TGCCATCACC GGCGTCAACA CGCTGTTCAA CGGCCTGCTC AACACCCCGG GCTTCGACGA GATCGACTTC
TCTTCGGTCA AGTTCACCCT GGGCGGCGGC ATGGCGGTGC AACGTGCCGT GGCCGAACGC TGGAAGAAGG
TCACCGGCGT GACCCTGGTC GAAGCCTATG GCCTGACCGA GACCTCGCCC GCGGCCTGCA TCAATCCGCT
CACCCTGCCC GAGTACAACG GTGCCATCGG CCTGCCGATC CCGTCTACCG ATGCCTGCAT CAAGGACGAC
AACGGCAACA TCCTGGCGCT GGGCGAAGTG GGCGAGCTGT GCATCAAGGG CCCGCAGGTA ATGAAGGGCT
ACTGGCAGCG TCCGGAAGAA ACCGCCACCG CCATCGATGC GGACGGCTGG CTGCACACCG GCGACATGGC
GAAGATGGAC GAACAGGGCT TCTTCTACAT CGTCGACCGC AAGAAGGACA TGATCCTGGT GTCCGGCTTC
AACGTGTACC CGAATGAGGT CGAAGACGTC ATCGCGATGA TGCCGGGCGT GCTGGAAGTC GCCGCCGTCG
GTGTCCCGGA CGAAAAGTCC GGCGAAGTGG TCAAGGTCGT GATCGTGAAG AAGGACCCGA ACCTGACCGC
GGAAATGGTC AAGGAACATG CGCGGGCAAA CCTGACCGGT TACAAGCACC CCAGAATCGT AGAATTCCGA
AAGGAGCTGC CGAAGACCAA CGTCGGCAAG ATCCTCCGTC GCGAGCTGCG TGATACGCCC GCCCCG**TAA**G
AATTC

FIG. 30

SEQ ID NO:14 – Protein sequence of ZP_01644857 from *Stenotrophomonas maltophilia* ATCC 17679.

MSLDRPWLQS YPKGVPAEID VNEFHSVASV FDASVAKFRD RPAYSSFGKV ITYGETDTLV
NQFAAYLLGE LKLKKGDRVA LMMPNCLQYP VATFGVLRAG LTVVNVNPLY TARELKHQLV
DAGVSALVVV DNFGDTVEQV IADTPVKHVI TTGLGDLLGA KGAIVNFVLK YVKKMVPNYH
IKGAVRFKQA LKLGSRHTLP AVEIDHDDIA FLQYTGGTTG VAKGAMLTNR NLIANMQQAS
AWLSTSGIEP GKEVIITALP LYHIFALTAN GLVFMKFGGC NHLITNPRDM KGFVKELKGT
RFTAITGVNT LFNGLLNTPG FDEIDFSSVK FTLGGGMAVQ RAVAERWKKT TGVTLVEAYG
LTETSPAACI NPLTLPEYNG SIGLPIPSTD ACIKDDNGNI LPLGEVGELC IKGPQVMKGY
WQRPEETATA IDADGWLHTG DMARMDEQGF FYIVDRKKDM ILVSGFNVYP NEVEDVIAMM
PGVLEVAAVG VPDEKSGEVV KVVIVKKDPN LTAEMVKEHA RANLTGYKHP RIVEFRKELP
KTNVGKILRR ELRDTPAP

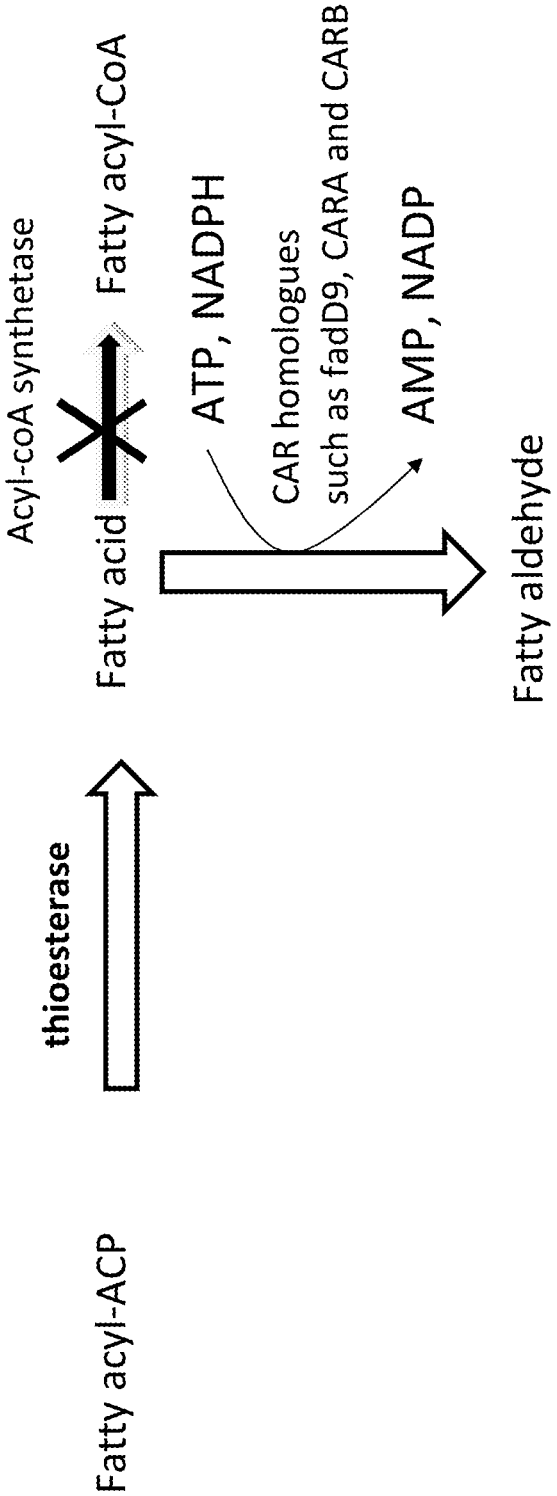

Fatty acyl-ACP
thioesterase
Fatty acid
Acyl-coA synthetase
Fatty acyl-CoA
ATP, NADPH
CAR homologues
such as fadD9, CARA and CARB
AMP, NADP
Fatty aldehyde

FIG. 31

FIG. 32

AAR91681.1

Nucleotide sequence (SEQ ID NO:15)

>gi|40796034:488-4012 Nocardia sp. NRRL 5646 ATP/NADPH-dependent carboxylic acid reductase (car) gene, complete cds

ATGGCAGTGGATTCACCGGATGAGCGGCTACAGCGCCGCATTGCACAGTTGTTTGCAGAAGATG
AGCAGGTCAAGGCCGCACGTCCGCTCGAAGCGGTGAGCGCGGCGGTGAGCGCGCCCGGTATGCG
GCTGGCGCAGATCGCCGCCACTGTTATGGCGGGTTACGCCGACCGCCCGGCCGCCGGGCAGCGT
GCGTTCGAACTGAACACCGACGACGCGACGGGCCGCACCTCGCTGCGGTTACTTCCCCGATTCG
AGACCATCACCTATCGCGAACTGTGGCAGCGAGTCGGCGAGGTTGCCGCGGCCTGGCATCATGA
TCCCGAGAACCCCTTGCGCGCAGGTGATTTCGTCGCCCTGCTCGGCTTCACCAGCATCGACTAC
GCCACCCTCGACCTGGCCGATATCCACCTCGGCGCGGTTACCGTGCCGTTGCAGGCCAGCGCGG
CGGTGTCCCAGCTGATCGCTATCCTCACCGAGACTTCGCCGCGGCTGCTCGCCTCGACCCCGGA
GCACCTCGATGCGGCGGTCGAGTGCCTACTCGCGGGCACCACACCGGAACGACTGGTGGTCTTC
GACTACCACCCCGAGGACGACGACCAGCGTGCGGCCTTCGAATCCGCCCGCCGCCGCCTTGCCG
ACGCGGGCAGCTTGGTGATCGTCGAAACGCTCGATGCCGTGCGTGCCCGGGGCCGCGACTTACC
GGCCGCGCCACTGTTCGTTCCCGACACCGACGACGACCCGCTGGCCCTGCTGATCTACACCTCC
GGCAGCACCGGAACGCCGAAGGGCGCGATGTACACCAATCGGTTGGCCGCCACGATGTGGCAGG
GGAACTCGATGCTGCAGGGGAACTCGCAACGGGTCGGGATCAATCTCAACTACATGCCGATGAG
CCACATCGCCGGTCGCATATCGCTGTTCGGCGTGCTCGCTCGCGGTGGCACCGCATACTTCGCG
GCCAAGAGCGACATGTCGACACTGTTCGAAGACATCGGCTTGGTACGTCCCACCGAGATCTTCT
TCGTCCCGCGCGTGTGCGACATGGTCTTCCAGCGCTATCAGAGCGAGCTGGACCGGCGCTCGGT
GGCGGGCGCCGACCTGGACACGCTCGATCGGGAAGTGAAAGCCGACCTCCGGCAGAACTACCTC
GGTGGGCGCTTCCTGGTGGCGGTCGTCGGCAGCGCGCCGCTGGCCGCGGAGATGAAGACGTTCA
TGGAGTCCGTCCTCGATCTGCCACTGCACGACGGGTACGGGTCGACCGAGGCGGGCGCAAGCGT
GCTGCTCGACAACCAGATCCAGCGGCCGCCGGTGCTCGATTACAAGCTCGTCGACGTGCCCGAA
CTGGGTTACTTCCGCACCGACCGGCCGCATCCGCGCGGTGAGCTGTTGTTGAAGGCGGAGACCA
CGATTCCGGGCTACTACAAGCGGCCCGAGGTCACCGCGGAGATCTTCGACGAGGACGGCTTCTA
CAAGACCGGCGATATCGTGGCCGAGCTCGAGCACGATCGGCTGGTCTATGTCGACCGTCGCAAC
AATGTGCTCAAACTGTCGCAGGGCGAGTTCGTGACCGTCGCCCATCTCGAGGCCGTGTTCGCCA
GCAGCCCGCTGATCCGGCAGATCTTCATCTACGGCAGCAGCGAACGTTCCTATCTGCTCGCGGT
GATCGTCCCCACCGACGACGCGCTGCGCGGCCGCGACACCGCCACCTTGAAATCGGCACTGGCC
GAATCGATTCAGCGCATCGCCAAGGACGCGAACCTGCAGCCCTACGAGATTCCGCGCGATTTCC
TGATCGAGACCGAGCCGTTCACCATCGCCAACGGACTGCTCTCCGGCATCGCGAAGCTGCTGCG
CCCCAATCTGAAGGAACGCTACGGCGCTCAGCTGGAGCAGATGTACACCGATCTCGCGACAGGC
CAGGCCGATGAGCTGCTCGCCCTGCGCCGCGAAGCCGCCGACCTGCCGGTGCTCGAAACCGTCA
GCCGGGCAGCGAAAGCGATGCTCGGCGTCGCCTCCGCCGATATGCGTCCCGACGCGCACTTCAC
CGACCTGGGCGGCGATTCCCTTTCCGCGCTGTCGTTCTCGAACCTGCTGCACGAGATCTTCGGG
GTCGAGGTGCCGGTGGGTGTCGTCGTCAGCCCGGCGAACGAGCTGCGCGATCTGGCGAATTACA
TTGAGGCGGAACGCAACTCGGGCGCGAAGCGTCCCACCTTCACCTCGGTGCACGGCGGCGGTTC

FIG. 32 (continued)

CGAGATCCGCGCCGCCGATCTGACCCTCGACAAGTTCATCGATGCCCGCACCCTGGCCGCCGCC
GACAGCATTCCGCACGCGCCGGTGCCAGCGCAGACGGTGCTGCTGACCGGCGCGAACGGCTAC
TCGGCCGGTTCCTGTGCCTGGAATGGCTGGAGCGGCTGGACAAGACGGGTGGCACGCTGATCG
CGTCGTGCGCGGTAGTGACGCGGCCGCGGCCCGTAAACGGCTGGACTCGGCGTTCGACAGCGGC
GATCCCGGCCTGCTCGAGCACTACCAGCAACTGGCCGCACGGACCCTGGAAGTCCTCGCCGGTG
ATATCGGCGACCCGAATCTCGGTCTGGACGACGCGACTTGGCAGCGGTTGGCCGAAACCGTCGA
CCTGATCGTCCATCCCGCCGCGTTGGTCAACCACGTCCTTCCCTACACCCAGCTGTTCGGCCCC
AATGTCGTCGGCACCGCCGAAATCGTCCGGTTGGCGATCACGGCGCGGCGCAAGCCGGTCACCT
ACCTGTCGACCGTCGGAGTGGCCGACCAGGTCGACCCGGCGGAGTATCAGGAGGACAGCGACGT
CCGCGAGATGAGCGCGGTGCGCGTCGTGCGCGAGAGTTACGCCAACGGCTACGGCAACAGCAAG
TGGGCGGGGGAGGTCCTGCTGCGCGAAGCACACGATCTGTGTGGCTTGCCGGTCGCGGTGTTCC
GTTCGGACATGATCCTGGCGCACAGCCGGTACGCGGGTCAGCTCAACGTCCAGGACGTGTTCAC
CCGGCTGATCCTCAGCCTGGTCGCCACCGGCATCGCGCCGTACTCGTTCTACCGAACCGACGCG
GACGGCAACCGGCAGCGGGCCCACTATGACGGCTTGCCGGCGGACTTCACGGCGGCGGCGATCA
CCGCGCTCGGCATCCAAGCCACCGAAGGCTTCCGGACCTACGACGTGCTCAATCCGTACGACGA
TGGCATCTCCCTCGATGAATTCGTCGACTGGCTCGTCGAATCCGGCCACCCGATCCAGCGCATC
ACCGACTACAGCGACTGGTTCCACCGTTTCGAGACGGCGATCCGCGCGCTGCCGGAAAAGCAAC
GCCAGGCCTCGGTGCTGCCGTTGCTGGACGCCTACCGCAACCCCTGCCCGGCGGTCCGCGGCGC
GATACTCCCGGCCAAGGAGTTCCAAGCGGCGGTGCAAACAGCCAAAATCGGTCCGGAACAGGAC
ATCCCGCATTTGTCCGCGCCACTGATCGATAAGTACGTCAGCGATCTGGAACTGCTTCAGCTGC
TCTGA

Amino acid sequence (SEQ ID NO:16)

>gi|40796035|gb|AAR91681.1| ATP/NADPH-dependent carboxylic acid reductase [Nocardia sp. NRRL 5646]

MAVDSPDERLQRRIAQLFAEDEQVKAARPLEAVSAAVSAPGMRLAQIAATVMAGYADRPAAGQR
AFELNTDDATGRTSLRLLPRFETITYRELWQRVGEVAAAWHHDPENPLRAGDFVALLGFTSIDY
ATLDLADIHLGAVTVPLQASAAVSQLIAILTETSPRLLASTPEHLDAAVECLLAGTTPERLVVF
DYHPEDDDQRAAFESARRRLADAGSLVIVETLDAVRARGRDLPAAPLFVPDTDDDPLALLIYTS
GSTGTPKGAMYTNRLAATMWQGNSMLQGNSQRVGINLNYMPMSHIAGRISLFGVLARGGTAYFA
AKSDMSTLFEDIGLVRPTEIFFVPRVCDMVFQRYQSELDRRSVAGADLDTLDREVKADLRQNYL
GGRFLVAVVGSAPLAAEMKTFMESVLDLPLHDGYGSTEAGASVLLDNQIQRPPVLDYKLVDVPE
LGYFRTDRPHPRGELLLKAETTIPGYYKRPEVTAEIFDEDGFYKTGDIVAELEHDRLVYVDRRN
NVLKLSQGEFVTVAHLEAVFASSPLIRQIFIYGSSERSYLLAVIVPTDDALRGRDTATLKSALA
ESIQRIAKDANLQPYEIPRDFLIETEPFTIANGLLSGIAKLLRPNLKERYGAQLEQMYTDLATG
QADELLALRREAADLPVLETVSRAAKAMLGVASADMRPDAHFTDLGGDSLSALSFSNLLHEIFG
VEVPVGVVVSPANELRDLANYIEAERNSGAKRPTFTSVHGGGSEIRAADLTLDKFIDARTLAAA
DSIPHAPVPAQTVLLTGANGYLGRFLCLEWLERLDKTGGTLICVVRGSDAAAARKRLDSAFDSG
DPGLLEHYQQLAARTLEVLAGDIGDPNLGLDDATWQRLAETVDLIVHPAALVNHVLPYTQLFGP
NVVGTAEIVRLAITARRKPVTYLSTVGVADQVDPAEYQEDSDVREMSAVRVVRESYANGYGNSK
WAGEVLLREAHDLCGLPVAVFRSDMILAHSRYAGQLNVQDVFTRLILSLVATGIAPYSFYRTDA
DGNRQRAHYDGLPADFTAAAITALGIQATEGFRTYDVLNPYDDGISLDEFVDWLVESGHPIQRI
TDYSDWFHRFETAIRALPEKQRQASVLPLLDAYRNPCPAVRGAILPAKEFQAAVQTAKIGPEQD
IPHLSAPLIDKYVSDLELLQLL

FIG. 33

Motif 1

-G-Y-X-X-S/A/T-K-W/L (SEQ ID NO:17); and

-G-X-X-G-X-L-G (SEQ ID NO:18); and

-L/V/I-G-G-D-S-X-X-A (SEQ ID NO:19); and

-[LIVMFY]-{E}-{VES}-[STG]-[STAG]-G-[ST]-[STEIA]-[SG]-X-[PASLIVM]-[KR] (SEQ ID NO:20), wherein {X} stands for any amino acid except X and [X_1X_2] stands for X_1 or X_2

Motif 2

RTVLLX_1GAX_2GX_3LGRX_4LX_5LX_6WL (SEQ ID NO:21)

wherein X_1 is S or T;

X_2 is T or N;

X_3 is F or W;

X_4 is F or Y;

X_5 is A or T; and

X_6 is E or Q

Motif 3

LXXGXXGXLGXXLXLXWLXR (SEQ ID NO:22)

Motif 4

WAXEVLLR (SEQ ID NO:23), where X can be any amino acid; or

LXXGXXGXLGXXLXX$_1$XX$_2$LX$_3$R (SEQ ID NO:24), wherein

X_1 is Leu or Ile;

X_2 is Trp or Leu; and

X_3 varies between 13 amino acids or 14 amino acids

Motif 5

-G-Y-X-X-S/A/T-K-W/L (SEQ ID NO:17); and

-L/V/I-G-G-D-S-X-X-A (SEQ ID NO:19); and

FIG. 33 (continued)

-[LIVMFY]-{E}-{VES}-[STG]-[STAG]-G-[ST]-[STEIA]-[SG]-X-[PASLIVM]-[KR] (SEQ ID NO:20), wherein {X} stands for any amino acid except X and [X_1X_2] stands for X_1 or X_2; and

RTVLLX_1GAX_2GX_3LGRX_4LX_5LX_6WL (SEQ ID NO:21), wherein

X_1 is S or T;

X_2 is I or N;

X_3 is F or W;

X_4 is F or Y;

X_5 is A or T; and

X_6 is E or Q

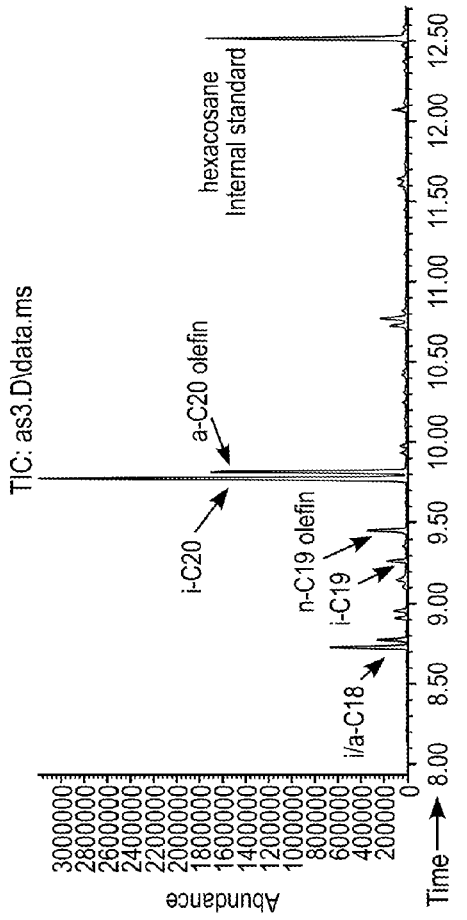


FIG. 34A

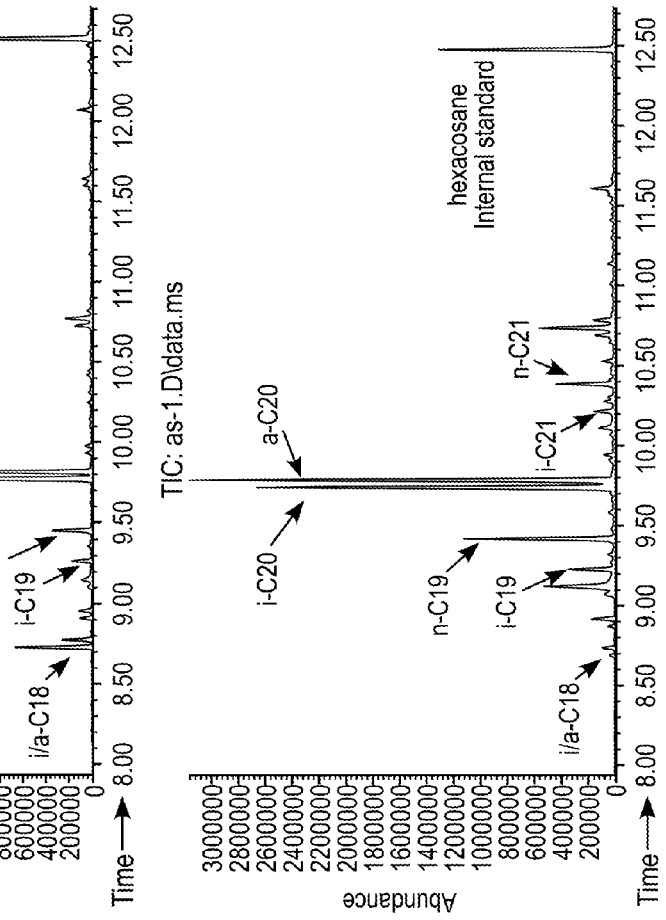


FIG. 34B

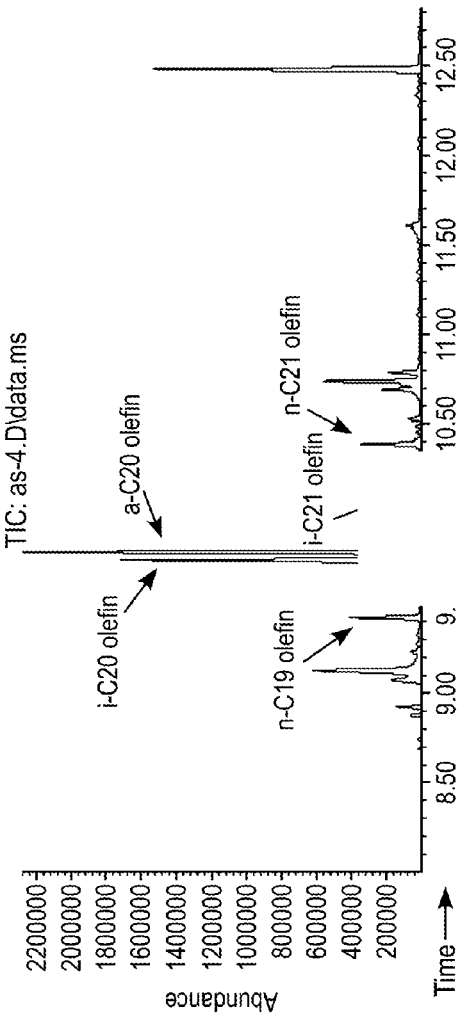


FIG. 35A

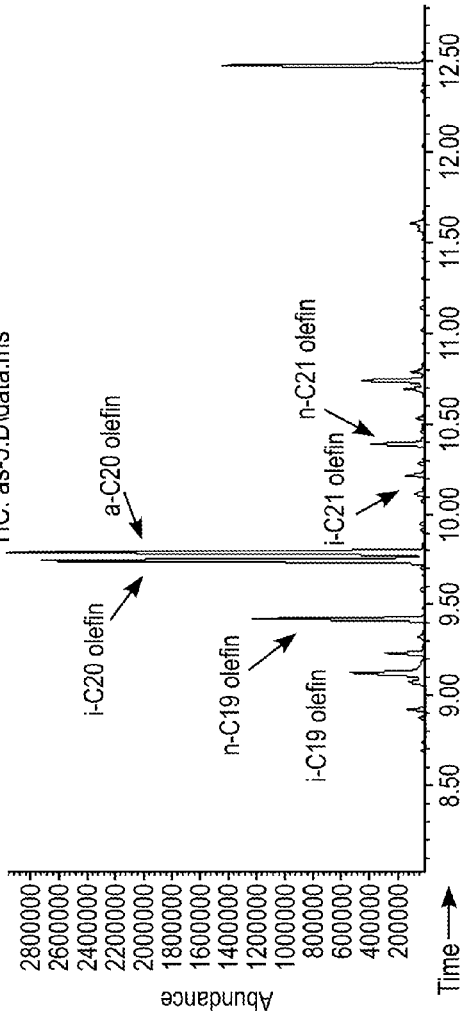


FIG. 35B

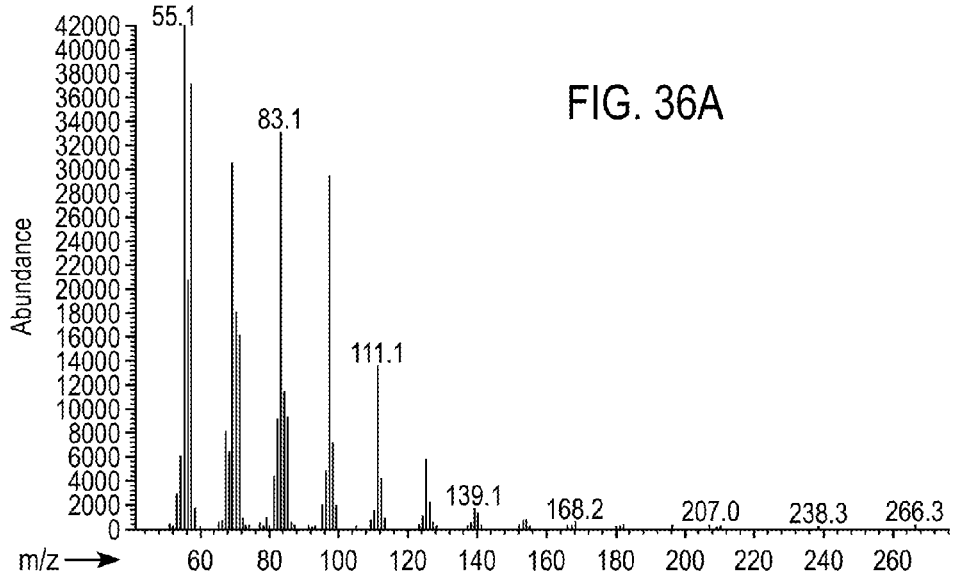


FIG. 36A

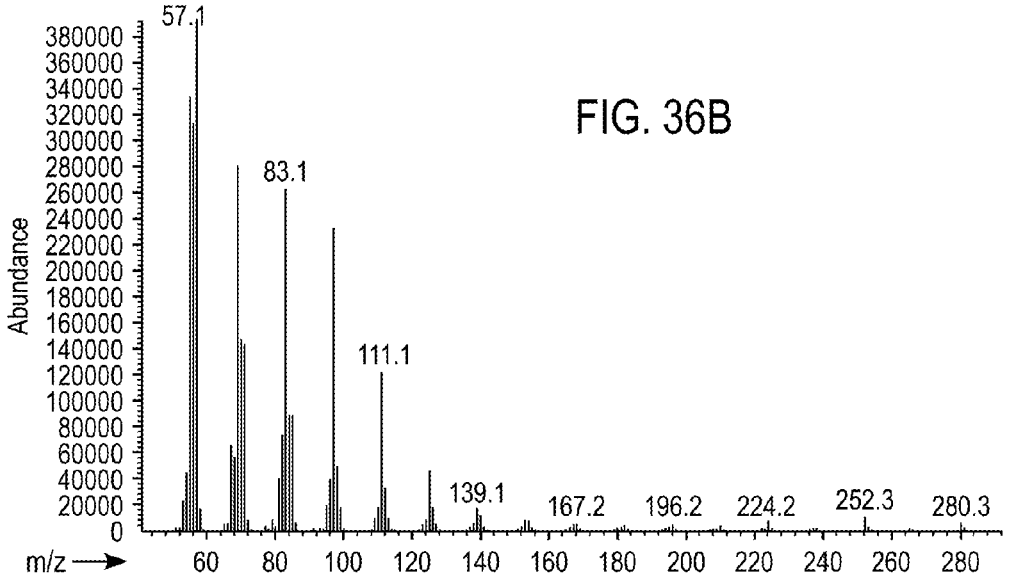


FIG. 36B

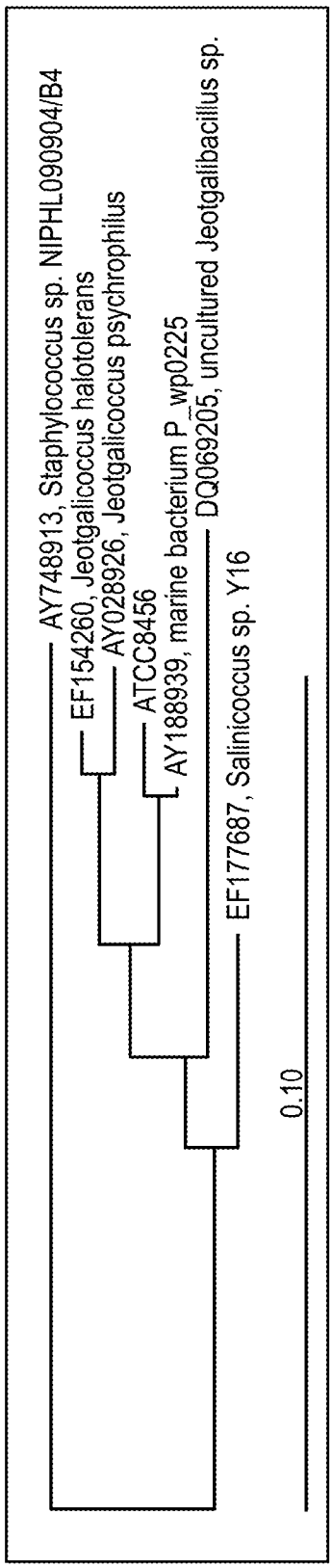

AY748913, Staphylococcus sp. NIPHL090904/B4
EF154260, Jeotgalicoccus halotolerans
AY028926, Jeotgalicoccus psychrophilus
ATCC8456
AY188939, marine bacterium P_wp0225
DQ069205, uncultured Jeotgalibacillus sp.
EF177687, Salinicoccus sp. Y16
0.10

FIG. 37

FIG. 38A

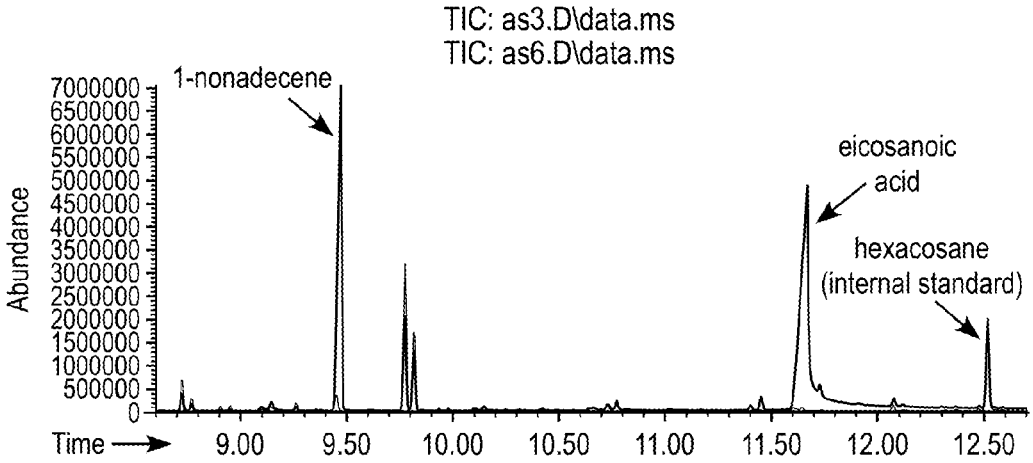
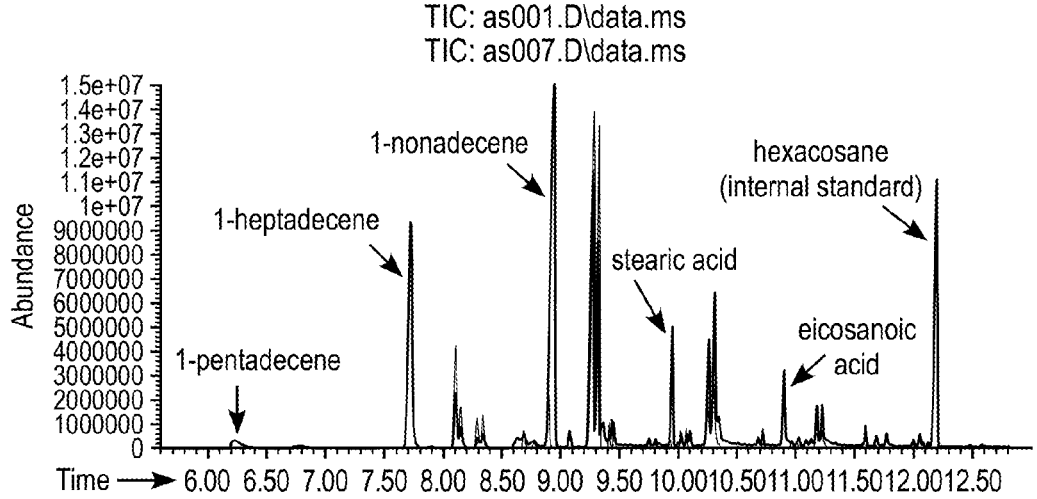


FIG. 38B



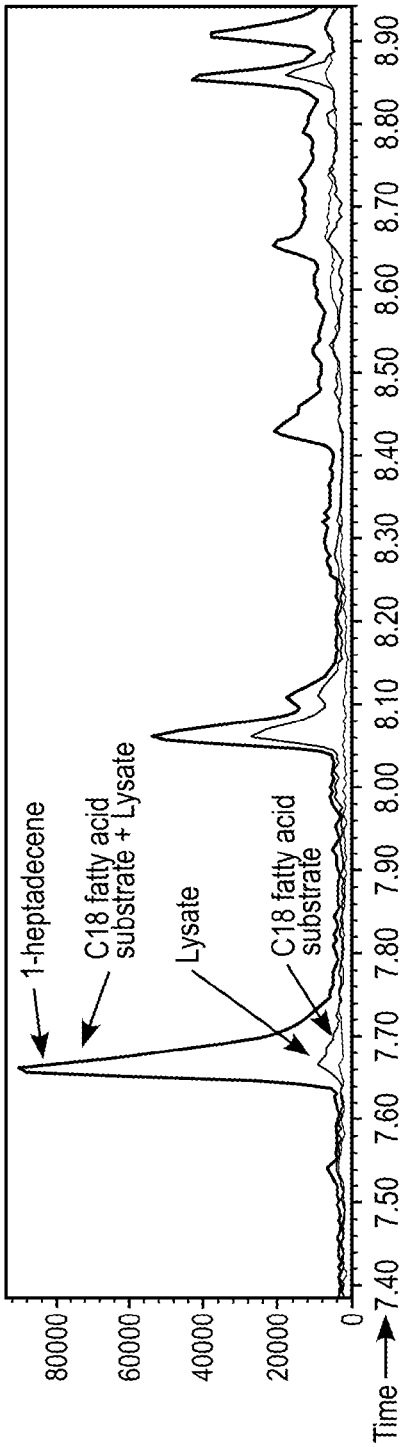

1-heptadecene
C18 fatty acid substrate + Lysate
Lysate
C18 fatty acid substrate
80000
60000
40000
20000
0
7.40
7.50
7.60
7.70
7.80
7.90
8.00
8.10
8.20
8.30
8.40
8.50
8.60
8.70
8.80
8.90
Time

FIG. 39

FIG. 40

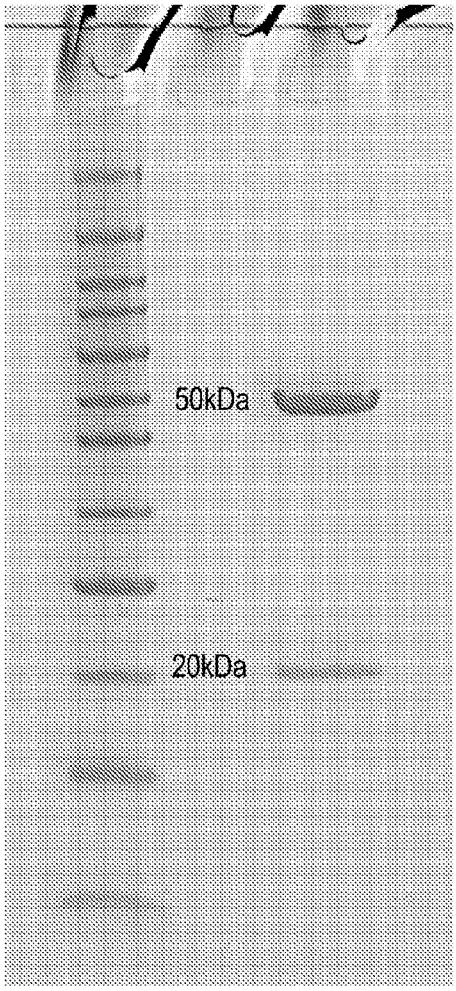


FIG. 41A

SEQ ID NO:25

```
ATGGCAACAC TTAAGAGGGA TAAGGGCTTA GATAATACTT TGAAAGTATT AAAGCAAGGT 60
TATCTTTACA CAACAAATCA GAGAAATCGT CTAAACACAT CAGTTTTCCA AACTAAAGCA 120
CTCGGTGGTA AACCATTCGT AGTTGTGACT GGTAAGGAAG GCGCTGAAAT GTTCTACAAC 180
AATGATGTTG TTCAACGTGA AGGCATGTTA CCAAAACGTA TCGTTAATAC GCTTTTTGGT 240
AAAGGTGCAA TCCATACGGT AGATGGTAAA AAACACGTAG ACAGAAAAGC ATTGTTCATG 300
AGCTTGATGA CTGAAGGTAA CTTGAATTAT GTACGAGAAT TAACGCGTAC ATTATGGCAT 360
GCGAACACAC AACGTATGGA AAGTATGCAT GAGGTAAATA TTTACCGTGA ATCTATCGTA 420
CTACTTACAA AAGTAGGAAC ACGTTGGCCA GGCGTTCAAG CACCACCTGA AGATATCGAA 480
AGAATCGCAA CAGACATGGA CATCATGATC GATTCATTTA GAGCACTTGG TGGTGCCTTT 540
AAAGGTTACA AGGCATCAAA AGAAGCACGT CGTCGTGTTG AAGATTGGTT AGAAGAACAA 600
ATTATTGAGA CTCGTAAAGG GAATATTCAT CCACCAGAAG GTACAGCACT TTACGAATTT 660
GCACATTGGG AAGACTACTT AGGTAACCCA ATGGACTCAA GAACTTGTGC GATTGACTTA 720
ATGAACACAT TCCGCCCATT AATCGCAATC AACAGATTCG TTTCATTCGG TTTACACGCG 780
ATGAACGAAA ACCCAATCAC ACGTGAAAAA ATTAAATCAG AACCTGACTA TGCATATAAA 840
TTCGCTCAAG AAGTTCGTCG TTACTATCCA TTCGTTCCAT TCCTTCCAGG TAAAGCGAAA 900
GTAGACATCG ACTTCCAAGG CGTTACAATT CCTGCAGGTG TAGGTCTTGC ATTAGATGTT 960
TATGGTACAA CGCATGATGA ATCACTTTGG GACGATCCAA ATGAATTCCG CCCAGAAAGA 1020
TTCGAAACTT GGGACGGATC ACCATTTGAC CTTATTCCAC AAGGTGGTGG AGATTACTGG 1080
ACAAATCACC GTTGTGCAGG TGAATGGATC ACAGTAATCA TCATGGAAGA AACAATGAAA 1140
TACTTTGCAG AAAAAATAAC TTATGATGTT CCAGAACAAG ATTTAGAAGT GGACTTAAAC 1200
AGTATCCCAG GATACGTTAA GAGTGGCTTT GTAATCAAAA ATGTTCGCGA AGTTGTAGAC 1260
ACAACATAA 1270
```

FIG. 41B

Jeotgalicoccus sp. ATCC8456 orf880 (SEQ ID NO:26)

```
MAILKRDKGL DNTLKVLKQG YLYTTNQRNR LNTSVFQTKA LGGKPFVVVT GKEGAEMFYN   60
NDVVQREGML PKRIVNTLFG KGAIHTVDGK KHVDRKALFM SLMTEGNLNY VRELIRILWH  120
ANTQRMESMD EVNIYRESIV LLTKVGIRWA GVQAPPEDIE RIATDMDIMI DSFRALGGAF  180
KGYKASKEAR RRVEDWLEEQ IIEIRKGNIH PPEGTALYEF AHWEDYLGNP MDSRTCAIDL  240
MNTFRPLIAI NRFVSFGLHA MNENPITREK IKSEPDYAYK FAQEVRRYYP FVPFLPGKAK  300
VDIDFQGVTI PAGVGLALDV YGTTHDESLW DDPNEFRPER FETWDGSPFD LIPQGGGDYW  360
TNHRCAGEWI TVIIMEETMK YFAEKITYDV PEQDLEVDLN SIPGYVKSGF VIKNVREVVD  420
RT         430
```

FIG. 41C

Jeotgalicoccus sp. ATCC8456 16s rRNA (partial sequence) (SEQ ID NO:27)

```
GGTTACCTTG TTACGACTTC ACCCCAATTA TCAATCCCAC CTTTGACGGC TACCTCCATT        60
AAGGTTAGTC CACCGGCTTC AGGTGTTAYC GACTTTCGTG GTGTGACGGG CGGTGTGTAC       120
AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG ATTCCAGCTT       180
CATGGAGTCG AGTTGCAGAC TCCAATCCGA ACTGAGAACA GTTTTATGGG ATTCGCTTGG       240
CCTCGCGGCT TCGCTGCCCT TTGTAACCTG CCCATTGTAG CACGTGTGTA GCCCAAATCA       300
TAAGGGGCAT GATGATTTGA CGTCATCCCC ACCTTCCTCC GGTTTGTCAC CGGCAGTCAA       360
TCTAGAGTGC CCAACTGAAT GATGGCAACT AAATTTAAGG GTTGCGCTCG TTGCGGGACT       420
TAACCCAACA TCTCACGACA CGAGCTGACG ACAACCATGC ACCACCTGTC TCTCTGCCCA       480
AAAGGGAAAC CATATCTCTR TGGCGATCAG AGGATGTCAA GATTTGGTAA GGTTCTTCGC       540
GTTGCTTCGA ATTAAACCAC ATGCTCCACC GCTTGTGCGG GTCCCCGTCA ATTCCTTTGA       600
GTTTCAACCT TGCGGTCGTA CTCCCCAGGC GGAGTGCTTA ATGCGTTAGC TGCAGCACTG       660
AGGGGCGGAA ACCCCCCAAC ACTTAGCACT CATCGTTTAC GGCGTGGACT ACCAGGGTAT       720
CTAATCCTGT TTGATCCCCA CGCTTTCGCA CCTCAGCGTC AGTTACAGAC CAGAGAGCCG       780
CCTTCGCCCA CTGGTGTTCC TCCATATCTC TGCGCATTTC ACCGCTACAC ATGGAATTCC       840
ACTCTCCTCT TCTGCACTCA AGTAAAACAG TTTCCAATGA CCCTCCCCGG TTGAGCCGGG       900
GGCTTTCACA TCAGACTTAT TCTACCGCCT ACGCGCGCTT TACGCCCAAT AATTCCGGAT       960
AACGCTTGCC ACCTACGTAT TACCGCGGCT GCTGGCACGT AGTTAGCCGT GGCTTTCTGG      1020
TTAAGTACCG TCATCTCTAG GCCAGTTACT ACCTAAAGTG TTCTTCCTTA ACAACAGAGT      1080
TTTACGAGCC GAAACCCTTC TTCACTCACG CGGCGTTGCT CCGTCAGACT TGCGTYCATT      1140
GCGGAAGATT CCCTACTGCT GCCTCCCGTA GGAGTCTGGG CCGTGTCTCA GTCCCAGTGT      1200
GGCCGATCAC CCTCTCAGGT CGGCTATGCA TCGTTGCCTT GGTGAGCCAC TACCTCACCA      1260
ACTAGCTAAT GCACCGCAGG CCCATCCTTT AGTGACAGAT AAATCCGCCT TTCATTAAGA      1320
TTACTTGTGT AATCCAACTT ATCCGGTATT AGCTACCGTT TCCGGTAGTT ATCCCAGTCT      1380
AAAGGGTAGG TTGCCCACGT GTTACTCACC CGTCCGCCGC TCGATTGTAA GGAGCAAGCT      1440
CCTTACGCTC GCGCTCGACT TGCATGTATT AGGCACGCCG CCAGCGTTCA TCCTGAGCCA      1500
GGATCAA                                                               1510
```

FIG. 42

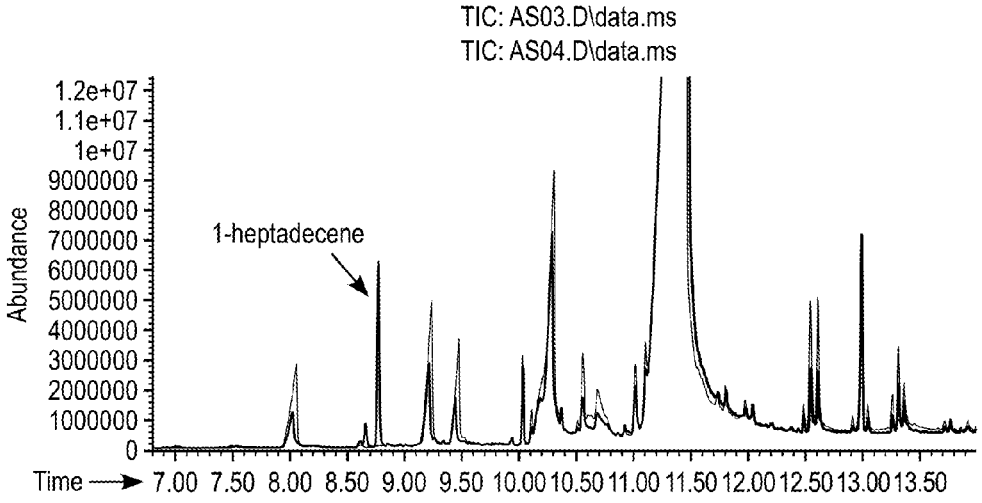

TIC: AS03.D\data.ms
TIC: AS04.D\data.ms
1-heptadecene
Abundance
1.2e+07
1.1e+07
1e+07
9000000
8000000
7000000
6000000
5000000
4000000
3000000
2000000
1000000
0
Time
7.00 7.50 8.00 8.50 9.00 9.50 10.00 10.50 11.00 11.50 12.00 12.50 13.00 13.50

FIG. 43

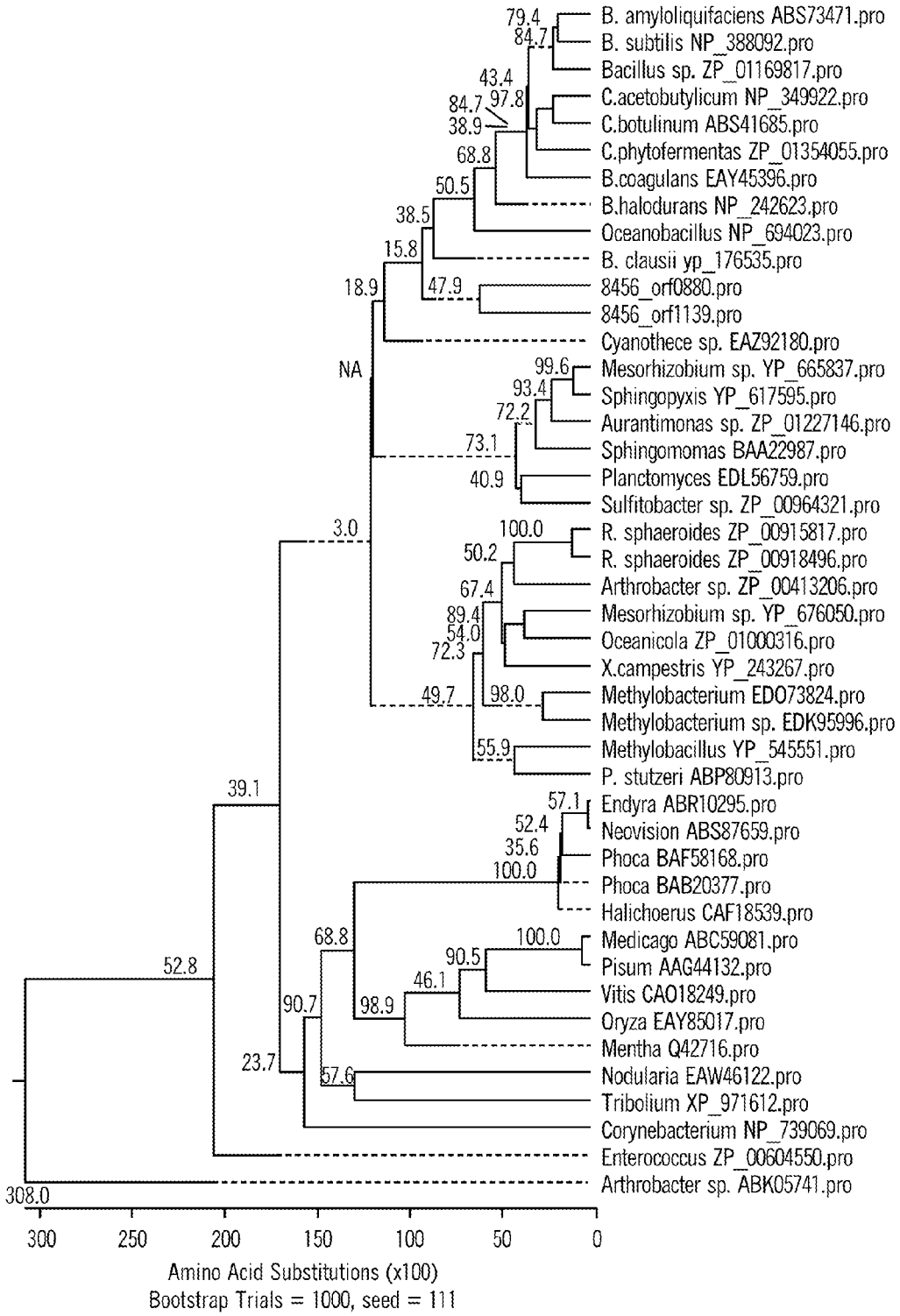

B. amyloliquifaciens ABS73471.pro
B. subtilis NP_388092.pro
Bacillus sp. ZP_01169817.pro
C.acetobutylicum NP_349922.pro
C.botulinum ABS41685.pro
C.phytofermentas ZP_01354055.pro
B.coagulans EAY45396.pro
B.halodurans NP_242623.pro
Oceanobacillus NP_694023.pro
B. clausii yp_176535.pro
8456_orf0880.pro
8456_orf1139.pro
Cyanothece sp. EAZ92180.pro
Mesorhizobium sp. YP_665837.pro
Sphingopyxis YP_617595.pro
Aurantimonas sp. ZP_01227146.pro
Sphingomomas BAA22987.pro
Planctomyces EDL56759.pro
Sulfitobacter sp. ZP_00964321.pro
R. sphaeroides ZP_00915817.pro
R. sphaeroides ZP_00918496.pro
Arthrobacter sp. ZP_00413206.pro
Mesorhizobium sp. YP_676050.pro
Oceanicola ZP_01000316.pro
X.campestris YP_243267.pro
Methylobacterium EDO73824.pro
Methylobacterium sp. EDK95996.pro
Methylobacillus YP_545551.pro
P. stutzeri ABP80913.pro
Endyra ABR10295.pro
Neovision ABS87659.pro
Phoca BAF58168.pro
Phoca BAB20377.pro
Halichoerus CAF18539.pro
Medicago ABC59081.pro
Pisum AAG44132.pro
Vitis CAO18249.pro
Oryza EAY85017.pro
Mentha Q42716.pro
Nodularia EAW46122.pro
Tribolium XP_971612.pro
Corynebacterium NP_739069.pro
Enterococcus ZP_00604550.pro
Arthrobacter sp. ABK05741.pro
79.4
84.7
43.4
84.7
97.8
38.9
68.8
50.5
38.5
15.8
18.9
47.9
NA
99.6
93.4
72.2
73.1
40.9
3.0
100.0
50.2
67.4
89.4
54.0
72.3
49.7
98.0
55.9
39.1
57.1
52.4
35.6
100.0
68.8
100.0
90.5
52.8
46.1
90.7
98.9
23.7
57.6
308.0
300
250
200
150
100
50
0
Amino Acid Substitutions (x100)
Bootstrap Trials = 1000, seed = 111

FIG. 44

G-D-S-L-X(5)-M (SEQ ID NO:28), wherein:

the Ser residue at position 3 is a catalytic residue;
the Asp residue at position 2 may be substituted with Asn or Thr; the Leu residue at position 4 may be substituted with Cys or Gln; the Met residue at position 10 may be substituted with Cys, Asp, Leu, Asn, Thr, or Val;

and

V-X(2)-G-X-N-D-X-L (SEQ ID NO:29), wherein:

the Asn residue at position 7 is in the oxyanion hole;
the Val residue at position 1 may be substituted with Leu;
the Asn residue at position 6 may be substituted with Val, Leu, Cys, Ala, Gly, His, Ile, Thr, or Trp;
the Asp residue at position 7 may be substituted with Glu;
the Leu residue at position 9 may be substituted with Ile, Trp, Phe, Thr, Met, Ala, Glu, Asn, or Val;

and

D-X(2)-H-P-X(7)-I (SEQ ID NO:30), wherein:

the Asp and His residues at positions 1 and 4, respectively, are the catalytic residues;
the Pro residue at position 5 may be substituted with Gly, Ala, Phe, Leu, Ser, or Val;
the Ile residue at position 13 may be substituted with Leu or Val.

FIG. 45A

POSITION	MUTATION	1PNP_MOD_Z_C10	1PNP_MOD_Z_C12	1PNP_MOD_Z_C14
1	A1S	6.394	11.580	20.629
7	L7M	6.757	10.090	5.929
7	L7V	8.265	9.279	2.303
9	D9N	15.267	13.647	15.639
12	S12A	4.555	3.215	1.903
13	A13D	3.735	0.903	-0.729
13	A13V	1.335	2.360	4.034
14	G14S	8.257	2.097	0.756
14	G14T	-1.567	0.967	4.298
14	G14V	11.223	18.158	34.850
15	Y15E	-4.756	2.142	10.078
15	Y15V	-7.702	-0.520	8.702
16	R16G	14.325	9.226	9.948
16	R16L	4.133	3.273	2.956
16	R16M	3.672	2.753	2.318
16	R16N	4.646	3.498	3.499
16	R16P	18.984	9.296	9.170
16	R16T	3.488	3.178	1.476
17	M17C	6.067	4.794	3.792
17	M17D	1.338	2.867	3.168
17	M17L	3.438	2.420	2.893
17	M17N	-0.090	3.106	4.076
17	M17T	4.221	3.513	3.074
17	M17V	6.474	2.281	2.390
20	S20A	4.359	3.370	3.415
20	S20C	4.227	3.784	2.849
20	S20D	5.378	4.972	4.722
20	S20G	8.105	7.279	7.378
20	S20L	5.108	4.383	4.563
20	S20T	4.956	4.936	4.330
20	S20W	3.016	3.156	3.283
21	A21G	2.006	2.215	3.213
21	A21P	2.704	3.717	1.674
22	A22N	5.224	3.894	6.827
24	P24V	6.943	3.729	2.463
25	A25D	2.272	3.185	2.194
25	A25E	4.782	4.521	6.391
25	A25L	4.174	4.394	2.472
25	A25N	3.676	3.556	5.959
25	A25Q	4.144	4.118	6.491
25	A25V	6.800	7.356	12.294
26	L26Q	2.404	2.435	4.533

FIG. 45A Cont.				
26	L26V	1.964	2.454	4.533
28	N28K	1.848	2.279	4.313
28	N28R	5.484	4.999	2.939
35	T35L	1.142	4.391	1.387
35	T35Y	1.199	3.823	1.851
36	S36H	1.023	1.356	3.701
38	V38F	2.942	3.043	4.848
39	N39A	10.899	5.838	2.829
39	N39Q	-4.841	0.211	4.206
40	A40G	1.657	1.721	4.380
40	A40V	1.830	5.274	6.003
42	I42A	3.954	6.892	4.294
42	I42C	2.384	3.148	1.925
42	I42D	-2.516	4.972	8.169
42	I42E	3.313	4.990	3.795
42	I42G	0.206	6.193	8.664
42	I42L	4.257	5.214	3.866
42	I42M	2.715	3.983	3.127
42	I42S	3.726	7.405	6.433
42	I42T	3.416	3.318	3.326
42	I42W	5.408	5.595	4.665
42	I42Y	3.969	4.791	3.842
43	S43A	3.516	6.311	3.717
43	S43D	5.985	8.842	6.907
43	S43E	3.582	4.171	3.005
43	S43F	-11.125	-0.402	12.329
43	S43L	16.778	17.685	15.484
43	S43M	2.612	5.188	4.064
43	S43N	9.913	6.791	3.931
43	S43W	-7.274	1.086	11.516
44	G44F	-5.359	0.298	13.270
44	G44M	-12.661	-2.567	4.780
44	G44Y	2.451	1.502	8.818
45	D45A	-0.294	7.110	12.755
45	D45C	-6.455	1.912	7.439
45	D45E	-1.230	3.649	3.532
45	D45F	-4.849	0.586	4.376
45	D45G	-6.106	2.534	16.202
45	D45Q	-7.477	0.879	9.370
45	D45S	-7.344	-0.597	7.240
45	D45T	-6.113	1.664	6.578
45	D45W	-1.352	3.401	5.645
46	T46A	-1.206	4.649	8.853

FIG. 45A Cont.				
46	T46C	-0.158	6.112	9.179
46	T46D	-2.233	4.810	18.146
46	T46G	-2.206	8.812	24.221
46	T46L	3.091	-9.678	-9.140
46	T46N	1.300	6.292	5.688
46	T46S	1.575	7.837	12.557
46	T46V	3.620	-0.054	-3.090
46	T46W	-8.251	0.760	13.198
47	S47A	3.529	-7.577	-12.577
47	S47M	9.633	-2.784	-5.012
48	Q48F	-1.201	1.752	6.042
48	Q48M	-0.580	1.282	4.104
48	Q48T	4.000	2.879	1.431
48	Q48V	3.521	5.933	11.056
48	Q48W	3.544	4.791	8.102
48	Q48Y	2.699	4.581	9.029
49	Q49A	3.075	7.455	13.528
49	Q49C	4.129	7.572	12.456
49	Q49D	3.858	7.266	15.064
49	Q49E	0.055	4.704	13.375
49	Q49G	4.621	9.500	17.760
49	Q49H	3.926	6.799	9.786
49	Q49I	1.460	6.572	13.667
49	Q49K	-1.162	2.210	3.123
49	Q49L	3.327	6.028	9.720
49	Q49M	3.427	5.613	8.580
49	Q49R	-1.520	1.685	3.754
49	Q49S	5.086	9.440	18.283
49	Q49V	2.715	7.616	14.223
49	Q49W	0.828	5.899	14.478
49	Q49Y	2.372	5.654	9.781
50	G50A	5.543	9.039	18.106
50	G50C	-3.097	4.373	16.692
50	G50F	-10.720	-3.587	9.503
50	G50L	-8.672	0.760	16.872
50	G50M	-4.800	3.932	21.633
50	G50N	-13.424	-7.278	4.358
50	G50Q	3.493	12.040	35.531
50	G50S	1.734	6.818	17.432
50	G50T	-5.130	0.190	10.072
51	L51A	3.336	3.415	3.086
51	L51C	1.954	2.391	3.215
52	A52H	1.944	2.621	4.263

FIG. 45A Cont.				
52	A52L	1.102	2.133	4.436
52	A52M	3.578	4.394	6.355
52	A52R	1.914	2.434	3.812
52	A52W	1.736	3.672	9.699
52	A52Y	0.370	1.666	3.212
53	R53A	1.209	7.046	13.260
53	R53E	-9.522	-4.303	4.973
53	R53I	-1.622	4.962	16.230
53	R53K	-1.692	1.524	6.340
53	R53L	-4.533	1.906	12.539
53	R53N	-2.528	2.000	7.059
53	R53S	-2.788	1.701	6.482
53	R53V	-0.921	5.737	17.575
56	A56R	2.198	2.171	3.566
56	A56W	2.282	2.445	5.129
56	A56Y	1.802	2.064	4.384
58	L58I	2.722	2.920	3.325
66	V66I	1.736	2.860	4.030
68	V68L	3.914	4.070	3.982
69	E69G	-2.706	0.579	3.911
69	E69Q	-3.745	-0.973	8.478
69	E69S	-1.111	1.609	7.270
70	L70T	-1.234	11.389	20.877
70	L70V	0.646	4.270	5.541
72	G72A	14.643	5.142	18.492
73	N73A	-2.509	0.071	7.473
73	N73C	0.690	2.962	14.842
73	N73G	-12.646	-5.398	13.811
73	N73L	2.964	10.775	46.587
73	N73V	-3.024	1.071	16.512
74	D74E	-7.071	0.624	11.720
75	G75A	2.975	-2.755	13.425
75	G75K	-1.950	-6.794	6.570
75	G75M	1.306	-8.006	3.391
76	L76A	-3.537	-8.281	7.135
76	L76E	-5.399	-9.182	3.000
76	L76F	1.580	1.298	24.980
76	L76I	3.841	5.135	28.435
76	L76M	5.727	3.927	11.869
76	L76N	-2.468	-6.507	6.317
76	L76T	-0.255	-4.430	12.575
76	L76V	-4.196	-4.995	3.901
76	L76W	13.746	6.221	34.187

FIG. 45A Cont.				
77	R77A	-3.079	-0.533	9.859
77	R77C	0.461	5.456	21.068
77	R77D	-2.838	2.127	12.211
77	R77E	-4.589	2.902	16.241
77	R77F	-1.292	2.850	22.678
77	R77G	7.203	11.587	27.111
77	R77H	-5.359	-2.852	8.936
77	R77K	1.376	3.625	6.073
77	R77L	10.539	10.057	17.946
77	R77N	-0.025	2.762	10.326
77	R77Q	6.394	4.821	3.779
77	R77S	0.104	4.522	13.675
77	R77V	-1.637	5.296	30.686
77	R77W	0.720	4.567	29.256
78	G78A	3.983	-0.533	-3.270
79	F79A	3.124	-3.257	-6.141
79	F79D	4.524	-4.371	-11.941
79	F79E	3.348	-5.838	-13.264
79	F79G	5.101	-2.922	-5.652
79	F79M	-0.425	1.923	10.143
79	F79V	0.611	2.531	3.984
79	F79W	4.875	-2.198	-5.513
79	F79Y	3.484	1.699	1.233
80	Q80G	-0.466	4.758	20.284
80	Q80L	0.197	1.684	5.931
80	Q80M	2.809	4.351	10.080
80	Q80S	0.014	3.640	12.533
80	Q80W	0.534	2.981	8.956
80	Q80Y	1.256	3.247	11.036
81	P81A	-0.430	3.378	5.476
81	P81E	1.832	4.174	7.861
81	P81K	1.207	3.924	8.595
81	P81L	0.378	4.145	3.931
81	P81M	-2.990	3.056	5.618
81	P81W	0.666	5.866	15.345
81	P81Y	3.189	5.997	9.827
82	Q82F	0.609	3.479	7.065
82	Q82I	1.002	2.176	5.633
82	Q82N	-1.675	1.981	3.202
82	Q82P	-1.744	2.992	8.294
82	Q82T	3.210	1.693	1.736
82	Q82V	2.235	3.292	3.811
82	Q82W	1.434	5.370	12.954

FIG. 45A Cont.

82	Q82Y	1.101	4.214	9.354
83	Q83A	6.362	7.643	5.270
84	T84S	0.270	2.141	3.881
86	Q86A	11.786	12.454	13.768
86	Q86T	10.110	11.117	15.340
87	T87A	-0.037	2.065	5.832
87	T87C	-0.229	2.934	9.499
87	T87E	1.415	3.575	5.069
87	T87F	-1.975	0.230	12.052
87	T87G	-0.739	2.096	6.515
87	T87H	-0.673	2.639	9.426
87	T87L	-0.419	3.398	14.653
87	T87M	-0.551	1.374	4.720
87	T87V	1.404	2.950	5.025
87	T87W	-0.755	2.064	10.109
91	I91L	2.206	2.297	3.351
91	I91V	6.585	5.278	4.212
92	L92V	3.616	3.994	4.208
93	Q93A	5.091	4.992	4.817
93	Q93E	3.105	2.687	2.646
93	Q93G	3.130	3.245	3.007
93	Q93H	3.975	3.697	4.434
93	Q93I	3.468	3.105	3.551
93	Q93Y	3.010	3.046	3.534
94	D94G	3.178	1.754	1.189
94	D94K	3.315	1.934	1.442
94	D94V	3.440	2.590	2.720
95	V95L	4.707	7.185	10.389
95	V95M	1.595	2.323	3.021
95	V95T	3.638	4.230	4.113
96	K96A	2.873	3.606	3.557
96	K96L	2.738	3.675	3.829
96	K96Y	3.791	4.548	4.760
97	A97K	2.718	3.068	2.788
97	A97W	2.510	2.579	3.691
98	A98K	2.626	2.900	3.829
98	A98L	2.724	3.677	5.565
98	A98W	3.024	3.845	5.805
99	N99C	2.700	3.443	2.569
99	N99G	4.074	4.878	3.934
99	N99L	4.330	4.878	4.479
99	N99M	2.867	3.104	2.038
99	N99P	3.020	3.900	3.152

FIG. 45A Cont.				
99	N99Q	3.088	3.415	3.069
99	N99R	4.286	5.058	4.131
99	N99W	2.850	3.827	1.514
99	N99Y	5.543	4.922	4.730
100	A100G	4.451	4.465	4.153
100	A100H	0.957	3.338	5.958
100	A100I	1.009	3.065	4.565
100	A100K	1.952	6.498	9.431
100	A100R	-0.695	1.432	3.879
100	A100T	0.930	2.475	4.441
100	A100V	3.365	7.715	11.388
101	E101A	3.144	2.270	1.757
101	E101G	5.108	4.874	5.154
101	E101L	7.257	7.646	8.984
101	E101M	3.983	4.000	3.570
101	E101S	4.213	4.112	4.699
101	E101T	5.114	4.805	6.246
101	E101V	4.472	5.342	5.700
102	P102S	4.145	5.235	6.224
105	M105C	3.337	3.633	7.462
105	M105I	3.337	2.850	5.146
105	M105L	0.486	0.666	4.783
105	M105V	5.143	5.027	11.562
106	Q106A	3.307	5.346	4.692
106	Q106C	1.652	3.004	3.267
106	Q106D	-0.831	-5.674	4.967
106	Q106G	0.911	3.061	6.930
106	Q106H	3.551	2.788	11.614
106	Q106K	0.523	4.879	6.237
106	Q106M	1.581	1.185	6.878
106	Q106R	1.323	4.645	8.251
106	Q106S	2.178	5.220	10.217
106	Q106T	2.225	3.935	5.199
106	Q106V	-0.434	0.829	6.395
106	Q106W	7.654	0.324	16.161
106	Q106Y	1.290	2.930	4.395
107	I107C	1.869	7.490	8.798
107	I107L	1.267	8.935	13.483
107	I107M	1.316	4.696	6.909
107	I107Q	-1.349	2.297	5.374
107	I107V	1.727	5.387	5.546
108	R108A	2.439	-2.014	5.537
108	R108D	6.314	-0.089	10.152

FIG. 45A Cont.				
108	R108F	5.682	3.958	4.773
108	R108I	3.876	-2.651	5.136
108	R108L	0.689	-6.243	5.281
108	R108S	3.181	-0.031	7.566
108	R108V	0.722	-3.072	6.040
108	R108W	18.196	12.645	5.488
108	R108Y	3.304	-0.165	7.301
109	L109M	0.743	4.940	8.682
109	L109V	1.441	-1.769	4.328
110	P110E	3.550	0.955	3.314
110	P110F	5.785	-6.804	-1.807
110	P110N	4.801	-5.215	3.764
110	P110W	3.459	-6.699	-1.484
111	A111C	12.672	4.560	6.257
111	A111L	5.262	1.291	4.013
111	A111Q	4.678	3.109	3.253
111	A111R	3.287	1.936	3.705
111	A111V	4.883	2.693	8.461
111	A111W	9.964	8.699	12.177
112	N112A	4.144	4.774	15.787
112	N112F	3.115	2.537	7.389
112	N112G	3.637	4.620	10.565
112	N112I	0.819	0.171	11.828
112	N112L	-3.870	-3.621	4.766
112	N112P	1.980	2.011	11.645
112	N112V	2.140	1.583	13.793
112	N112W	3.839	4.910	19.845
112	N112Y	-0.190	1.507	11.835
113	Y113A	3.598	4.764	9.665
113	Y113D	0.785	2.906	4.157
113	Y113G	3.788	3.762	4.740
113	Y113I	5.657	5.345	7.568
113	Y113M	3.602	2.503	5.842
114	G114F	0.911	1.324	4.351
114	G114K	4.656	4.586	4.314
114	G114L	3.867	5.743	12.412
114	G114M	2.565	5.242	13.172
114	G114W	0.253	0.903	3.468
114	G114Y	1.840	4.894	14.604
115	R115A	4.529	3.272	8.124
115	R115C	4.177	3.552	6.305
115	R115E	4.847	3.429	8.136
115	R115G	4.070	5.954	16.468

FIG. 45A Cont.				
115	R115I	2.218	2.090	4.740
115	R115N	3.044	4.272	7.232
115	R115Q	2.297	2.565	3.644
115	R115S	3.737	4.546	7.056
115	R115W	3.879	2.470	7.235
115	R115Y	3.224	3.648	9.522
116	R116C	2.854	2.857	3.579
116	R116D	3.327	2.880	2.274
116	R116H	2.748	3.277	4.951
116	R116T	2.464	2.657	3.147
116	R116V	2.951	2.874	4.116
116	R116W	3.104	5.198	14.499
117	Y117C	6.675	6.817	4.454
117	Y117H	2.743	4.861	4.621
117	Y117I	5.647	5.993	4.154
117	Y117L	4.993	7.391	6.723
117	Y117M	2.081	5.075	5.217
117	Y117N	3.349	4.700	3.926
117	Y117S	5.030	5.742	4.660
117	Y117T	5.542	5.207	1.889
117	Y117V	6.015	5.039	1.300
117	Y117W	-2.334	0.471	7.263
118	N118H	0.512	1.428	6.319
118	N118L	1.598	0.958	8.703
118	N118M	2.010	2.961	6.341
118	N118P	-0.832	-1.966	5.482
118	N118W	3.397	1.114	4.463
119	E119C	6.373	5.141	7.221
119	E119D	2.931	2.142	4.557
119	E119F	5.693	5.823	10.266
119	E119K	7.496	8.591	15.835
119	E119M	4.702	3.479	5.351
119	E119P	0.089	-3.003	9.754
119	E119R	8.707	9.759	17.979
119	E119T	2.287	2.383	3.146
119	E119W	9.580	10.352	19.702
119	E119Y	9.350	9.436	15.291
120	A120D	4.191	3.321	3.841
120	A120G	4.420	5.180	8.547
120	A120I	0.912	3.418	7.663
120	A120L	1.580	1.987	3.530
120	A120T	1.659	3.057	4.009
120	A120W	3.462	6.175	16.518

FIG. 45A Cont.

121	F121A	-3.589	-10.094	5.171
121	F121C	-0.082	-2.789	9.095
121	F121L	-5.058	-5.323	11.514
121	F121M	5.655	0.053	7.119
121	F121V	0.041	0.880	3.163
121	F121Y	5.012	2.070	12.144
122	S122A	2.242	1.706	6.562
122	S122C	-0.273	-0.816	4.001
122	S122D	1.254	-0.098	3.277
122	S122E	1.103	-4.994	7.905
122	S122F	7.194	10.424	21.883
122	S122G	0.956	0.171	7.614
122	S122I	4.496	10.648	14.247
122	S122L	3.754	7.072	21.707
122	S122M	3.706	5.077	4.995
122	S122P	-1.009	-2.338	10.147
122	S122V	3.999	8.868	16.170
122	S122W	4.006	6.033	19.886
122	S122Y	5.510	9.236	22.214
123	A123C	2.585	4.047	3.338
123	A123E	2.551	2.618	3.222
123	A123F	2.687	3.711	5.874
123	A123H	3.250	6.451	5.071
123	A123L	3.577	6.736	6.773
123	A123R	1.525	4.273	2.798
123	A123T	2.814	4.735	7.298
123	A123V	3.161	6.871	7.478
123	A123W	2.648	6.055	7.330
123	A123Y	2.962	4.380	8.914
124	I124A	-0.562	1.899	3.815
124	I124C	0.236	1.648	3.855
124	I124L	1.512	3.595	4.736
125	Y125F	4.483	4.223	8.143
125	Y125W	5.467	0.988	2.558
126	P126H	2.813	4.522	3.032
126	P126Y	3.280	4.782	4.765
132	F132E	3.891	2.969	1.705
133	D133K	4.876	4.529	5.272
133	D133Y	3.220	2.963	3.695
134	V134S	3.028	2.367	3.015
136	L136M	2.870	2.522	6.068
139	F139W	3.157	0.616	-0.147
140	F140C	5.288	-1.783	-1.192

FIG. 45A Cont.				
140	F140M	9.127	7.726	9.142
141	M141A	19.387	7.458	8.597
141	M141C	24.744	13.096	16.316
141	M141D	3.833	-9.983	-11.956
141	M141F	7.928	-0.323	-1.087
141	M141G	8.556	0.266	-1.457
141	M141L	26.699	7.856	12.106
141	M141P	28.456	11.233	15.930
141	M141T	16.276	-2.612	-3.803
141	M141V	5.450	2.714	2.404
141	M141W	22.542	-6.189	-11.732
141	M141Y	7.007	-2.350	-2.470
142	E142C	8.448	3.735	9.778
142	E142L	-3.282	-4.875	3.795
142	E142M	-2.761	-2.385	3.791
142	E142N	1.555	1.436	4.438
142	E142P	3.497	-5.193	5.681
142	E142Q	0.112	-5.551	3.055
142	E142W	5.517	-0.083	1.084
143	E143P	1.430	1.276	3.559
145	Y145A	7.436	2.636	1.728
145	Y145C	3.459	-0.037	-1.380
145	Y145D	14.809	2.255	0.802
145	Y145E	17.603	3.655	1.660
145	Y145G	6.679	1.119	0.709
145	Y145L	19.163	2.153	0.684
145	Y145M	20.306	2.929	2.071
145	Y145N	5.399	1.985	1.132
145	Y145Q	10.267	1.374	1.497
145	Y145T	12.043	1.401	0.033
145	Y145W	3.067	0.831	1.859
146	L146A	3.575	1.649	1.428
146	L146C	4.149	1.316	1.323
146	L146D	4.297	1.036	0.012
146	L146E	3.500	1.346	0.616
146	L146G	6.333	1.300	2.477
146	L146H	4.022	0.923	0.846
146	L146S	4.476	1.765	2.197
146	L146W	6.590	1.383	1.912
147	K147P	12.887	0.241	0.155
149	Q149L	1.904	3.314	1.490
151	M151C	5.917	-0.371	2.395
151	M151I	8.570	-1.585	3.131

FIG. 45A Cont.				
151	M151T	4.843	-0.831	2.369
151	M151V	12.233	-0.991	3.783
152	Q152L	8.055	2.425	1.226
153	D153I	-0.251	-1.341	5.536
153	D153K	0.496	4.381	24.183
153	D153M	-0.031	-0.252	6.594
153	D153W	0.825	1.942	5.668
155	G155F	0.748	4.224	17.841
155	G155H	0.577	0.713	4.600
155	G155W	1.260	3.722	25.886
155	G155Y	1.028	4.734	24.337
156	I156C	0.643	4.084	14.550
156	I156F	-1.220	5.882	21.266
156	I156M	1.352	3.366	5.773
156	I156V	1.058	8.647	28.646
158	P158A	28.337	25.604	23.049
158	P158F	4.767	-13.452	-15.087
158	P158G	15.067	18.931	18.163
158	P158S	1.396	2.691	3.567
159	N159C	3.930	2.253	1.220
159	N159G	5.704	6.742	8.472
159	N159I	6.698	0.339	-1.825
159	N159K	3.480	1.811	0.050
159	N159T	9.890	5.559	4.096
159	N159V	7.525	3.005	0.453
160	R160A	9.519	6.024	3.348
160	R160C	3.506	2.581	1.641
160	R160D	8.278	4.382	2.706
160	R160E	5.409	3.130	1.951
160	R160G	7.865	5.128	4.129
160	R160H	5.935	4.122	4.113
160	R160N	6.060	4.902	3.730
160	R160Q	5.514	3.157	0.989
160	R160S	7.526	4.396	1.913
160	R160W	4.083	3.664	4.125
161	D161G	3.772	2.804	4.563
161	D161I	4.057	3.561	5.100
161	D161K	4.293	3.763	5.362
161	D161L	4.309	5.132	5.641
161	D161M	4.022	4.129	4.522
161	D161N	1.985	3.184	4.521
161	D161Q	3.578	3.372	4.481
161	D161R	3.649	2.933	4.841

FIG. 45A Cont.				
161	D161S	2.066	2.033	3.739
161	D161V	2.584	2.273	4.309
161	D161W	6.250	5.868	8.648
162	A162G	1.092	2.969	4.532
163	Q163G	9.939	14.921	22.736
163	Q163L	5.669	7.675	11.903
163	Q163M	6.592	6.612	10.149
163	Q163S	11.573	17.725	20.165
164	P164A	3.492	2.729	3.086
164	P164C	7.690	10.246	19.449
164	P164D	3.378	2.709	1.181
164	P164K	2.978	2.832	3.739
164	P164L	2.884	2.488	3.158
164	P164M	4.425	4.031	3.981
164	P164N	3.045	2.408	3.364
164	P164R	3.349	2.698	4.469
164	P164T	2.855	1.824	3.006
164	P164V	3.112	2.173	2.366
164	P164W	3.153	2.758	3.762
165	F165G	2.593	0.257	3.167
165	F165H	4.419	2.655	6.687
165	F165K	4.942	-2.230	-3.292
165	F165M	7.251	0.917	-0.403
165	F165R	4.877	-2.313	-1.664
165	F165S	4.960	1.864	3.145
165	F165T	5.339	-2.331	-3.829
165	F165W	0.010	0.235	4.654
165	F165Y	3.225	2.345	3.191
166	I166L	18.318	14.606	16.175
166	I166V	4.327	4.575	6.647
167	A167C	4.510	3.914	1.380
167	A167T	11.776	8.525	9.337
168	D168A	2.457	2.548	4.035
168	D168G	3.636	4.073	4.581
168	D168H	2.674	3.053	3.474
168	D168R	3.855	3.280	6.154
168	D168T	2.600	2.800	3.557
169	W169A	2.642	5.199	5.873
169	W169E	4.386	6.114	6.052
169	W169K	4.477	3.840	13.096
169	W169Q	5.338	6.843	7.989
169	W169R	1.304	1.991	5.210
169	W169S	2.189	3.655	4.112

FIG. 45A Cont.

169	W169T	1.785	2.162	6.470
169	W169V	1.067	0.726	3.672
170	M170F	4.885	3.909	3.829
170	M170V	3.485	3.100	4.452
172	K172M	4.747	3.595	2.023
173	Q173N	4.134	3.905	5.313
173	Q173W	1.146	1.915	3.827
175	Q175I	3.342	3.221	3.491
175	Q175Y	2.746	2.780	3.254
176	P176H	4.015	4.074	5.270
176	P176K	3.495	3.084	3.649
176	P176L	2.672	3.069	3.829
176	P176N	3.029	3.025	2.671
176	P176R	2.964	2.174	3.241
176	P176W	3.269	3.097	3.591
176	P176Y	2.764	2.738	3.305
178	V178T	3.190	2.694	4.114
178	V178W	3.680	2.786	3.353
179	N179G	3.629	2.391	1.826
179	N179H	4.365	3.812	4.765
179	N179R	4.654	3.519	5.557
179	N179T	3.572	2.829	5.611
179	N179V	4.917	2.799	6.588
179	N179Y	4.669	3.002	3.265
180	H180A	2.979	3.267	2.634
180	H180G	3.183	3.983	3.849
180	H180R	4.458	2.264	4.203
180	H180S	1.578	1.692	4.349
180	H180V	3.685	2.490	2.811
180	H180W	3.961	2.513	6.242
181	D181A	3.031	2.584	3.438
181	D181H	5.520	3.286	7.065
181	D181I	3.956	3.717	5.388
181	D181L	5.749	4.543	9.373
181	D181P	3.013	2.523	2.960
181	D181Q	2.775	2.594	3.340
181	D181R	4.136	3.057	5.542
181	D181S	2.912	2.871	3.726
181	D181W	3.880	3.401	4.580
182	S182A	3.017	2.728	3.484
182	S182G	3.546	2.190	6.319
182	S182I	2.625	2.695	3.706
182	S182K	8.925	8.192	7.944

FIG. 45A Cont.				
182	S182L	5.685	4.213	6.957
182	S182P	5.587	4.401	8.903
182	S182Q	2.495	0.896	4.219
182	S182R	4.486	3.007	6.811
182	S182T	2.619	1.235	5.003

FIG. 45B

POSITION	MUTATION	[1]MOD_Z_SUBSSPEC_C10	[1]MOD_Z_SUBSSPEC_C12	[1]MOD_Z_SUBSSPEC_C14
1	A1L	48.514	-37.653	-2.752
1	A1Q	-2.486	6.325	-9.186
1	A1S	-23.759	5.850	28.101
1	A1V	-2.350	7.164	-11.124
2	D2E	-0.668	3.150	-5.543
2	D2K	-0.305	5.631	-11.357
2	D2P	-6.441	5.960	-1.667
2	D2W	-3.805	7.712	-9.961
3	T3K	5.877	-2.945	-3.760
3	T3R	-2.123	5.157	-7.326
3	T3W	-2.285	3.375	-4.461
4	L4A	3.568	3.162	-14.912
4	L4S	0.968	-2.325	3.295
4	L4Y	-15.139	4.369	17.118
5	L5F	-3.514	8.841	-8.569
5	L5G	-11.850	9.755	-0.504
5	L5H	-5.668	-18.894	49.806
5	L5S	-6.262	6.972	-0.005
5	L5Y	-19.759	10.741	10.891
6	I6T	-3.743	7.482	-5.797
6	I6V	-9.941	6.836	2.442
7	L7A	-5.015	11.193	-9.807
7	L7C	-9.123	4.609	5.775
7	L7M	-1.148	3.062	-3.124
7	L7N	-23.486	17.456	3.062
7	L7S	-21.759	9.573	16.783
7	L7T	-17.077	11.361	5.000
7	L7V	3.865	1.108	-9.460
7	L7Y	-24.305	10.558	19.031
8	G8S	-13.718	2.133	11.525
9	D9N	5.692	-7.515	5.187
9	D9T	-40.636	-2.082	46.771
11	L11C	-35.128	-5.595	46.137
11	L11I	-13.652	-0.536	15.468

FIG. 45B Cont.				
11	L11M	-32.833	6.911	24.870
11	L11Q	-41.620	-0.115	44.870
11	L11V	-19.849	-6.977	31.806
12	S12A	6.708	-2.948	-2.736
12	S12I	-26.505	14.101	7.264
12	S12L	-21.879	0.349	26.470
12	S12M	-17.035	0.167	20.715
12	S12T	-7.390	2.766	3.778
12	S12V	-25.521	15.319	4.377
13	A13C	-9.325	4.944	2.581
13	A13D	32.086	-15.227	-22.702
13	A13G	-28.452	26.850	-2.137
13	A13H	-12.806	8.058	5.847
13	A13I	-14.177	3.234	10.398
13	A13L	-30.387	5.884	35.766
13	A13N	-3.062	3.141	-1.433
13	A13T	-12.269	3.614	12.379
13	A13V	-4.275	-0.630	5.539
13	A13W	-26.301	23.469	0.282
14	G14A	15.742	-13.198	-1.573
14	G14E	5.397	0.611	-6.750
14	G14F	-44.312	6.850	55.040
14	G14I	-37.226	8.878	26.630
14	G14K	-24.419	35.111	-22.056
14	G14M	-16.669	15.904	-6.011
14	G14P	15.233	-7.375	-5.306
14	G14Q	25.688	-15.179	-13.185
14	G14R	6.925	-14.406	13.589
14	G14S	22.348	-11.496	-6.715
14	G14T	-12.570	1.759	10.891
14	G14V	-18.570	-5.806	28.673
15	Y15A	-75.656	19.556	80.927
15	Y15C	-39.128	12.344	23.426
15	Y15D	-74.258	43.275	39.073
15	Y15E	-32.800	6.091	26.067
15	Y15G	-47.292	12.391	32.158
15	Y15I	-44.407	13.117	27.968
15	Y15L	-73.290	30.039	59.718
15	Y15M	-73.452	24.000	70.121
15	Y15N	-43.062	23.117	11.489
15	Y15Q	-72.323	25.932	65.202
15	Y15R	-92.269	17.478	109.234
15	Y15S	-75.065	25.546	69.960
15	Y15V	-41.259	7.801	32.581

FIG. 45B Cont.				
16	R16D	-8.774	7.575	0.524
16	R16E	-5.011	7.720	-5.363
16	R16G	28.215	-21.411	-6.573
16	R16H	-7.914	9.169	-3.427
16	R16I	-0.280	3.855	-6.008
16	R16L	8.269	-4.406	-5.040
16	R16M	9.344	-4.647	-6.250
16	R16N	9.935	-6.821	-3.508
16	R16P	51.387	-35.710	-17.460
16	R16Q	4.075	-0.155	-5.847
16	R16S	-5.871	4.193	1.815
16	R16T	3.495	-0.583	-2.877
16	R16V	-6.086	8.203	-4.556
16	R16W	-23.129	7.092	22.863
17	M17A	-3.645	3.664	-2.657
17	M17C	6.282	-3.557	-1.398
17	M17G	-9.032	5.122	3.684
17	M17K	-13.259	7.042	6.617
17	M17L	4.052	-3.628	1.102
17	M17N	-11.390	4.171	5.996
17	M17P	-20.005	6.222	21.479
17	M17Q	-5.632	3.510	1.479
17	M17R	-35.521	17.215	12.264
17	M17S	-11.030	5.576	3.461
17	M17T	3.889	-2.597	-0.271
17	M17V	14.905	-9.201	-2.173
18	S18M	0.112	7.232	-3.934
18	S18N	0.015	9.473	-5.033
19	A19L	-6.717	17.108	-2.989
21	A21I	-3.083	3.373	0.989
21	A21L	-4.278	4.701	1.385
21	A21Y	-5.124	4.452	-2.411
22	A22C	6.943	-2.433	-3.957
22	A22D	14.773	-5.646	-7.477
22	A22E	11.129	-2.711	-8.694
22	A22F	-12.514	11.321	-6.786
22	A22G	4.332	-4.220	-1.670
22	A22H	8.390	-2.695	-5.240
22	A22I	8.287	-2.334	-5.832
22	A22K	9.295	0.125	-12.082
22	A22L	-19.620	23.539	5.209
22	A22M	-11.636	6.813	1.109
22	A22N	4.307	-7.830	0.264
22	A22R	-6.132	11.008	-0.286

FIG. 45B Cont.				
22	A22Y	-19.310	6.748	11.043
23	W23Y	-1.403	-0.711	3.214
24	P24A	6.161	-3.805	-3.538
24	P24C	9.579	-3.072	-6.030
24	P24D	9.398	-5.564	-0.832
24	P24F	15.315	-4.793	-9.878
24	P24G	-7.553	4.764	0.056
24	P24I	13.817	1.190	-19.977
24	P24S	3.455	-1.630	-1.128
24	P24T	10.354	-2.892	-7.378
24	P24V	13.455	-6.072	-4.944
24	P24W	5.419	-0.007	-6.885
25	A25R	-5.375	3.096	0.902
26	L26C	-6.311	2.183	3.029
26	L26D	-6.712	6.234	-2.083
26	L26E	-2.278	3.954	-0.044
26	L26F	-16.378	7.429	5.473
26	L26G	-6.244	5.883	-2.051
26	L26H	-8.302	6.568	4.000
26	L26I	-1.937	3.000	0.176
26	L26K	-4.717	3.498	2.396
26	L26N	-8.819	6.422	-0.305
26	L26R	-3.717	3.166	1.670
26	L26S	-8.217	4.080	2.235
26	L26W	-9.254	6.984	-0.717
26	L26Y	-14.706	5.977	5.854
27	L27A	-8.050	7.944	-3.130
27	L27C	-5.059	9.017	-0.242
27	L27F	-6.512	3.963	0.806
27	L27M	-2.595	3.705	0.374
27	L27W	-12.365	14.970	-8.559
27	L27Y	-6.815	7.772	2.044
28	N28A	4.358	-1.564	-2.019
28	N28P	-5.254	2.668	3.319
28	N28W	-1.947	3.038	-1.930
29	D29P	-5.799	5.545	-1.589
29	D29V	-2.063	0.188	3.333
30	K30P	-4.941	4.702	0.439
31	W31E	-2.309	3.466	-2.047
31	W31N	-3.410	3.069	-0.543
32	Q32V	3.151	-1.954	-2.135
32	Q32Y	3.842	-2.646	-2.135
33	S33F	-1.224	-0.570	3.187
36	S36H	-0.796	-1.048	3.275

FIG. 45B Cont.				
37	V37F	-1.234	7.783	-4.023
37	V37H	-23.808	0.319	18.465
37	V37Q	1.461	-7.507	3.723
37	V37S	-11.174	17.420	-2.521
37	V37W	-4.480	4.142	0.643
38	V38D	-13.150	21.406	-3.554
38	V38E	8.287	-3.522	-4.164
38	V38G	-3.210	14.667	-6.981
38	V38K	3.078	-1.348	-1.535
38	V38P	-15.665	31.043	-7.826
38	V38R	4.395	-4.029	-0.831
39	N39A	7.740	-5.051	-4.795
39	N39C	-3.868	4.812	-0.080
39	N39E	-9.497	23.942	-8.061
39	N39F	-11.076	-1.921	23.099
39	N39G	-1.114	11.188	-6.371
39	N39M	-4.250	-0.603	8.626
39	N39Q	-34.766	16.333	16.681
39	N39T	8.287	-1.565	-5.526
39	N39V	-2.894	-1.279	3.632
39	N39W	-18.000	10.536	7.291
39	N39Y	-29.138	-9.609	29.122
40	A40D	6.311	7.420	-9.751
40	A40G	-2.671	-4.754	5.178
40	A40H	3.201	0.142	-2.847
40	A40L	-9.253	6.102	2.391
40	A40M	-2.431	4.957	-1.300
40	A40P	-30.635	15.391	14.052
40	A40T	-7.222	0.826	5.131
40	A40V	-7.301	1.738	4.670
40	A40Y	-2.431	11.696	-5.667
41	S41C	-8.846	6.593	1.365
41	S41P	-22.604	2.786	16.815
41	S41T	-28.989	16.352	9.998
42	I42D	-12.486	0.852	6.716
42	I42G	-10.282	-0.119	5.994
42	I42K	-4.953	4.980	-0.273
42	I42P	-19.197	10.716	5.013
42	I42S	-6.509	2.387	3.429
43	S43A	-4.055	3.085	0.698
43	S43C	3.201	-0.232	-2.530
43	S43F	-33.923	5.379	24.151
43	S43G	-22.314	13.085	7.221
43	S43H	-24.346	9.594	12.120

FIG. 45B Cont.				
43	S43L	-1.259	-3.574	4.309
43	S43P	8.821	-3.125	-4.720
43	S43R	-15.955	13.110	1.781
43	S43T	-14.768	9.244	4.264
43	S43V	-8.541	3.833	3.835
43	S43W	-25.190	2.711	19.095
44	G44A	-8.980	2.981	3.501
44	G44C	-31.232	10.541	17.176
44	G44E	-24.556	6.985	10.219
44	G44F	-20.625	-3.499	20.810
44	G44H	-29.042	9.120	16.612
44	G44K	-17.377	7.053	6.033
44	G44L	-42.261	13.110	24.309
44	G44M	-20.466	2.419	10.431
44	G44N	-19.648	5.213	8.372
44	G44Q	-36.536	13.110	19.388
44	G44R	-11.367	5.775	3.290
44	G44S	-24.088	4.446	11.374
44	G44W	-12.402	-7.257	11.249
44	G44Y	-4.272	-8.961	7.534
45	D45A	-27.495	3.323	57.388
45	D45C	-21.997	7.000	12.481
45	D45E	-10.071	5.579	3.564
45	D45F	-29.067	8.007	46.447
45	D45G	-48.829	0.424	119.153
45	D45H	-18.448	6.929	23.624
45	D45I	-6.720	5.653	0.630
45	D45K	-37.257	31.502	-7.671
45	D45L	-7.433	6.277	0.675
45	D45M	-26.257	11.576	28.094
45	D45P	-42.156	7.773	29.050
45	D45Q	-24.346	4.756	16.521
45	D45S	-21.074	3.733	14.648
45	D45T	-20.414	6.825	11.284
45	D45V	-10.335	5.180	4.151
45	D45W	-11.232	3.359	6.567
46	T46A	-14.214	2.511	9.862
46	T46C	-13.923	3.284	8.937
46	T46D	-36.257	-4.446	103.506
46	T46E	18.609	-6.192	-10.318
46	T46F	20.410	-4.483	-36.259
46	T46G	-45.971	-1.509	118.329
46	T46I	19.981	-1.435	-44.847
46	T46K	-11.876	7.822	4.565

FIG. 45B Cont.				
46	T46L	34.731	-19.608	-11.966
46	T46N	-9.385	4.506	3.971
46	T46R	-13.114	10.684	-1.435
46	T46S	-14.108	1.040	11.126
46	T46V	19.600	-4.892	-32.965
46	T46W	-28.066	2.012	22.210
47	S47A	57.886	-16.416	-91.082
47	S47C	21.248	-11.254	-7.971
47	S47E	-45.162	-9.539	141.859
47	S47F	8.082	-4.845	-2.530
47	S47G	18.557	-9.209	-7.564
47	S47L	29.665	-15.743	-11.131
47	S47M	27.607	-15.693	-9.415
47	S47P	-38.971	24.810	17.741
47	S47Q	-66.257	5.703	145.741
47	S47T	4.863	-3.648	-0.860
47	S47V	34.652	-19.085	-12.372
47	S47W	-27.776	-8.761	31.668
47	S47Y	-49.305	-2.513	129.741
48	Q48C	-2.921	-0.781	3.203
48	Q48D	19.124	-1.546	-42.376
48	Q48E	3.933	10.164	-41.906
48	Q48F	-9.042	-0.332	8.034
48	Q48G	4.230	-1.454	-2.327
48	Q48I	-3.554	0.017	3.023
48	Q48M	-5.876	-0.406	5.393
48	Q48S	6.886	-0.320	-16.024
48	Q48T	8.648	-3.257	-11.082
48	Q48V	-9.114	-5.450	39.624
48	Q48W	-4.114	-5.078	26.094
48	Q48Y	-7.876	-4.892	34.918
49	Q49A	-32.553	5.896	34.139
49	Q49C	-9.095	-2.526	10.088
49	Q49D	-28.813	-4.625	39.485
49	Q49E	-42.634	0.688	51.267
49	Q49G	-35.398	1.833	41.366
49	Q49H	-7.222	-1.529	7.582
49	Q49I	-40.276	7.667	41.762
49	Q49K	-7.776	3.185	3.767
49	Q49L	-20.195	3.604	21.267
49	Q49M	-16.211	2.771	17.109
49	Q49P	-28.383	16.576	9.275
49	Q49R	-27.431	15.167	18.990
49	Q49S	-32.959	-2.542	42.554

FIG. 45B Cont.				
49	Q49V	-36.455	7.354	37.406
49	Q49W	-43.122	3.188	49.485
49	Q49Y	-25.236	6.000	25.030
50	G50A	-28.650	-7.750	42.158
50	G50C	-69.057	7.250	77.208
50	G50E	-125.886	-16.708	169.188
50	G50F	-100.114	6.833	115.426
50	G50I	-119.951	14.646	132.158
50	G50K	-114.098	34.333	106.317
50	G50L	-104.341	10.167	117.406
50	G50M	-86.537	-1.708	107.109
50	G50N	-110.114	7.354	127.109
50	G50P	-20.185	5.821	24.955
50	G50Q	-68.081	-17.958	99.980
50	G50R	-18.604	6.226	21.722
50	G50S	-9.658	0.432	15.431
50	G50T	-19.026	5.720	23.175
50	G50W	-138.488	-14.833	182.752
50	G50Y	-132.797	3.188	158.693
51	L51C	-3.366	-0.563	4.634
51	L51D	-21.821	14.750	12.554
51	L51F	6.797	0.479	-8.733
51	L51H	3.463	1.000	-5.267
51	L51N	-2.959	5.583	-1.703
51	L51S	-2.472	-2.438	5.327
51	L51T	-6.134	5.568	1.972
51	L51V	-13.528	10.271	6.812
51	L51W	2.813	3.188	-6.356
51	L51Y	5.008	2.458	-8.436
52	A52C	-3.691	3.083	1.564
52	A52D	15.577	-4.417	-14.772
52	A52H	-6.293	-1.813	9.386
52	A52I	-10.927	1.938	11.465
52	A52L	-10.439	-1.500	14.139
52	A52M	-6.537	-2.333	10.079
52	A52P	-12.248	8.034	8.464
52	A52R	-4.911	-1.917	7.703
52	A52V	-5.967	0.375	6.911
52	A52W	-21.171	-7.958	33.347
52	A52Y	-2.715	0.889	3.175
53	R53A	-23.023	11.009	15.186
53	R53C	-17.173	8.372	16.158
53	R53D	-61.107	5.393	62.316
53	R53E	-53.598	10.416	49.405

FIG. 45B Cont.				
53	R53F	-22.670	7.561	26.509
53	R53G	-27.889	13.292	18.392
53	R53I	-33.215	7.447	29.700
53	R53K	-9.026	3.101	10.419
53	R53L	-39.575	9.411	34.848
53	R53N	-25.092	10.598	17.844
53	R53S	-25.284	11.146	17.591
53	R53T	-16.014	9.740	12.198
53	R53V	-32.257	6.580	29.489
53	R53W	-51.375	11.146	46.241
53	R53Y	-44.556	23.064	27.717
54	L54A	-0.494	6.215	-5.194
54	L54C	-0.341	3.566	-2.916
54	L54E	-7.697	11.055	-1.734
54	L54F	-8.732	13.064	-2.451
54	L54G	-8.195	11.922	-1.987
54	L54M	-4.517	11.100	-5.278
54	L54N	-8.540	11.192	-0.932
54	L54S	-5.360	10.598	-3.844
54	L54T	4.218	0.279	-4.857
54	L54W	-16.433	14.023	5.143
54	L54Y	-36.088	21.192	20.165
55	P55Y	-2.716	10.187	-6.460
56	A56P	4.908	-3.557	-2.114
56	A56W	-1.261	-3.740	4.848
56	A56Y	-1.682	-2.826	4.468
57	L57A	-0.292	3.416	-7.234
57	L57C	-1.542	3.810	-5.863
57	L57F	-10.431	4.348	8.411
57	L57K	-3.069	5.351	-6.669
57	L57P	-2.068	4.419	-3.115
57	L57Q	-0.708	9.401	-19.895
57	L57R	-4.042	6.427	-7.395
57	L57Y	-4.690	3.953	-0.702
58	L58A	-8.023	7.108	-1.992
58	L58D	-10.755	16.068	-17.476
58	L58E	-11.079	10.011	-3.202
58	L58F	-5.616	1.373	6.718
58	L58G	-16.773	13.129	-0.298
58	L58H	-11.727	9.652	-1.266
58	L58N	-9.227	9.545	-5.460
58	L58R	-4.523	5.466	-0.559
58	L58S	-9.782	9.509	-4.411
58	L58W	-8.903	8.434	-3.444

FIG. 45B Cont.				
58	L58Y	-20.199	11.659	8.976
59	K59R	3.366	-1.817	-1.750
60	Q60M	4.708	-2.892	-1.669
60	Q60P	-1.727	4.814	-7.879
61	H61D	-2.368	4.942	-1.778
61	H61G	-0.677	5.349	-3.583
61	H61P	-5.801	9.826	-2.426
62	Q62P	-1.522	6.163	-3.537
62	Q62W	0.517	3.663	-3.398
63	P63I	-1.672	5.116	-2.519
63	P63L	-3.313	8.779	-3.907
63	P63N	-3.800	6.514	-3.341
63	P63S	-6.199	9.244	-1.639
63	P63T	-5.552	7.035	-0.435
63	P63V	-1.821	3.314	-0.944
63	P63W	-8.488	14.360	-3.491
64	R64D	4.846	-1.337	-3.444
64	R64E	4.000	-0.930	-2.981
64	R64F	-0.229	4.186	-3.167
64	R64P	-10.975	17.791	-3.907
64	R64Q	4.000	-3.779	-0.713
64	R64W	-5.652	13.895	-5.759
64	R64Y	-3.512	4.709	-0.435
65	W65A	-0.180	7.222	-7.393
65	W65E	-4.203	10.470	-6.143
65	W65G	-3.453	5.128	-1.837
65	W65K	-2.289	3.077	-0.607
65	W65M	-1.820	5.812	-4.000
65	W65N	1.969	3.504	-5.920
65	W65V	2.867	3.205	-6.634
66	V66I	-4.164	0.598	4.125
66	V66M	-3.578	4.658	-0.786
66	V66S	-2.986	4.976	-2.414
67	L67A	-3.969	4.402	-0.071
67	L67T	-7.016	5.427	2.295
68	V68A	-6.742	6.453	0.955
68	V68M	-1.352	11.410	-10.384
68	V68S	-11.469	20.983	-8.777
68	V68T	-1.586	3.162	-1.545
69	E69A	-22.982	16.124	25.784
69	E69C	-27.267	18.336	32.255
69	E69D	-12.881	9.166	7.837
69	E69F	-8.037	-2.814	27.745
69	E69G	-19.465	8.204	33.922

FIG. 45B Cont.				
69	E69H	-29.722	23.071	28.431
69	E69K	-31.846	29.398	20.098
69	E69L	-31.663	23.292	33.137
69	E69M	-20.088	14.265	22.157
69	E69N	-24.264	20.903	18.529
69	E69P	-8.107	8.625	0.694
69	E69Q	-12.685	0.500	20.368
69	E69S	-7.881	1.378	11.070
69	E69V	-17.560	12.274	19.902
69	E69Y	-14.996	9.708	18.627
70	L70A	-15.803	12.459	7.812
70	L70C	-25.143	25.504	10.784
70	L70E	-13.800	8.929	9.742
70	L70F	-39.355	28.425	42.353
70	L70H	-65.873	36.582	13.112
70	L70I	-0.564	4.531	-8.529
70	L70K	-31.663	54.796	-36.667
70	L70Q	-38.916	26.168	46.176
70	L70S	-29.832	28.027	17.745
70	L70T	-40.915	15.063	16.072
70	L70V	-13.714	9.442	15.784
70	L70W	-49.136	2.894	125.098
71	G71A	-8.513	16.566	-13.824
72	G72A	22.432	-24.937	8.474
72	G72C	21.780	-32.504	13.627
72	G72P	10.352	-30.115	39.118
72	G72S	21.377	-40.558	32.549
73	N73A	-29.185	-1.819	32.298
73	N73C	-24.471	-13.119	36.623
73	N73G	-60.831	4.272	42.783
73	N73H	-74.207	3.435	75.507
73	N73I	-69.846	2.305	71.833
73	N73L	-51.872	-22.497	73.274
73	N73P	-49.890	-4.079	56.019
73	N73R	-58.084	25.638	40.205
73	N73S	-58.040	4.960	57.181
73	N73T	-73.034	8.354	48.013
73	N73V	-26.508	-2.816	23.507
73	N73W	-74.912	0.723	76.484
74	D74E	-41.254	9.715	21.961
74	D74G	-38.954	4.667	89.632
75	G75A	9.297	-24.747	18.474
75	G75C	23.923	-64.804	47.614
75	G75D	15.818	-49.619	42.702

FIG. 45B Cont.				
75	G75E	27.467	-60.889	32.263
75	G75F	40.940	-80.201	30.596
75	G75I	56.288	-47.816	6.007
75	G75K	7.136	-23.671	19.033
75	G75L	40.186	-37.753	8.046
75	G75M	28.831	-33.386	12.322
75	G75N	12.028	-49.143	51.298
75	G75P	11.221	-46.762	49.456
75	G75T	31.818	-72.476	40.684
75	G75V	63.116	-96.709	2.526
75	G75W	38.449	-79.196	35.158
75	G75Y	33.712	-71.630	34.544
76	L76A	4.254	-26.297	24.066
76	L76C	-3.767	-33.401	31.460
76	L76D	11.872	-33.853	15.321
76	L76E	2.008	-21.772	21.039
76	L76F	-13.754	-17.278	28.638
76	L76G	11.076	-26.171	18.605
76	L76I	-15.703	-13.259	25.974
76	L76K	3.502	-46.226	34.344
76	L76M	4.075	-25.209	16.437
76	L76N	4.000	-21.108	18.836
76	L76P	5.176	-40.689	28.019
76	L76Q	4.075	-42.610	30.763
76	L76R	9.978	-45.153	26.623
76	L76T	2.008	-23.259	22.618
76	L76V	-14.075	-40.576	48.251
76	L76W	8.661	-28.449	22.816
77	R77A	-22.007	-7.714	67.702
77	R77C	-25.130	-8.190	76.386
77	R77D	-28.288	3.503	64.895
77	R77E	-36.975	6.013	22.454
77	R77F	-28.674	-18.032	101.561
77	R77G	-16.254	-3.544	16.303
77	R77H	-28.393	-9.884	87.351
77	R77K	-8.288	3.291	15.246
77	R77L	0.864	-7.152	6.763
77	R77N	-15.340	-2.899	43.140
77	R77Q	9.993	-8.455	-10.982
77	R77S	-20.639	0.540	50.684
77	R77V	-36.636	-4.367	32.980
77	R77W	-26.814	-26.127	110.421
78	G78A	22.730	-17.820	-27.298
78	G78C	36.028	-33.799	-34.053

FIG. 45B Cont.				
78	G78D	-4.147	15.831	-15.895
78	G78E	40.144	-9.272	-21.526
78	G78F	43.831	-23.671	-9.421
78	G78M	49.932	-21.392	-16.526
78	G78N	33.677	-19.460	-51.947
78	G78P	-15.060	-11.524	56.737
78	G78Q	20.695	-8.878	-37.123
78	G78R	77.008	-35.000	-23.401
78	G78S	36.034	-12.184	-15.309
78	G78T	40.625	-28.984	-53.526
78	G78V	47.305	-21.994	-13.829
78	G78Y	51.432	-48.085	-48.877
79	F79A	6.341	-4.286	-10.157
79	F79D	43.407	-15.253	-17.842
79	F79E	46.373	-16.677	-18.697
79	F79G	7.214	-5.504	-10.133
79	F79H	17.305	-4.778	-8.467
79	F79M	-3.406	-1.510	14.105
79	F79N	6.131	-4.183	-9.759
79	F79P	-36.890	7.215	21.138
79	F79Q	5.265	-2.800	-10.157
79	F79V	-1.942	0.926	3.988
79	F79W	6.393	-4.327	-10.227
80	Q80A	-1.822	1.091	3.239
80	Q80E	22.898	-6.456	-11.033
80	Q80G	-26.000	-1.108	21.368
80	Q80L	-7.949	-0.316	6.500
80	Q80M	-7.186	-1.804	7.454
80	Q80S	-17.483	0.475	13.079
80	Q80W	-3.107	-0.478	10.827
80	Q80Y	-10.915	-2.120	10.711
81	P81A	-3.368	2.009	6.002
81	P81E	-8.966	1.329	5.579
81	P81K	-3.077	0.245	9.094
81	P81M	-5.049	3.516	7.852
81	P81N	4.802	-2.748	-8.845
81	P81T	3.413	-1.675	-6.878
81	P81W	-21.339	2.690	13.737
81	P81Y	-3.032	0.678	7.993
82	Q82F	-2.987	0.750	7.665
82	Q82I	-5.831	-0.538	5.086
82	Q82N	-3.092	2.329	4.410
82	Q82P	-4.556	1.380	11.155
82	Q82R	4.297	-0.253	-3.072

FIG. 45B Cont.				
82	Q82S	4.932	-1.994	-1.757
82	Q82W	-4.287	0.028	13.356
82	Q82Y	-3.413	0.348	9.913
83	Q83C	31.076	-11.709	-11.954
83	Q83F	23.703	-8.418	-9.651
83	Q83G	40.229	-16.044	-14.553
83	Q83K	25.992	-10.063	-9.684
83	Q83L	43.110	-17.532	-15.243
83	Q83M	23.110	-8.449	-9.158
83	Q83N	23.873	-9.367	-8.796
83	Q83R	27.305	-10.728	-10.046
83	Q83S	26.288	-9.684	-10.375
83	Q83T	22.856	-8.513	-8.895
83	Q83V	16.338	-5.835	-9.834
83	Q83W	10.890	-4.968	-4.990
83	Q83Y	10.200	-4.159	-5.385
84	T84A	32.364	-14.910	-14.615
84	T84E	-7.487	7.532	-2.495
84	T84F	21.114	-9.535	-9.813
84	T84L	76.709	-40.900	-29.197
84	T84M	28.726	-12.829	-13.555
84	T84N	28.558	-11.962	-14.615
84	T84Q	12.308	-3.090	-9.272
84	T84R	-3.233	5.841	-4.782
84	T84S	-6.479	0.379	6.694
84	T84V	29.006	-13.841	-12.432
84	T84W	1.580	3.529	-6.840
84	T84Y	20.591	-7.382	-12.328
85	E85A	4.771	-2.367	-1.892
85	E85C	3.185	0.075	-3.659
85	E85D	-7.151	2.864	3.846
85	E85L	4.976	-1.948	-2.744
85	E85Q	6.729	-2.829	-3.430
85	E85R	4.043	-1.081	-2.952
85	E85S	3.241	-0.171	-3.368
85	E85T	7.812	-2.121	-5.655
85	E85W	3.222	-0.416	-2.994
85	E85Y	4.043	-1.283	-2.661
86	Q86G	4.938	-2.540	-1.850
86	Q86K	3.147	-1.038	-2.017
86	Q86T	-1.930	-1.657	3.976
86	Q86V	-3.700	0.465	3.451
86	Q86W	-4.017	0.682	3.493
87	T87A	-11.920	1.314	20.762

FIG. 45B Cont.				
87	T87C	-18.065	0.661	33.629
87	T87D	16.335	-7.543	-18.399
87	T87E	-5.938	0.017	6.590
87	T87F	-21.738	-10.278	59.434
87	T87G	-16.102	3.355	25.238
87	T87H	-19.447	1.110	35.448
87	T87L	-23.665	-4.033	52.510
87	T87M	-8.718	-0.373	10.270
87	T87P	23.571	-12.808	-23.364
87	T87S	-4.575	0.824	7.406
87	T87V	-6.865	0.988	11.531
87	T87W	-18.829	-2.482	40.483
88	L88C	-6.393	7.763	-0.986
89	R89A	3.607	0.988	-8.608
89	R89G	12.153	-4.849	-15.112
89	R89H	-0.829	-1.094	3.420
89	R89L	-1.338	3.029	-2.594
89	R89P	0.298	8.131	-14.483
89	R89T	-6.247	2.090	8.385
89	R89V	-4.875	1.491	3.285
89	R89W	-3.156	0.212	5.727
90	Q90E	5.607	-2.073	-7.210
90	Q90N	-2.684	3.355	-0.566
90	Q90P	-7.580	7.084	-1.746
90	Q90W	-5.338	7.559	-2.664
90	Q90Y	3.062	-3.420	-0.007
91	I91G	-2.783	8.825	-7.128
91	I91L	-1.200	-3.476	5.349
91	I91M	-3.783	18.667	-17.404
91	I91S	-7.700	13.825	-7.495
91	I91V	11.800	-7.603	-4.193
91	I91Y	-130.617	56.048	79.018
92	L92A	-7.033	10.175	-4.009
92	L92C	-3.700	4.937	-1.624
92	L92G	-11.533	16.286	-6.119
92	L92H	-0.367	7.635	-8.321
92	L92N	-11.533	17.397	-7.404
92	L92S	-4.987	4.064	-0.291
92	L92T	-9.367	7.635	1.495
92	L92Y	-29.117	37.714	-11.532
93	Q93E	4.133	-4.032	0.119
93	Q93H	2.300	-5.460	3.789
93	Q93I	3.133	-4.984	2.321
93	Q93L	3.050	-3.317	0.486

FIG. 45B Cont.				
93	Q93P	-48.617	39.143	8.284
93	Q93S	3.717	-4.190	0.761
93	Q93W	5.217	-3.794	-1.349
93	Q93Y	0.300	-3.000	3.147
94	D94E	7.467	-3.397	-4.284
94	D94F	6.967	-5.063	-1.899
94	D94G	11.800	-7.762	-4.009
94	D94H	13.800	-8.476	-5.385
94	D94K	11.383	-7.762	-3.550
94	D94N	7.967	-5.222	-2.725
94	D94P	-1.759	3.442	-2.973
94	D94Q	8.300	-5.063	-3.275
94	D94R	8.883	-7.365	-1.165
94	D94S	11.883	-7.603	-4.284
94	D94V	6.800	-6.571	0.119
95	V95F	-14.444	19.641	-2.010
95	V95G	-3.341	4.897	-0.833
95	V95L	-2.454	-0.446	5.163
95	V95N	-5.730	8.519	-1.552
95	V95Q	-9.824	15.955	-4.036
95	V95W	-14.919	18.147	5.089
96	K96P	-11.034	13.513	3.644
96	K96V	3.128	-2.117	-3.207
97	A97P	-11.793	15.571	-1.193
98	A98L	-0.757	-1.326	3.089
98	A98P	-9.850	15.654	-1.281
98	A98V	-1.084	3.199	-1.912
98	A98W	-0.383	-1.853	3.015
98	A98Y	-1.766	3.167	-1.029
99	N99D	-4.549	11.436	-6.029
99	N99Y	3.045	-2.132	-0.924
100	A100D	-7.199	9.321	-0.539
100	A100E	-5.283	7.590	-1.160
100	A100H	-7.605	1.927	9.161
100	A100I	-5.441	2.429	4.297
100	A100K	-12.555	4.919	11.534
100	A100L	-9.798	6.115	5.931
100	A100M	-7.905	2.654	8.144
100	A100Q	-8.669	7.686	2.958
100	A100R	-7.803	3.071	6.618
100	A100T	-4.549	0.827	4.788
100	A100V	-11.755	3.637	12.720
100	A100W	-23.755	20.774	-0.839
100	A100Y	-5.362	3.519	3.056

FIG. 45B Cont.				
101	E101A	3.495	-1.919	-2.110
101	E101D	3.895	-1.748	-3.127
101	E101L	0.095	-1.876	3.568
101	E101P	-9.055	15.944	-16.263
101	E101T	1.245	-2.731	3.314
102	P102E	-12.081	17.750	-3.056
102	P102F	-9.305	13.893	-11.686
102	P102H	-12.475	18.744	-3.578
102	P102L	-7.436	8.199	0.899
102	P102Q	-4.706	10.474	-4.820
102	P102R	-10.454	15.699	-2.990
102	P102S	-2.255	0.132	3.568
102	P102W	-2.711	4.769	-1.487
102	P102Y	-14.505	21.457	-17.873
103	L103E	0.706	4.474	-3.054
103	L103G	4.690	0.635	-6.454
103	L103K	-4.458	9.958	-3.083
103	L103N	0.589	3.481	-2.413
103	L103Q	-1.164	3.581	-1.378
103	L103R	0.799	3.605	-2.617
104	L104C	-6.164	8.519	-1.159
104	L104P	-4.154	6.608	-1.276
104	L104S	-8.906	10.603	0.278
104	L104W	-3.547	10.801	-4.133
105	M105A	-0.717	-2.474	3.415
105	M105C	-0.822	-5.327	6.454
105	M105E	-6.570	3.647	4.461
105	M105G	-11.635	7.558	6.781
105	M105I	1.934	-5.712	3.415
105	M105L	-2.711	-4.494	7.958
105	M105V	-0.244	-9.269	9.788
106	Q106D	7.079	-27.635	19.330
106	Q106G	-7.042	0.250	8.513
106	Q106H	-0.927	-12.442	13.840
106	Q106K	-11.084	7.910	5.735
106	Q106L	1.383	-12.763	11.291
106	Q106M	-1.346	-8.115	9.951
106	Q106R	-9.142	2.750	8.578
106	Q106S	-8.407	0.218	10.245
106	Q106T	-7.776	-0.290	5.036
106	Q106V	-7.173	-2.763	11.748
106	Q106W	12.407	-34.141	19.330
106	Q106Y	-8.150	-0.092	5.138
107	I107C	-1.534	0.799	3.913

FIG. 45B Cont.				
107	I107E	-4.030	3.950	3.734
107	I107G	-1.332	-1.499	11.249
107	I107K	-3.634	5.924	-5.054
107	I107L	-3.000	1.239	8.823
107	I107M	-1.049	0.068	4.390
107	I107Q	-3.567	2.070	8.366
107	I107S	-29.598	3.928	0.798
107	I107Y	36.578	-5.114	-0.752
108	R108A	3.281	-6.028	6.974
108	R108C	2.405	-4.806	6.497
108	R108D	5.395	-8.381	6.020
108	R108E	26.776	-5.423	0.965
108	R108F	3.857	-4.120	-2.370
108	R108G	12.329	-2.682	0.611
108	R108H	31.677	-5.713	0.507
108	R108I	5.242	-7.874	4.887
108	R108L	3.565	-8.683	15.185
108	R108M	15.246	-4.409	1.742
108	R108R	3.003	-2.983	-2.668
108	R108S	2.814	-5.409	6.815
108	R108V	1.613	-5.353	11.944
108	R108W	8.281	-6.954	-11.813
108	R108Y	3.048	-5.582	6.417
109	L109A	7.292	-7.405	-5.849
109	L109C	1.708	-3.847	6.159
109	L109D	6.047	-5.175	-8.314
109	L109E	7.922	-7.238	-9.229
109	L109F	38.618	-8.122	1.663
109	L109G	3.920	-4.806	-0.203
109	L109K	5.579	-7.378	1.626
109	L109M	-1.997	0.453	7.213
109	L109P	7.333	-7.249	-6.584
109	L109Q	-2.254	-0.032	10.076
109	L109R	33.518	-6.685	1.118
109	L109S	6.960	-6.714	-6.843
109	L109T	2.715	-5.509	7.630
109	L109V	2.162	-4.505	6.497
109	L109Y	5.570	-8.370	5.205
110	P110A	2.679	-6.318	10.672
110	P110C	41.790	-7.316	0.470
110	P110D	35.246	-6.316	0.528
110	P110E	25.303	-5.151	0.936
110	P110F	11.249	-12.603	-4.795
110	P110G	22.385	-5.018	1.243

FIG. 45B Cont.				
110	P110H	3.511	-7.456	11.050
110	P110K	50.147	-8.246	0.084
110	P110L	47.994	-6.901	-0.814
110	P110M	39.297	-6.690	0.271
110	P110N	7.949	-10.958	3.913
110	P110R	7.863	-11.231	5.245
110	P110S	29.892	-6.653	1.617
110	P110V	3.893	-6.814	7.074
110	P110W	8.879	-10.612	-1.435
111	A111C	18.210	-13.170	-4.264
111	A111E	4.235	-0.045	-5.452
111	A111L	10.134	-9.844	1.347
111	A111M	6.125	-1.287	0.262
111	A111P	9.977	-2.263	0.578
111	A111Q	4.058	-2.121	-2.152
111	A111V	2.767	-7.589	7.617
111	A111Y	10.686	-0.775	-0.868
112	N112A	-7.410	-4.888	16.891
112	N112F	-4.527	-2.871	3.255
112	N112G	-6.119	-0.915	9.300
112	N112I	-4.954	-11.138	22.931
112	N112K	8.311	-7.746	0.620
112	N112L	-7.258	-10.647	25.175
112	N112P	-5.663	-6.719	17.320
112	N112R	4.992	-0.296	-0.461
112	N112V	-5.309	-10.022	21.743
112	N112W	-10.220	-6.585	23.063
112	N112Y	-11.461	-4.286	21.281
113	Y113A	-6.094	0.223	7.617
113	Y113C	11.856	-6.585	-5.749
113	Y113D	-7.587	4.576	3.129
113	Y113M	1.071	-3.906	4.383
113	Y113W	-17.785	-0.784	3.317
114	G114F	-14.414	-1.098	3.101
114	G114L	-8.575	0.558	10.356
114	G114M	-11.511	1.004	13.525
114	G114P	8.958	-0.057	-1.263
114	G114W	-18.493	-0.453	3.122
114	G114Y	-13.511	0.335	17.122
115	R115A	2.071	-21.595	11.017
115	R115C	1.509	-13.387	6.638
115	R115E	2.970	-22.000	10.431
115	R115G	-14.783	-18.936	24.914
115	R115I	-1.375	-10.092	7.328

FIG. 45B Cont.				
115	R115N	-6.805	-4.486	8.983
115	R115P	-3.772	-2.867	5.190
115	R115Q	-1.375	-3.792	3.534
115	R115S	-4.258	-5.757	7.362
115	R115V	-0.588	-4.659	3.328
115	R115W	3.745	-3.737	2.823
115	R115Y	-6.393	-15.584	15.190
116	R116D	4.169	-3.561	-1.707
116	R116E	4.281	-2.058	-2.707
116	R116H	-2.873	-4.370	5.293
116	R116V	0.311	-6.393	3.534
116	R116W	-15.532	-15.410	23.500
117	Y117A	8.618	-0.333	-0.960
117	Y117C	4.169	0.948	-4.397
117	Y117E	13.547	-1.374	-0.748
117	Y117H	-7.404	8.000	2.052
117	Y117L	-6.393	7.538	1.397
117	Y117M	-11.749	11.584	3.879
117	Y117N	-3.397	5.341	-0.052
117	Y117Q	9.722	-0.448	-1.022
117	Y117R	8.844	0.284	-1.554
117	Y117T	6.940	2.220	-7.707
117	Y117V	10.124	0.023	-9.328
117	Y117W	-24.071	-3.272	24.121
118	N118A	-0.663	-9.399	6.224
118	N118C	5.667	-25.526	9.983
118	N118E	0.086	-15.410	9.121
118	N118G	8.101	-17.838	3.190
118	N118H	-9.764	-9.977	14.983
118	N118I	14.918	-47.665	14.707
118	N118K	8.213	1.699	-8.569
118	N118L	-5.157	-26.509	20.569
118	N118M	-6.955	-6.335	10.190
118	N118P	-4.371	-30.902	22.466
118	N118Q	2.933	-12.289	4.603
118	N118S	3.150	-0.526	0.013
118	N118T	15.330	-44.197	12.259
118	N118V	19.150	-54.081	14.672
118	N118W	8.176	-24.023	6.845
119	E119C	3.998	-4.613	1.487
119	E119D	1.897	-3.588	5.105
119	E119F	0.766	-3.860	9.645
119	E119G	4.624	-5.115	1.026
119	E119K	-0.810	-4.215	15.895

FIG. 45B Cont.				
119	E119M	3.554	-4.257	1.816
119	E119P	0.442	-13.546	41.158
119	E119R	-0.547	-4.843	17.013
119	E119W	-0.184	-5.722	18.592
119	E119Y	1.695	-5.052	10.368
120	A120D	3.291	-2.918	-1.605
120	A120E	3.377	-0.130	-0.382
120	A120G	-0.386	-2.228	8.263
120	A120I	-5.537	0.743	15.697
120	A120L	-0.527	-0.931	4.645
120	A120T	-1.982	0.847	3.789
120	A120W	-6.143	-2.981	29.382
121	F121A	5.352	-25.847	63.855
121	F121C	-0.022	-12.312	38.789
121	F121D	20.543	-30.262	28.263
121	F121E	15.756	-25.052	27.474
121	F121K	-9.116	-2.226	3.346
121	F121L	-11.497	-11.203	72.671
121	F121M	9.614	-13.839	12.211
121	F121P	9.109	-26.203	52.737
121	F121Q	6.240	-19.111	39.776
121	F121R	14.604	-25.554	32.803
121	F121S	6.523	-22.772	50.303
121	F121Y	3.392	-11.036	23.658
122	S122A	0.160	-4.467	13.526
122	S122C	-1.214	-3.985	16.487
122	S122D	10.119	-5.248	3.251
122	S122E	7.149	-19.592	38.329
122	S122F	-4.952	-3.504	27.145
122	S122G	-1.154	-6.182	23.197
122	S122I	-7.962	4.069	13.066
122	S122L	-8.042	-4.320	39.776
122	S122P	-3.558	-10.115	43.395
122	S122V	-7.739	1.015	21.947
122	S122W	-5.941	-5.659	37.145
122	S122Y	-6.931	-3.337	33.066
123	A123F	-5.958	-0.357	6.272
123	A123T	-10.509	2.225	7.988
123	A123V	-3.817	-0.031	4.011
123	A123W	-4.095	-0.373	4.667
123	A123Y	-10.030	-2.335	12.426
124	I124A	-5.925	1.023	5.095
124	I124C	-3.568	-0.943	4.728
124	I124G	-36.078	27.280	6.272

FIG. 45B Cont.				
124	I124H	-2.221	4.313	-2.310
124	I124K	-8.107	6.450	1.537
124	I124L	-2.997	-0.473	3.629
124	I124R	-3.539	4.043	-0.631
124	I124S	1.707	4.203	-6.213
124	I124T	38.234	-15.577	-21.006
124	I124Y	-60.150	34.258	22.544
125	Y125C	11.946	-28.984	19.408
125	Y125F	-0.389	-7.830	8.817
125	Y125G	6.710	-11.556	5.385
125	Y125I	-28.114	-11.401	40.059
125	Y125L	-1.665	-11.584	14.148
125	Y125P	4.631	-9.803	5.660
125	Y125Q	-26.916	-3.654	30.533
125	Y125R	-68.533	19.368	46.805
125	Y125S	42.186	-49.313	11.420
125	Y125T	-12.485	-12.995	26.331
125	Y125V	3.323	-24.588	23.136
125	Y125W	10.092	-9.533	-0.310
126	P126C	-60.210	44.423	11.657
126	P126F	-4.940	5.962	-1.538
126	P126R	7.874	2.280	-10.237
126	P126T	8.473	-5.247	-2.722
126	P126V	4.701	-1.346	-3.195
127	K127I	-0.569	3.214	-2.840
127	K127P	-1.202	5.012	-5.867
127	K127S	3.994	-1.002	-5.753
128	L128A	0.269	7.225	-8.047
128	L128C	9.371	-0.192	-9.053
128	L128S	-0.030	9.643	-10.296
128	L128T	7.275	5.082	-12.663
128	L128V	4.118	-0.884	-6.171
129	A129H	-4.820	3.819	0.651
129	A129I	-4.439	7.465	-3.852
129	A129K	-11.287	9.423	1.065
129	A129N	-6.557	8.819	-2.959
129	A129W	-5.944	12.347	-8.947
129	A129Y	-6.852	12.229	-7.084
130	K130E	3.231	-3.927	0.407
130	K130I	3.683	-3.434	0.000
130	K130P	-2.893	5.932	-4.232
130	K130V	6.198	-2.500	-3.491
131	E131A	-4.419	3.237	1.541
131	E131C	-6.547	5.699	0.395

FIG. 45B Cont.				
131	E131F	-6.074	4.757	1.478
131	E131G	-4.926	7.523	-6.548
131	E131I	-6.277	2.568	6.446
131	E131K	-4.641	3.599	0.769
131	E131L	-5.770	3.328	3.898
131	E131N	-5.359	5.082	-0.178
131	E131V	-5.534	3.906	2.242
131	E131W	-4.622	5.091	-1.962
132	F132D	3.453	1.596	-9.860
132	F132E	8.293	-3.049	-4.911
132	F132N	3.250	0.684	-7.567
132	F132T	3.486	0.137	-6.930
133	D133R	3.323	-2.665	-0.414
133	D133S	3.443	-3.654	0.533
133	D133T	3.024	-3.984	1.302
133	D133V	3.503	-2.445	-0.828
134	V134D	-21.228	24.423	-5.325
134	V134E	-7.814	10.027	-3.077
134	V134I	4.939	-3.602	-1.771
134	V134K	-0.365	3.997	-7.694
134	V134M	5.838	0.632	-6.450
134	V134N	-0.736	3.298	-5.465
134	V134Q	-1.277	4.635	-7.312
134	V134R	-1.750	5.243	-7.694
134	V134W	-26.198	33.489	-10.178
134	V134Y	-10.928	13.049	-3.254
136	L136A	-7.528	6.456	1.185
136	L136C	-6.018	-0.852	6.864
136	L136D	-9.614	9.162	0.628
136	L136E	-5.846	5.338	0.598
136	L136F	-4.136	4.132	0.070
136	L136G	-10.658	8.926	1.889
136	L136H	-3.933	5.368	-1.367
136	L136K	-6.600	11.103	-4.358
136	L136M	-0.449	-7.500	8.580
136	L136N	-3.296	6.015	-2.628
136	L136P	-8.426	14.397	-5.824
136	L136Q	-18.174	11.731	5.266
136	L136R	-4.948	7.574	-2.540
136	L136S	-21.766	11.236	9.408
136	L136T	-7.788	5.309	2.592
137	L137E	-4.281	11.397	-7.026
137	L137G	-3.962	4.221	-0.164
137	L137H	-8.165	11.221	-2.921

FIG. 45B Cont.				
137	L137P	-9.383	3.103	6.405
137	L137Q	-7.528	9.897	-2.246
137	L137S	-10.658	9.426	1.390
137	L137Y	-5.528	3.985	1.625
138	P138E	3.719	-6.985	3.208
138	P138N	14.328	-10.809	-3.713
138	P138R	9.255	-12.868	3.472
138	P138T	6.646	-10.279	3.531
138	P138V	8.443	-8.750	0.217
139	F139A	13.261	-9.939	-12.583
139	F139D	22.456	-13.350	-28.446
139	F139G	11.100	-11.047	-4.964
139	F139H	21.136	-18.248	-15.173
139	F139M	4.233	-10.551	11.048
139	F139S	14.845	-11.207	-13.923
139	F139W	4.315	-0.967	-0.962
140	F140C	13.261	-12.504	-7.315
140	F140G	22.180	-21.615	-10.857
140	F140M	6.586	-6.484	-3.060
140	F140N	14.509	-12.504	-10.440
140	F140P	14.521	-14.254	-6.929
140	F140S	13.285	-17.402	2.565
141	M141A	18.951	-17.373	-11.512
141	M141C	17.618	-16.863	-9.250
141	M141D	31.280	-26.367	-23.714
141	M141E	34.413	-29.516	-25.054
141	M141F	9.687	-2.686	-1.501
141	M141G	16.238	-13.277	-13.179
141	M141K	35.697	-31.601	-23.982
141	M141L	24.101	-23.350	-12.077
141	M141P	21.952	-21.397	-10.738
141	M141Q	31.268	-28.598	-19.101
141	M141R	8.419	-2.332	-1.309
141	M141T	30.715	-26.878	-21.244
141	M141V	3.541	-0.867	-0.696
141	M141W	45.505	-37.388	-36.482
141	M141Y	13.755	-4.050	-1.834
142	E142A	5.325	-15.609	18.667
142	E142C	8.747	-11.688	2.179
142	E142L	-5.095	-5.857	24.560
142	E142M	-6.139	-1.163	17.595
142	E142N	0.451	-2.854	4.708
142	E142P	11.340	-20.566	13.905
142	E142Q	5.445	-14.414	15.929

FIG. 45B Cont.				
142	E142S	1.892	-10.974	17.714
142	E142W	10.739	-10.595	-4.994
142	E142Y	4.725	-12.563	13.935
143	E143I	-0.176	-1.331	3.466
143	E143P	-1.049	-0.495	4.376
144	V144D	4.483	-1.002	-1.005
144	V144E	4.422	-0.983	-0.994
144	V144G	4.613	-1.149	-0.882
144	V144H	4.672	-4.731	-4.312
144	V144N	4.180	-0.926	-0.946
144	V144P	3.802	-3.760	-3.706
144	V144Q	4.314	-4.232	-4.280
144	V144R	4.387	-4.254	-4.460
144	V144S	3.922	-3.958	-3.648
144	V144W	5.056	-5.435	-3.976
144	V144Y	3.251	-3.786	-1.919
145	Y145D	4.432	-4.427	-4.222
145	Y145E	4.063	-3.921	-4.165
145	Y145I	5.026	-1.079	-1.181
145	Y145L	5.654	-5.844	-4.960
145	Y145M	5.093	-5.521	-3.911
145	Y145Q	3.497	-4.090	-2.025
145	Y145T	4.445	-4.363	-4.402
145	Y145W	3.246	-1.035	-0.331
147	K147G	11.439	-6.436	-4.857
147	K147P	23.533	-13.093	-10.453
147	K147R	-2.386	0.133	4.839
147	K147W	10.731	-6.162	-4.184
148	P148D	3.769	-0.621	-6.375
148	P148E	3.503	-0.504	-6.137
148	P148W	-1.846	-0.230	4.796
150	W150C	18.216	-17.412	-4.912
150	W150D	72.093	-67.695	-20.400
150	W150E	52.797	-45.435	-18.400
150	W150G	3.150	-7.412	2.763
150	W150L	5.529	-7.017	-0.074
150	W150Q	30.683	-27.638	-9.656
150	W150T	20.639	-27.638	0.949
151	M151A	14.428	-9.579	-1.495
151	M151C	12.550	-8.997	0.805
151	M151E	17.466	-11.230	-2.970
151	M151F	4.904	-1.559	-0.507
151	M151G	13.789	-8.155	-4.597
151	M151I	17.938	-12.805	0.978

FIG. 45B Cont.				
151	M151Q	8.538	-7.121	3.711
151	M151S	14.949	-9.319	-3.490
151	M151T	11.075	-8.442	2.302
151	M151V	21.832	-14.853	-1.126
151	M151W	30.917	-18.538	-9.499
152	Q152A	-28.877	18.915	14.949
152	Q152D	9.714	7.277	-16.260
152	Q152E	-1.960	13.887	-9.377
152	Q152F	27.379	-12.045	-19.005
152	Q152H	-19.405	37.616	-10.493
152	Q152I	34.251	-17.356	-21.935
152	Q152K	-28.260	19.085	14.158
152	Q152L	35.176	-28.994	-13.284
152	Q152R	-0.286	15.299	-12.307
152	Q152S	-3.458	0.667	3.042
152	Q152T	30.947	-17.017	-18.726
152	Q152Y	-19.185	37.616	-10.726
156	I156C	-11.137	-3.481	18.057
156	I156F	-20.314	-1.126	26.721
156	I156L	16.668	-12.287	-6.370
156	I156Q	-4.765	-5.965	13.019
156	I156R	-11.137	-7.481	22.790
156	I156S	-11.564	-7.932	23.859
158	P158A	9.534	-9.674	-0.454
158	P158F	127.486	-65.116	-30.085
158	P158G	-1.503	-1.061	3.172
158	P158H	37.125	-18.739	-24.309
158	P158I	54.844	-27.076	-14.134
158	P158L	97.675	-53.754	-18.385
158	P158Q	52.627	-20.266	-20.449
158	P158S	-6.099	1.794	3.032
158	P158T	22.156	-8.306	-8.911
158	P158V	80.929	-40.233	-20.449
159	N159C	8.099	-3.322	-2.960
159	N159E	7.095	1.487	-10.683
159	N159G	-0.832	-2.545	4.050
159	N159I	29.137	-13.189	-8.951
159	N159K	5.540	-2.932	-3.431
159	N159L	7.460	-0.674	-8.546
159	N159M	6.495	0.532	-6.279
159	N159Q	0.814	3.100	-4.653
159	N159R	6.307	-3.887	-0.652
159	N159T	17.061	-8.306	-4.538
159	N159V	20.222	-8.173	-7.413

FIG. 45B Cont.				
160	R160A	10.296	-7.094	-4.500
160	R160C	3.487	-1.140	-5.209
160	R160D	11.400	-6.335	-10.830
160	R160E	7.313	-3.793	-7.627
160	R160G	8.009	-4.380	-7.758
160	R160H	5.313	-3.486	-3.902
160	R160N	4.655	-3.674	-1.485
160	R160Q	7.491	-4.513	-4.042
160	R160S	9.412	-6.126	-4.538
161	D161E	4.656	-2.857	-0.490
161	D161K	1.024	-3.223	3.032
161	D161N	-2.357	-0.352	3.363
161	D161R	1.495	-3.887	3.478
161	D161S	-1.241	-2.093	3.599
161	D161V	-0.344	-3.090	4.045
161	D161W	-0.392	-3.953	5.138
162	A162G	-6.020	3.218	6.033
162	A162I	20.328	-12.592	-16.386
162	A162L	45.052	-32.508	-25.536
162	A162T	15.023	-11.531	-6.908
162	A162V	4.168	-4.513	0.118
162	A162Y	38.646	-24.547	-29.719
163	Q163A	-7.019	4.607	2.920
163	Q163C	-3.679	5.155	-4.156
163	Q163G	-5.180	1.692	5.678
163	Q163L	-2.460	0.436	3.452
163	Q163S	-6.777	0.745	7.599
163	Q163T	-9.289	9.808	-3.757
164	P164C	-3.585	-0.626	7.638
165	F165D	8.103	-4.668	-4.721
165	F165E	4.989	-3.493	-1.631
165	F165G	3.488	-4.056	2.156
165	F165I	23.345	-17.771	-8.202
165	F165K	13.525	-8.775	-5.850
165	F165L	4.126	-0.465	-6.349
165	F165M	11.424	-6.874	-6.050
165	F165R	12.962	-9.467	-3.425
165	F165S	5.364	-4.121	-1.033
165	F165T	14.576	-9.225	-6.781
165	F165V	11.668	-6.858	-6.515
165	F165W	-2.723	-3.448	7.447
166	I166F	37.399	-30.900	-10.263
166	I166L	9.198	-11.481	2.065
166	I166M	5.235	-6.223	0.805

FIG. 45B Cont.				
167	A167C	5.857	2.000	-4.993
167	A167E	-3.668	5.326	-1.714
167	A167F	2.286	18.325	-15.878
167	A167G	-1.869	3.648	-1.981
167	A167K	-7.595	12.598	-5.673
167	A167L	-4.976	21.915	-14.585
167	A167M	3.192	-2.803	-0.721
167	A167N	-16.524	26.701	-11.796
167	A167Q	-7.833	15.248	-7.646
167	A167R	5.024	8.581	-9.687
167	A167T	16.095	-7.060	-3.565
167	A167V	0.738	9.692	-8.122
167	A167Y	-1.107	6.487	-6.294
168	D168L	-16.048	9.521	1.605
168	D168P	22.857	-55.287	36.798
168	D168V	-7.000	3.795	0.993
168	D168W	-4.738	4.393	-0.776
169	W169A	-6.365	0.702	5.848
169	W169D	-7.402	6.347	-1.283
169	W169E	-3.004	-0.617	4.143
169	W169G	-7.527	3.923	2.395
169	W169K	-1.442	-9.900	13.477
169	W169M	-5.079	1.163	3.740
169	W169Q	-2.921	-2.365	6.565
169	W169R	-4.000	-3.009	8.673
169	W169S	-3.627	-0.064	4.009
169	W169T	-2.204	-3.868	7.294
169	W169V	-0.345	-3.610	4.698
170	M170A	-0.832	-3.029	4.622
170	M170F	4.609	-4.006	-1.590
170	M170G	-3.962	4.296	-0.169
170	M170H	6.415	-4.788	0.108
170	M170L	5.004	-3.347	-0.520
170	M170N	-5.711	6.765	-1.262
170	M170Q	-13.710	16.776	-9.668
170	M170S	-5.041	5.346	-0.005
170	M170T	3.297	2.198	-10.060
170	M170V	1.052	-4.130	5.350
170	M170W	-12.257	9.383	-0.475
170	M170Y	3.469	-2.887	0.466
171	A171E	3.220	-1.322	-1.552
171	A171F	4.133	-1.567	-2.179
171	A171I	0.265	-2.216	3.383
171	A171V	3.137	-2.365	0.063

FIG. 45B Cont.				
171	A171W	7.120	-3.715	-2.224
172	K172A	3.967	-0.463	-3.614
172	K172M	5.834	-2.825	-2.135
172	K172P	-11.469	9.537	-1.552
173	Q173N	0.469	-3.667	5.623
173	Q173W	-2.314	-0.079	5.349
173	Q173Y	-0.479	-1.102	4.169
174	L174A	-5.962	8.637	-6.778
174	L174F	-3.087	4.019	-1.262
174	L174G	2.067	3.469	-12.791
174	L174Q	-11.267	-17.425	66.163
174	L174T	-5.267	5.927	-2.007
174	L174W	-6.644	5.130	3.383
176	P176H	-0.434	-2.463	5.240
176	P176L	-1.717	-0.549	4.202
177	L177D	-0.977	4.112	-7.366
177	L177G	-1.006	3.497	-5.928
177	L177M	3.081	-1.028	-4.556
177	L177T	3.197	-2.899	-0.438
178	V178A	-1.717	-0.673	4.421
178	V178W	3.793	-4.685	1.197
179	N179G	3.130	-0.720	-1.281
179	N179V	3.340	-3.342	1.391
179	N179Y	3.718	-1.414	-0.923
180	H180E	6.029	-1.825	-1.997
180	H180R	4.391	-2.879	0.207
181	D181A	1.694	-3.574	3.219
181	D181H	3.550	-3.316	1.253
181	D181Q	0.644	-2.494	3.219
181	D181S	0.003	-2.185	3.874
181	D181W	1.606	-4.160	4.421
182	S182A	1.111	-2.895	3.055
182	S182E	-0.551	-1.630	3.929
182	S182I	-0.638	-2.031	4.803
182	S182K	-2.644	-1.270	3.607

FIG. 46A

Mutations that increase % Ester	
MUTATION	Z Score
A1R	5.03
D2H	4.09
D2R	3.60
L4G	5.04
L4M	3.47
L5Q	3.20
I6A	4.33
I6L	5.83
L7E	6.00
G8A	3.98
S12N	4.13
A13I	4.23
A13L	7.83
A13S	8.38
A13T	11.78
A13W	3.67
A13Y	6.66
G14K	4.45
G14R	4.70
G14S	5.27
G14T	3.50
A22D	4.29
A22E	3.44
A22H	3.34
A22Y	9.47
W23Y	7.30
P24C	5.98
P24G	5.08
P24T	5.11
A25P	3.19
L26C	6.61
L26D	3.91
L26E	3.56
L26G	3.09
L26N	4.91
N28A	4.17
N28M	4.76
D29V	3.50
S33G	3.89

FIG. 46A Cont.

S33M	6.90
K34A	3.82
K34H	4.00
K34M	4.59
T35G	7.42
T35M	4.77
S36A	5.89
V37A	3.32
V37G	12.12
V37H	6.80
V37S	6.18
V38D	3.78
V38G	3.04
V38P	7.99
N39E	8.55
N39Q	10.27
N39R	8.30
A40M	8.09
A40P	4.48
S41T	3.18
G44F	15.32
G44Y	18.61
D45P	7.22
D45Q	6.10
T46W	5.89
S47F	11.65
Q49I	3.53
G50A	4.02
G50K	8.94
G50M	7.53
G50S	4.66
R53S	3.50
L58D	4.15
L58M	4.67
L58R	4.08
W65L	4.97
L67G	5.61
V68G	6.96
V68M	5.55
V68N	3.76
E69P	7.37
E69Q	4.96
L70A	3.26
L70E	5.28
L70H	6.20

FIG. 46A Cont.

G71C	5.41
G72A	8.49
N73C	43.13
N73G	20.82
N73L	99.80
N73R	55.92
N73T	21.73
N73V	23.14
D74C	3.40
D74S	6.08
D74W	3.06
G75A	5.56
G75K	9.24
G75L	4.21
G75M	5.22
L76A	8.09
L76F	6.06
L76G	9.97
L76I	12.96
L76M	8.95
L76N	7.26
L76T	8.29
L76W	3.88
R77G	3.68
F79A	4.32
F79M	3.53
F79P	5.17
P81E	3.67
P81W	9.66
T84F	3.46
T84H	6.48
T84Y	5.60
Q86P	5.77
Q86W	3.12
T87M	5.05
T87S	10.43
T87W	6.37
L88C	4.90
L88F	4.64
L88G	5.68
L88H	5.96
L88Y	6.92
R89G	3.31
Q90P	5.13
Q90W	4.08

FIG. 46A Cont.

I91M	3.07
I91S	3.57
L92C	3.80
L92G	3.16
Q93F	3.11
Q93P	4.58
V95A	4.03
V95D	12.50
V95E	5.71
V95L	4.40
V95M	5.04
K96P	4.05
N99L	3.35
N99M	4.20
N99S	4.70
A100D	3.22
A100K	4.15
A100L	7.81
A100M	4.13
A100V	3.06
A100Y	4.65
L103A	6.13
L104A	15.18
L104C	5.30
L104P	4.74
L104Q	9.63
L104W	10.14
M105A	5.23
Q106A	5.08
Q106C	3.89
Q106T	4.25
Q106W	3.32
I107C	3.47
I107M	3.01
R108E	4.03
L109F	6.41
L109M	3.71
G114F	3.10
R115W	3.53
Y117P	3.67
E119D	3.15
E119P	3.57
A120P	3.78
F121A	5.76
F121C	3.24

FIG. 46A Cont.

F121W	3.48
K127P	3.78
L128F	3.52
A129L	3.29
A129Y	3.90
E131A	3.45
F132P	4.96
V134P	5.07
P135A	5.45
L136A	6.42
F139M	4.10
M141A	5.51
M141P	5.32
E142A	3.32
E143P	3.02
V144A	3.51
W150D	7.23
W150E	3.06
M151S	3.79
G155V	5.25
I156K	5.55
I156M	3.06
P158A	5.79
P158G	10.16
P158Q	3.77
P158S	4.57
N159E	3.77
N159I	5.22
R160H	3.92
R160I	5.09
R160K	5.34
D161G	4.10
A162T	3.68
A162Y	8.66
Q163A	7.29
Q163C	7.72
Q163E	5.85
Q163G	11.71
Q163I	9.28
Q163M	4.29
Q163S	4.82
Q163T	3.00
Q163V	6.11
P164C	12.04
F165D	3.42

FIG. 46A Cont.

F165S	3.30
I166A	3.85
I166L	3.59
W169M	3.29
M170E	3.05
M170G	9.99
M170N	8.03
M170S	7.12
Q173P	3.78
L174A	3.78

FIG. 46B

Mutations that Decrease % Ester	
MUTATION	Z Score
T3E	-3.75
T3G	-3.15
T3K	-4.44
T3L	-5.16
L5C	-3.52
L5G	-7.94
Y15A	-9.80
Y15L	-7.41
Y15Q	-9.62
Y15R	-12.86
Y15V	-5.13
R16D	-5.44
R16E	-7.34
R16G	-5.66
R16I	-5.18
R16V	-4.68
S18E	-3.37
L27V	-4.40
N28G	-3.88
N28I	-4.84
S33I	-3.77
S33R	-4.67
K34R	-6.85
T35F	-3.95
T35K	-4.93
T35L	-5.21
T35Q	-6.00
T35V	-4.28
S36F	-3.06
S36I	-3.20
S36L	-4.70
S36W	-3.22
V37L	-7.70
V38E	-3.29
V38F	-3.81
V38K	-5.68
V38L	-4.19
A40D	-3.30
A40G	-7.18
I42T	-3.61

FIG. 46B Cont.

T46L	-3.27
L57A	-4.83
L57F	-4.37
L57G	-4.12
L57H	-6.58
L57K	-5.98
L57N	-5.05
L57P	-5.74
L57R	-5.38
L57S	-6.16
L57T	-4.19
L57V	-4.08
L57W	-3.71
L57Y	-5.01
K59V	-4.45
Q60E	-3.55
Q60P	-3.08
Q62G	-4.53
W65V	-4.41
V68L	-7.42
R77L	-3.91
G78M	-4.30
V95F	-3.85
V95N	-3.33
K96C	-4.65
K96L	-3.67
K96N	-4.18
K96Q	-5.36
K96R	-7.65
K96Y	-5.38
A97E	-4.36
A97F	-4.27
A97R	-4.60
A97W	-5.12
A98E	-3.70
N99A	-4.21
N99D	-3.30
A100S	-4.38
P102I	-3.39
L103Q	-3.11
L103W	-3.89
M105L	-3.83
Q106G	-5.28
Q106H	-5.37
Q106K	-3.30

FIG. 46B Cont.

Q106S	-4.63
Q106V	-5.60
F121P	-3.07
A123E	-4.90
Q152D	-4.56
Q152E	-9.86
Q152F	-11.08
Q152H	-12.47
Q152I	-8.55
Q152K	-6.37
Q152L	-7.44
Q152S	-5.03
Q152T	-7.31
Q152Y	-14.60
D153P	-4.17
D153V	-4.45
D154E	-3.11
A167V	-3.05
Q175L	-3.76
P176D	-3.67
V178K	-3.94
N179H	-3.14
N179W	-5.01
H180E	-3.01
H180L	-3.82
H180P	-3.19
H180R	-5.37
D181C	-3.81
D181E	-3.98
S182K	-5.10
S182L	-9.96
S182N	-3.24
S182R	-3.03
S182T	-3.14
S182V	-4.94

FIG. 46C

Mutation	Total Fatty Acid Derivative Z-Score
D2L	3.1
D2P	3.09
D2R	5.27
L5G	9.06
L11I	10.41
S12N	19.35
S12T	5.24
A13N	9.86
G14C	10.55
G14P	3.91
G14S	11.7
G14T	15.3
G14V	10.24
Y15C	15.73
Y15I	4.12
Y15V	14.38
R16T	10.83
M17D	5.66
M17E	13.02
M17N	12.87
M17R	8.13
M17S	17.91
M17V	14.03
A19C	8.28
A21G	3.99
A22L	8.35
A22R	9.85
A22T	11.82
A25P	4.3
L26D	6.02
L26G	5.13
L26W	3.97
L27C	18.8
L27F	4.85
L27W	4.46
L27Y	17.6
N28I	3.54
N28P	10.46

FIG. 46C Cont.

D29P	4.5
K30P	4.51
W31D	3.34
W31G	3.44
W31N	7.18
W31P	9.84
W31R	8.12
W31S	5.62
W31T	3.45
V37Y	3.31
N39P	4.07
S41C	6.16
I42D	3.81
I42G	5.49
S43E	5.31
G44K	4.38
G44R	5.74
G44W	4.52
D45G	2.99
Q49E	5.84
G50A	4.07
G50K	3.41
G50M	5.65
G50Q	3.87
L51D	7.74
L51T	3.23
R53A	14.19
R53G	19.1
R53L	3.99
R53N	19.72
R53S	10.86
R53V	8.46
L54E	10.38
L54F	7.61
L54G	16.55
L54N	18.34
L54S	6.45
L54W	7.15
L58R	4.52
P63G	3.98
P63M	3.85

FIG. 46C Cont.

P63N	4.85
P63T	3.32
P63W	3.16
W65E	3.44
W65G	3.87
V66G	3.15
V66S	5.47
L67T	2.95
V68S	3.59
E69F	4.13
E69V	6.21
L70C	12.11
L70F	6.04
L70Q	6.61
L70S	9.83
L70T	6.68
L70V	3.8
G71A	10.48
N73G	6.55
N73L	3.47
D74A	11.53
D74C	19.11
G75A	3.47
G75C	4.7
G75F	11.23
G75R	9.68
G75W	3.24
L76I	7.06
R77A	5.59
R77C	24.14
R77D	17.67
R77F	19.44
R77G	6.42
R77H	18.69
R77K	4.45
R77L	3.18
R77N	27.44
R77Q	5.4
R77S	26.28
R77W	14.62
G78D	30.26

FIG. 46C Cont.

G78E	7.28
F79K	3.58
Q80G	5.77
T84H	4.38
T84N	4.63
T84Q	3.61
T87A	4.56
T87F	10.68
T87H	3.02
T87W	4.76
L88A	3.11
L88C	5.35
L88H	5.98
Q90N	3.66
Q90W	10.88
I91G	40.44
I91L	7.89
I91M	8.25
I91S	50.1
L92G	48.24
L92N	56.72
L92Q	34.3
L92S	6.32
L92T	14.59
L92Y	35.1
Q93P	15.14
D94P	6.43
V95F	3.15
V95N	5.79
V95Q	9.2
K96P	7.91
A97C	3.52
A97P	11.7
A98P	5.42
A98V	5.62
A100D	12.11
A100E	8.23
A100Q	9.29
A100Y	3.33
P102L	5.39
P102Q	4.73

FIG. 46C Cont.

P102R	9.77
L103E	6.37
L103K	4.03
L104A	34.92
L104Q	14.84
L104W	14.88
L104Y	3.25
M105C	4.72
M105E	4.3
M105F	4.17
M105L	4.82
Q106D	4.12
Q106G	7.15
Q106L	4.33
Q106V	3.38
Q106W	3.87
Q106Y	6.66
I107A	38.63
I107C	19.37
I107E	7.18
I107G	11.8
I107K	29.78
I107L	38.5
I107Q	25.71
I107S	4.17
I107T	8.3
R108G	8.53
L109F	5.13
L109V	32.35
L109Y	13.22
P110A	20.08
P110E	3.92
P110F	4.31
P110G	4.8
P110H	22.31
P110N	24.19
P110S	3.14
P110V	11.63
A111Y	4.58
N112F	3.1
N112P	3.5

FIG. 46C Cont.

Y113D	7.02
Y113E	3.14
Y113P	6.39
R115W	13.16
Y117A	4.83
Y117D	6.71
Y117E	4.27
Y117G	7.9
Y117P	8.97
Y117Q	4.65
N118F	6.41
E119P	5.92
A120P	7.4
F121C	7.33
F121L	2.95
F121M	4.56
F121N	5.99
F121Q	7.56
F121R	5.7
F121V	5.95
F121W	8.69
F121Y	5.61
S122D	4.01
S122F	3.37
S122L	5.09
S122P	5.48
S122W	5.64
S122Y	7.13
I124A	3.2
I124G	4.26
I124H	3.91
I124K	4.95
I124R	5.09
K127P	4.82
L128S	5.28
A129I	7.03
A129W	5.66
A129Y	4.68
K130P	5.67
L136A	5.53
L136D	6.18

FIG. 46C Cont.

L136E	14.63
L136G	16.68
L136K	4.2
L136N	6.97
L136P	5.97
L136Q	3.19
L136S	3.2
L136T	9.17
L137A	13.72
L137C	4.56
L137H	17.74
L137K	4.68
L137Q	16.1
L137S	16.41
L137Y	4.51
P138F	8.47
F139L	4
F139M	9.77
F140C	8.5
F140I	5.75
F140L	7.6
F140M	11.44
F140V	5.4
M141T	3.63
E143P	8.01
V144H	3.57
Y145I	6.61
L146G	3
L146P	10.14
W150G	2.98
W150I	6.42
W150V	12.18
M151F	6.24
M151L	5.43
M151R	8.2
M151S	3.62
M151T	5.19
M151W	3.09
Q152N	4.22
Q152V	7.76
Q152Y	4.88

FIG. 46C Cont.

D154C	12.35
D154E	5.76
G155I	4.41
I156C	5.24
I156K	7.75
I156T	6.63
I156V	4.43
P158G	3.01
P158T	7.31
A162T	6.21
Q163A	5.37
Q163C	5.25
Q163E	5.17
Q163I	4.83
Q163S	5.27
Q163T	3.47
Q163V	3.25
I166C	3.39
A167E	8.68
A167F	8.37
A167L	5.18
A167N	6.56
A167R	4.61
A167V	3.39
A167Y	7.5
W169K	5.3
M170N	3.97
M170S	4.35
Q173D	3.48
L174A	7.12
L174T	11.05
L174W	3.59

FIG. 46D

Mutation	% Short Chain Z-Score
A13V	7.09
R16A	11.68
M17T	7.96
A25S	3.27
D29M	3.68
W31L	3.55
T35Y	4.06
S36W	3.53
V38S	3.40
P55A	3.39
P55G	4.06
L57I	4.09
L58M	3.45
L58V	4.08
K59E	3.50
H61W	3.16
Q62M	3.02
P63V	3.29
R64M	3.08
W65L	3.30
V66C	5.60
L67C	5.55
L67M	3.18
G78F	3.39
G78M	3.80
G78R	3.31
G78T	6.98
G78V	4.03
F79K	5.25
F79Y	3.92
Q82A	3.27
Q82M	3.26
Q82R	3.05
Q83G	3.70
Q83K	4.81
T84M	3.89
T84V	3.61
E85A	3.07

FIG. 46D Cont.

E85C	4.50
E85G	4.06
E85Q	4.15
E85S	3.63
E85T	3.30
E85V	3.44
E85W	3.96
E85Y	3.69
Q86H	3.43
Q86Y	3.32
T87R	3.52
R89V	3.51
Q90L	3.16
Q93M	3.31
Q93N	3.61
Q93V	3.18
D94C	3.53
D94L	3.52
V95G	3.30
K96C	3.24
A97N	4.73
A97V	4.59
A98G	3.67
A98Y	4.87
M105I	3.47
Q106K	3.18
Q106R	4.48
R108W	3.83
A111E	4.12
A111N	5.07
A111S	4.21
A111W	6.93
A111Y	4.86
Y113A	3.19
Y113S	3.04
Y113V	4.98
G114K	3.54
G114Y	3.66
Y117R	5.13
E119M	4.08
E119Q	3.49

FIG. 46D Cont.

E119R	3.28
S122F	3.57
S122I	5.40
S122M	6.27
S122R	5.14
P126K	3.97
F132C	4.67
F132D	4.72
F132K	3.54
F132L	4.13
F132N	4.95
F132V	4.28
P135A	3.60
P135E	4.28
P135K	3.75
P135Q	3.37
L136H	4.45
F139L	3.92
E142W	3.17
V144Y	3.35
Y145A	6.56
Y145C	8.23
Y145D	4.08
Y145E	7.49
Y145G	4.43
Y145I	5.79
Y145L	9.47
Y145M	4.49
Y145N	4.71
Y145R	7.80
Y145S	6.13
Y145T	5.12
D153K	3.32
D153Q	3.10
D161K	3.21
A162I	3.34
F165K	3.34
D168W	3.59
Q173I	4.32
Q175M	3.35
P176Q	4.15

FIG. 46D Cont.

P176R	4.03
P176V	31.09
V178F	6.09
V178G	4.08
V178L	4.38
V178R	6.56
V178S	4.09
V178T	7.82
N179H	3.08
H180E	3.85
H180P	3.13
H180R	4.08
H180S	4.02
H180V	3.27
H180W	3.32
D181R	3.24
D181T	3.06
S182C	3.07
S182D	5.28
S182G	3.84
S182P	5.05
S182R	3.11

FIG. 46E

Mutation	% Short Chain Z-Score
A1C	-63.21
A1F	-9.02
A1L	-44.70
A1Y	-8.32
D2L	-5.90
D2M	-4.92
D2P	-19.11
D2W	-20.50
T3R	-26.69
L4A	-6.44
L4M	-4.38
L4N	-42.37
L4S	-40.54
L4V	-5.67
L4Y	-5.91
L5E	-35.71
L5F	-4.80
L5G	-7.53
L5K	-30.43
L5N	-42.32
L5S	-4.31
L5W	-31.99
I6T	-14.34
L7A	-3.04
L7E	-42.41
L7K	-37.04
L7M	-21.53
L7W	-57.14
G8K	-214.60
D9N	-14.32
D9T	-120.67
L11A	-18.08
L11C	-107.22
L11I	-7.83
L11M	-101.21
L11Q	-91.91
L11V	-116.56
S12I	-93.25
S12L	-12.25

FIG. 46E Cont.

S12M	-4.54
S12N	-18.74
S12T	-3.35
S12V	-78.58
S12Y	-12.22
A13C	-3.99
G14C	-39.75
G14E	-100.31
G14I	-102.00
G14M	-111.79
G14N	-35.52
G14P	-60.98
G14S	-5.26
G14T	-21.65
G14V	-9.41
Y15C	-18.57
Y15E	-80.36
Y15G	-77.73
Y15I	-62.75
Y15N	-102.87
Y15V	-25.60
R16T	-7.14
M17D	-11.63
M17E	-27.51
M17G	-4.41
M17L	-7.33
M17N	-8.89
M17P	-3.70
M17R	-46.44
M17S	-16.39
M17V	-22.23
S18M	-5.57
S18N	-35.29
S18T	-7.42
A19E	-4.77
A19L	-22.51
A19V	-25.84
A21P	-3.45
A22D	-3.98
A22E	-12.41
A22F	-23.02

FIG. 46E Cont.

A22H	-15.49
A22I	-12.96
A22K	-18.01
A22L	-24.96
A22P	-11.17
A22R	-19.43
A22S	-4.85
A22T	-4.65
A22Y	-10.55
W23A	-24.50
W23H	-87.01
W23N	-13.53
W23P	-19.15
P24A	-6.88
P24C	-8.82
P24D	-16.32
P24E	-17.09
P24F	-26.45
P24G	-17.75
P24I	-4.37
P24M	-22.41
P24N	-13.92
P24S	-12.83
P24T	-9.58
P24V	-4.54
P24W	-30.72
L26P	-21.59
L27A	-19.17
L27C	-8.14
L27F	-4.31
L27H	-61.92
L27R	-58.76
L27S	-62.16
L27T	-45.28
L27W	-8.60
L27Y	-17.79
K30P	-4.76
W31D	-4.32
W31P	-4.55
W31R	-3.68
S36F	-4.42

FIG. 46E Cont.

S36L	-4.11
V37G	-11.20
V37H	-10.89
V37N	-33.74
V37Q	-10.59
V37W	-30.09
V37Y	-12.66
V38P	-3.60
N39E	-6.92
N39G	-3.17
N39K	-46.33
N39M	-39.26
N39P	-4.38
N39Q	-3.40
N39Y	-7.53
I42D	-12.43
I42G	-3.39
I42P	-18.84
G44A	-12.40
G44E	-16.26
G44K	-7.30
G44M	-11.89
G44N	-13.25
G44R	-3.19
G44S	-18.29
G44W	-15.05
G44Y	-10.81
D45G	-5.89
D45M	-4.57
T46D	-7.57
S47E	-3.25
S47P	-21.28
S47Q	-5.63
S47R	-6.47
S47Y	-8.31
Q48Y	-3.34
G50C	-8.06
G50E	-31.84
G50F	-19.16
G50I	-19.41
G50K	-16.73

FIG. 46E Cont.

G50L	-19.75
G50M	-14.11
G50N	-20.46
G50P	-53.52
G50Q	-16.90
G50R	-45.44
G50S	-17.05
G50T	-36.12
G50W	-26.95
G50Y	-26.67
L51D	-10.49
L51P	-44.08
L51T	-4.49
A52P	-40.24
R53A	-6.83
R53C	-48.10
R53D	-16.24
R53E	-15.22
R53F	-60.20
R53G	-6.40
R53I	-15.55
R53K	-3.63
R53L	-14.72
R53N	-4.40
R53S	-6.28
R53T	-38.15
R53V	-13.28
R53W	-15.21
R53Y	-16.67
L54C	-5.06
L54E	-5.47
L54G	-3.80
L54N	-5.95
L54Y	-17.42
P55Y	-3.37
L57P	-3.06
H61A	-7.21
H61D	-5.86
H61E	-9.15
P63D	-98.14
P63E	-42.96

FIG. 46E Cont.

P63G	-28.12
P63K	-70.32
P63M	-5.00
P63N	-19.05
P63Q	-34.79
P63R	-64.59
R64L	-4.58
W65G	-12.80
W65P	-8.14
W65R	-3.23
V66N	-5.41
V66Q	-6.18
V66S	-6.63
V66W	-3.70
V66Y	-6.28
L67E	-8.21
L67G	-6.01
L67Q	-60.05
L67R	-12.02
L67S	-6.98
L67W	-4.14
V68E	-11.51
V68G	-60.22
V68N	-4.74
V68P	-3.83
V68Q	-5.95
E69A	-28.03
E69C	-27.17
E69D	-61.95
E69F	-24.68
E69G	-28.66
E69H	-28.86
E69K	-32.28
E69L	-25.27
E69M	-27.85
E69N	-27.47
E69P	-25.46
E69Q	-35.73
E69S	-49.76
E69V	-18.30
E69W	-66.11

FIG. 46E Cont.

E69Y	-37.18
L70A	-42.86
L70C	-3.55
L70E	-42.71
L70F	-19.50
L70G	-94.13
L70H	-25.17
L70K	-29.95
L70Q	-20.11
L70S	-7.68
L70T	-14.42
L70W	-57.74
G71C	-32.31
G71S	-56.24
G72A	-26.23
G72M	-33.06
G72P	-47.28
N73A	-4.63
N73G	-13.51
N73H	-10.61
N73I	-8.43
N73L	-7.30
N73P	-9.25
N73R	-6.25
N73S	-8.04
N73T	-28.23
N73W	-7.23
D74A	-45.23
D74C	-31.24
D74F	-28.47
D74G	-60.70
D74Q	-24.51
D74S	-38.03
D74W	-49.27
D74Y	-99.77
G75A	-20.56
G75C	-48.09
G75D	-81.21
G75E	-42.01
G75F	-48.35
G75I	-32.43

FIG. 46E Cont.

G75K	-26.48
G75L	-32.30
G75M	-24.38
G75N	-52.61
G75P	-62.43
G75R	-31.94
G75T	-53.18
G75V	-57.06
G75W	-56.35
G75Y	-57.62
L76A	-22.79
L76C	-7.92
L76D	-12.58
L76E	-30.25
L76F	-19.25
L76G	-26.23
L76I	-6.81
L76K	-4.47
L76M	-4.68
L76N	-31.55
L76P	-8.17
L76Q	-9.92
L76R	-6.71
L76T	-25.66
L76V	-6.91
L76W	-5.04
R77A	-26.49
R77C	-9.00
R77D	-30.03
R77E	-20.54
R77F	-24.10
R77G	-9.49
R77H	-24.48
R77N	-8.48
R77S	-10.71
R77V	-22.45
R77W	-28.93
G78A	-6.52
G78C	-8.34
G78D	-9.99
G78E	-3.95

FIG. 46E Cont.

G78N	-8.13
G78P	-10.38
G78Q	-18.48
G78Y	-21.82
F79P	-28.76
F79Q	-6.47
F79S	-4.11
F79V	-3.46
P81E	-3.29
P81W	-3.14
T84D	-88.05
T84E	-41.00
T84G	-26.25
T84H	-10.81
T84K	-63.88
T84L	-23.82
T84N	-7.78
T84Q	-3.62
T84R	-46.36
T84W	-38.11
T84Y	-24.81
E85F	-13.79
E85P	-53.55
Q86A	-5.22
T87F	-4.59
L88A	-25.28
L88E	-37.11
L88G	-32.24
L88H	-20.68
L88Q	-42.32
L88S	-46.95
L88W	-30.65
L88Y	-29.41
R89P	-24.05
Q90P	-31.92
Q90W	-3.38
I91E	-79.82
I91L	-5.73
I91M	-30.56
I91N	-42.09
I91Q	-38.31

FIG. 46E Cont.

I91S	-4.95
I91Y	-43.76
L92C	-4.99
L92E	-73.12
L92G	-5.00
L92H	-9.88
L92N	-7.93
L92Q	-19.11
L92R	-84.60
L92S	-8.48
L92Y	-13.84
Q93P	-32.68
D94P	-7.30
D94V	-3.57
V95A	-3.75
V95C	-5.62
V95D	-29.29
V95E	-30.46
V95F	-20.99
V95I	-8.56
V95P	-59.35
V95Q	-22.52
V95W	-24.15
V95Y	-33.39
K96P	-8.92
A97C	-7.38
A97P	-15.17
N99D	-33.21
A100Q	-5.06
A100Y	-4.26
P102E	-46.58
P102G	-3.79
P102H	-45.32
P102L	-3.44
P102R	-10.05
P102V	-8.26
P102W	-22.77
L103C	-3.18
L103E	-24.55
L103I	-3.75
L103K	-5.44

FIG. 46E Cont.

L103N	-11.31
L103R	-4.04
L103S	-4.81
L103T	-11.37
L103V	-6.38
L104A	-11.07
L104C	-3.49
L104E	-28.11
L104G	-31.37
L104I	-7.05
L104N	-32.01
L104P	-3.12
L104Q	-22.01
L104S	-61.20
L104W	-18.48
L104Y	-23.89
M105A	-28.83
M105C	-10.71
M105E	-8.53
M105F	-3.85
M105G	-18.71
M105K	-34.14
M105L	-5.29
M105P	-102.51
M105T	-11.34
M105W	-50.61
Q106D	-10.02
Q106G	-9.34
Q106H	-14.02
Q106L	-20.17
Q106W	-11.32
I107A	-17.31
I107E	-32.09
I107F	-20.95
I107G	-28.47
I107K	-22.87
I107L	-3.00
I107Q	-18.95
I107S	-23.44
I107T	-7.98
I107Y	-22.72

FIG. 46E Cont.

R108A	-10.47
R108C	-9.20
R108D	-13.69
R108E	-9.20
R108F	-5.75
R108G	-10.70
R108H	-9.69
R108I	-6.35
R108L	-8.87
R108M	-5.49
R108S	-11.02
R108V	-9.68
R108Y	-9.49
L109C	-41.59
L109F	-28.41
L109G	-42.09
L109K	-69.64
L109Q	-50.80
L109R	-29.08
L109T	-41.67
L109V	-23.71
L109Y	-43.56
P110A	-33.63
P110C	-25.47
P110D	-24.31
P110E	-17.72
P110F	-43.41
P110G	-23.80
P110H	-34.80
P110K	-30.19
P110L	-23.19
P110M	-23.20
P110N	-33.38
P110R	-51.79
P110S	-22.47
P110V	-33.71
P110W	-39.36
A111C	-9.89
A111L	-3.57
A111P	-4.23
A111Q	-5.35

FIG. 46E Cont.

A111R	-8.12
A111V	-4.23
N112I	-10.62
N112L	-4.98
N112P	-11.54
N112Y	-5.03
Y113D	-11.51
Y113E	-3.61
Y113Q	-3.02
G114A	-9.61
R115W	-10.95
Y117D	-6.37
Y117G	-4.14
Y117P	-4.06
N118F	-3.92
E119C	-3.87
E119L	-7.23
A120P	-6.88
F121A	-28.88
F121C	-5.63
F121D	-42.24
F121E	-39.48
F121G	-15.38
F121K	-42.52
F121L	-19.00
F121N	-18.73
F121P	-41.32
F121Q	-11.85
F121R	-13.32
F121S	-29.43
F121V	-9.75
F121W	-3.56
F121Y	-13.42
S122D	-9.90
S122E	-7.17
S122L	-5.66
S122P	-10.63
I124D	-37.98
I124E	-27.01
I124G	-8.97
I124H	-10.69

FIG. 46E Cont.

I124K	-4.59
I124R	-4.97
I124W	-15.37
I124Y	-23.96
Y125C	-19.66
Y125G	-21.01
Y125H	-30.52
Y125I	-17.04
Y125L	-24.91
Y125P	-21.87
Y125Q	-23.99
Y125R	-20.53
Y125S	-21.85
Y125T	-21.27
Y125V	-21.89
K127A	-6.42
L128E	-27.59
L128F	-22.69
L128G	-29.74
L128K	-21.82
L128Q	-18.58
L128R	-41.57
L128S	-6.88
L128W	-40.49
A129D	-32.30
A129F	-17.62
A129L	-20.77
A129W	-8.30
A129Y	-11.75
K130P	-8.51
K130V	-4.75
E131A	-12.26
E131C	-7.90
E131D	-3.75
E131P	-60.42
E131V	-3.20
F132P	-67.58
D133C	-5.33
V134C	-3.68
V134D	-5.51
V134N	-14.94

FIG. 46E Cont.

V134P	-64.09
V134W	-9.68
L136A	-4.43
L136D	-25.03
L136E	-9.24
L136G	-11.96
L136N	-12.24
L136P	-12.86
L136T	-5.66
L137D	-77.81
L137E	-44.88
L137G	-64.00
L137H	-9.52
L137K	-21.51
L137P	-59.72
L137Q	-3.55
L137R	-45.70
L137S	-12.66
P138G	-7.85
P138N	-66.99
P138V	-7.12
F139A	-39.52
F139C	-19.20
F139D	-51.25
F139E	-54.34
F139G	-23.27
F139H	-47.30
F139M	-14.75
F139N	-20.27
F139S	-28.56
F139T	-25.28
F139V	-51.37
F139W	-26.49
F140A	-23.45
F140C	-17.35
F140G	-59.93
F140I	-8.48
F140L	-11.28
F140M	-6.79
F140N	-34.77
F140P	-35.35

FIG. 46E Cont.

F140S	-46.16
F140T	-47.57
F140V	-11.26
F140W	-20.83
M141C	-5.00
M141D	-22.31
M141E	-28.46
M141F	-26.20
M141G	-16.10
M141K	-32.04
M141L	-6.54
M141P	-5.70
M141Q	-22.98
M141R	-33.51
M141T	-10.69
M141W	-48.57
M141Y	-29.44
E142A	-5.76
E142C	-23.94
E142G	-4.51
E142I	-3.28
E142L	-13.49
E142M	-3.24
E142P	-5.72
E142Q	-6.34
E142R	-6.85
E142T	-4.28
E142V	-4.47
E143A	-7.08
E143D	-5.09
E143F	-5.68
E143G	-3.69
E143I	-4.21
E143M	-8.02
E143P	-6.28
E143W	-4.76
V144A	-3.67
V144D	-17.15
V144E	-13.28
V144G	-18.12
V144H	-15.74

FIG. 46E Cont.

V144N	-19.72
V144P	-9.89
V144Q	-11.28
V144R	-14.09
V144S	-16.74
Y145Q	-16.20
Y145W	-24.17
L146C	-5.36
L146P	-7.13
W150P	-8.88
W150R	-3.07
M151A	-22.29
M151C	-13.48
M151D	-53.94
M151E	-36.34
M151F	-6.85
M151G	-28.78
M151I	-12.66
M151L	-7.96
M151Q	-14.75
M151R	-6.83
M151S	-18.89
M151T	-5.52
M151V	-12.16
M151W	-18.58
Q152P	-4.80
D153A	-7.19
D153E	-3.25
D153F	-4.87
D154A	-23.82
D154C	-3.67
D154E	-22.22
D154F	-58.92
D154G	-25.00
D154H	-31.59
D154I	-64.36
D154K	-29.79
D154L	-60.21
D154M	-25.21
D154N	-28.72
D154P	-58.38

FIG. 46E Cont.

D154R	-28.30
D154S	-39.88
D154T	-59.86
D154V	-59.21
D154W	-60.95
G155A	-3.44
G155P	-27.12
G155V	-5.61
I156A	-11.30
I156C	-7.69
I156E	-30.46
I156F	-12.66
I156G	-54.46
I156K	-19.45
I156M	-11.92
I156Q	-12.81
I156R	-12.93
I156S	-15.73
I156T	-19.26
I156Y	-20.27
H157C	-5.78
H157E	-22.88
P158F	-13.72
P158H	-12.61
P158I	-21.00
P158L	-11.13
P158Q	-11.63
P158V	-10.02
P158W	-30.29
N159P	-31.69
N159W	-15.96
A162K	-21.65
A162L	-20.87
A162N	-24.35
A162R	-17.88
A162Y	-21.36
Q163A	-7.69
Q163D	-52.48
Q163E	-5.19
Q163F	-30.51
Q163I	-4.62

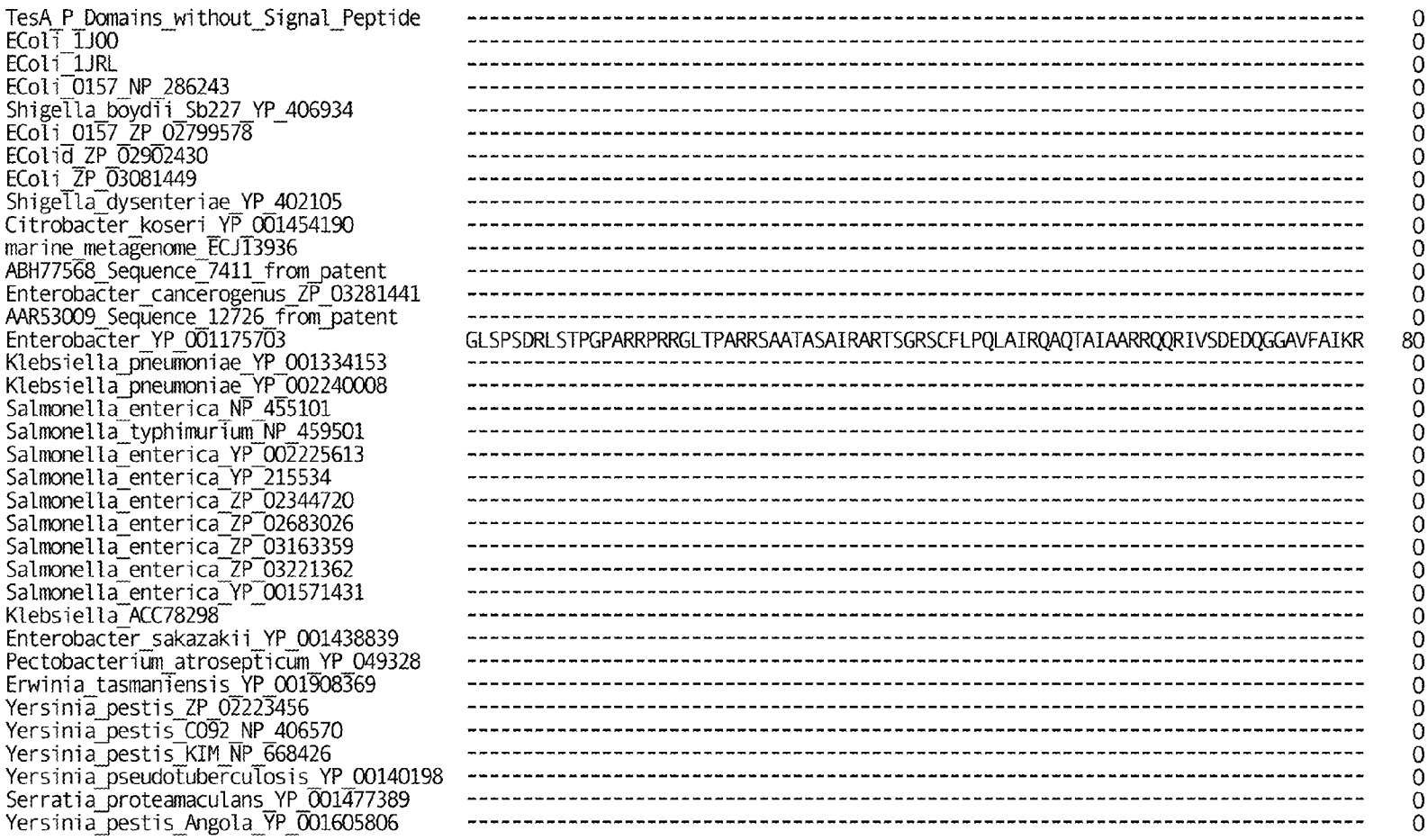
FIG. 46E Cont.

Q163V	-10.61
Q163W	-18.60
Q163Y	-24.52
F165L	-16.66
I166A	-12.07
I166F	-18.25
I166M	-7.12
I166S	-55.69
I166Y	-14.41
A167C	-4.32
A167D	-22.48
A167E	-3.95
A167F	-13.29
A167L	-6.74
A167N	-10.52
A167R	-8.46
A167V	-5.29
A167W	-81.07
A167Y	-7.34
D168M	-3.18
D168R	-3.50
M170E	-5.17
M170F	-4.50
M170G	-34.58
M170N	-11.65
M170S	-11.08
M170T	-9.46
A171S	-26.54
Q173D	-10.77
Q173P	-44.81
L174A	-12.29
L174G	-29.08
L174S	-44.11
L174T	-4.63
L174W	-7.19
L174Y	-47.03
Q175F	-38.91
P176L	-8.35
P176Y	-4.38
L177F	-4.63
L177M	-4.34

FIG. 46E Cont.

L177S	-3.75
D181C	-6.46
D181E	-6.68
D181G	-3.39

FIG. 47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Erwinia_tasmaniensis_YP_001908369 0
Yersinia_pestis_ZP_02223456 0
Yersinia_pestis_CO92_NP_406570 0
Yersinia_pestis_KIM_NP_668426 0
Yersinia_pseudotuberculosis_YP_00140198 0
Serratia_proteamaculans_YP_001477389 0
Yersinia_pestis_Angola_YP_001605806 0

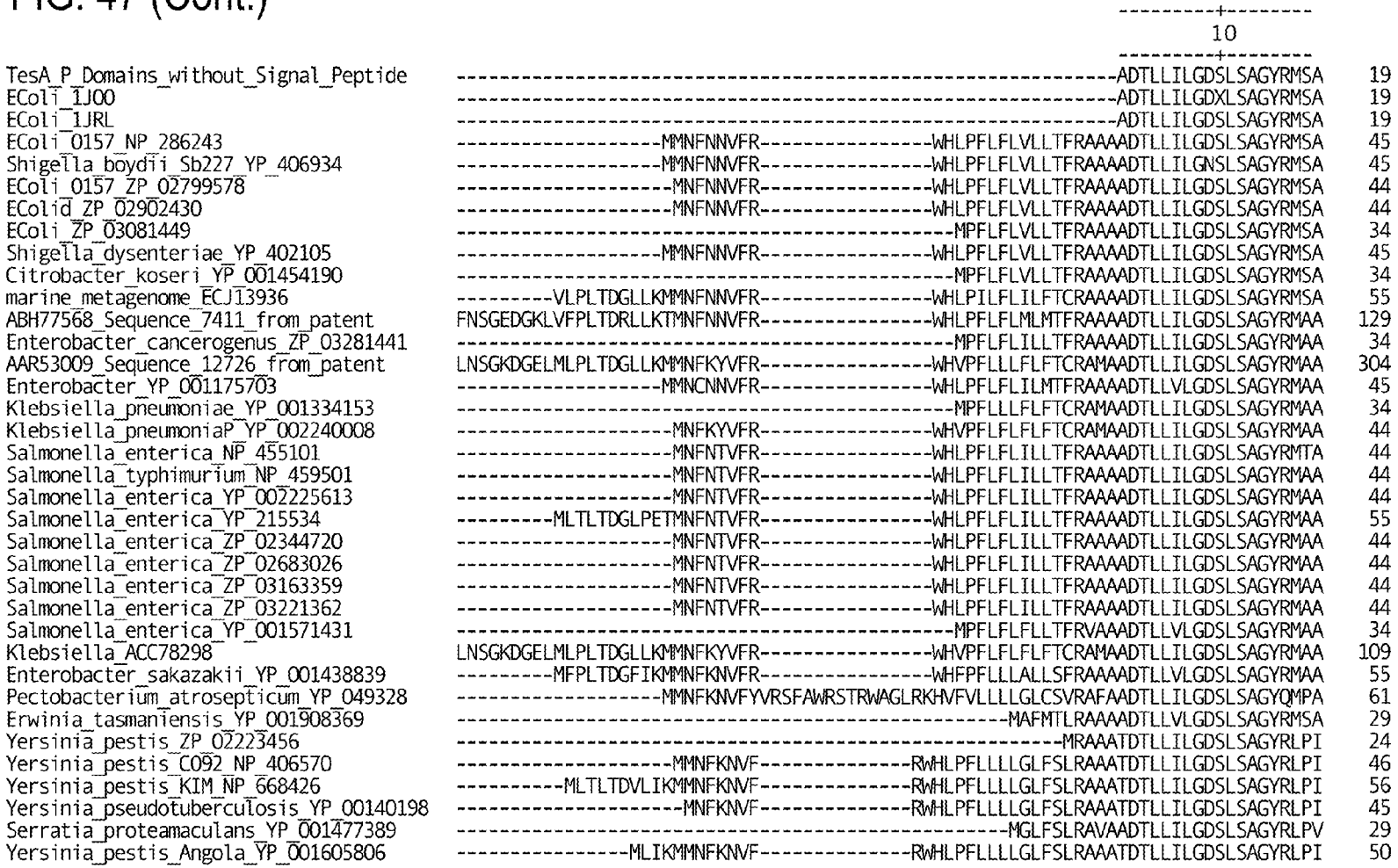
FIG. 47 (Cont.)

TesA_P_Domains_without_Signal_Peptide	--	0
EColi_1JO0	--	0
EColi_1JRL	--	0
EColi_0157_NP_286243	--	0
Shigella_boydii_Sb227_YP_406934	--	0
EColi_0157_ZP_02799578	--	0
EColid_ZP_02902430	--	0
EColi_ZP_03081449	--	0
Shigella_dysenteriae_YP_402105	--	0
Citrobacter_koseri_YP_001454190	--	0
marine_metagenome_ECJ13936	--	0
ABH77568_Sequence_7411_from_patent	--	0
Enterobacter_cancerogenus_ZP_03281441	--	0
AAR53009_Sequence_12726_from_patent	EQQIGNFVPGLAIEVAGGLIGEQNGRAPVKGPGQRHPLLFAAGELRRQVVQAFAKSQLLKQRAGIAPALAIAGAAQQRRQ	160
Enterobacter_YP_001175703	--	0
Klebsiella_pneumoniae_YP_001334153	--	0
Klebsiella_pneumoniae_YP_002240008	--	0
Salmonella_enterica_NP_455101	--	0
Salmonella_typhimurium_NP_459501	--	0
Salmonella_enterica_YP_002225613	--	0
Salmonella_enterica_YP_215534	--	0
Salmonella_enterica_ZP_02344720	--	0
Salmonella_enterica_ZP_02683026	--	0
Salmonella_enterica_ZP_03163359	--	0
Salmonella_enterica_ZP_03221362	--	0
Salmonella_enterica_YP_001571431	--	0
Klebsiella_ACC78298	--	0
Enterobacter_sakazakii_YP_001438839	--	0
Pectobacterium_atrosepticum_YP_049328	--	0
Erwinia_tasmaniensis_YP_001908369	--	0
Yersinia_pestis_ZP_02223456	--	0
Yersinia_pestis_CO92_NP_406570	--	0
Yersinia_pestis_KIM_NP_668426	--	0
Yersinia_pseudotuberculosis_YP_00140198	--	0
Serratia_proteamaculans_YP_001477389	--	0
Yersinia_pestis_Angola_YP_001605806	--	0

FIG. 47 (Cont.)

```
TesA_P_Domains_without_Signal_Peptide   ----------------------------------------------------------------------------------------   0
EColi_1J00                              ----------------------------------------------------------------------------------------   0
EColi_1JRL                              ----------------------------------------------------------------------------------------   0
EColi_0157_NP_286243                    ----------------------------------------------------------------------------------------   0
Shigella_boydii_Sb227_YP_406934         ----------------------------------------------------------------------------------------   0
EColi_0157_ZP_02799578                  ----------------------------------------------------------------------------------------   0
EColid_ZP_02902430                      ----------------------------------------------------------------------------------------   0
EColi_ZP_03081449                       ----------------------------------------------------------------------------------------   0
Shigella_dysenteriae_YP_402105          ----------------------------------------------------------------------------------------   0
Citrobacter_koseri_YP_001454190         ----------------------------------------------------------------------------------------   0
marine_metagenome_ECJ13936              ----------------------------------------------------------------------------------------   0
ABH77568_Sequence_7411_from_patent      ---------------LKDKPDMPGSQRGAGLFIKRVEGLADQVHFPTAAIVQTGENGQQRGLTGTGFTNQGDGFGTFDNE   65
Enterobacter_cancerogenus_ZP_03281441   ----------------------------------------------------------------------------------------   0
AAR53009_Sequence_12726_from_patent     LDVLQGVERRDQHKRLKNKTNVLRPQRRPRLFIHPVQRFAQHRYFPAAAIVEAGEDRQQGRFTGTRLADQGDGLPRFDNQ   240
Enterobacter_YP_001175703               ----------------------------------------------------------------------------------------   0
Klebsiella_pneumoniae_YP_001334153      ----------------------------------------------------------------------------------------   0
Klebsiella_pneumoniae_YP_002240008      ----------------------------------------------------------------------------------------   0
Salmonella_enterica_NP_455101           ----------------------------------------------------------------------------------------   0
Salmonella_typhimurium_NP_459501        ----------------------------------------------------------------------------------------   0
Salmonella_enterica_YP_002225613        ----------------------------------------------------------------------------------------   0
Salmonella_enterica_YP_215534           ----------------------------------------------------------------------------------------   0
Salmonella_enterica_ZP_02344720         ----------------------------------------------------------------------------------------   0
Salmonella_enterica_Zp_02683026         ----------------------------------------------------------------------------------------   0
Salmonella_enterica_ZP_03163359         ----------------------------------------------------------------------------------------   0
Salmonella_enterica_ZP_03221362         ----------------------------------------------------------------------------------------   0
Salmonella_enterica_YP_001571431        ----------------------------------------------------------------------------------------   0
Klebsiella_ACC78298                     ----------------------------------MQRFAQHRYFPAAAIVQAGEDRQQGRFTGARLADQGDGLPRFDNQ   45
Enterobacter_sakazakii_Yp_001438839     ----------------------------------------------------------------------------------------   0
Pectobacterium_atrosepticum_YP_049328   ----------------------------------------------------------------------------------------   0
Erwinia_tasmaniensis_YP_001908369       ----------------------------------------------------------------------------------------   0
Yersinia_pestis_ZP_02223456             ----------------------------------------------------------------------------------------   0
Yersinia_pestis_C092_NP_406570          ----------------------------------------------------------------------------------------   0
Yersinia_pestis_KIM_NP_668426           ----------------------------------------------------------------------------------------   0
Yersinia_pseudotuberculosis_YP_00140198 ----------------------------------------------------------------------------------------   0
Serratia_proteamaculans_YP_001477389    ----------------------------------------------------------------------------------------   0
Yersinia_pestis_Angola_YP_001605806     ----------------------------------------------------------------------------------------   0
```

FIG. 47 (Cont.)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TesA_P_Domains_without_Signal_Peptide
EColi_1J00
EColi_1JRL
EColi_0157_NP_286243
Shigella_boydii_Sb227_YP_406934
EColi_0157_ZP_02799578
EColid_ZP_02902430
EColi_ZP_03081449
Shigella_dysenteriae_YP_402105
Citrobacter_koseri_YP_001454190
marine_metagenome_ECJ13936
ABH77568_Sequence_7411_from_patent
Enterobacter_cancerogenus_ZP_03281441
AAR53009_Sequence_12726_from_patent
Enterobacter_YP_001175703
Klebsiella_pneumoniae_YP_001334153
KlebsiellA_pneumoniaP_YP_002240008
Salmonella_enterica_NP_455101
Salmonella_typhimurium_NP_459501
Salmonella_enterica_YP_002225613
Salmonella_enterica_YP_215534
Salmonella_enterica_ZP_02344720
Salmonella_enterica_ZP_02683026
Salmonella_enterica_ZP_03163359
Salmonella_enterica_ZP_03221362
Salmonella_enterica_YP_001571431
Klebsiella_ACC78298
Enterobacter_sakazakii_YP_001438839
Pectobacterium_atrosepticum_YP_049328
Erwinia_tasmaniensis_YP_001908369
Yersinia_pestis_ZP_02223456
Yersinia_pestis_C092_NP_406570
Yersinia_pestis_KIM_NP_668426
Yersinia_pseudotuberculosis_YP_00140198
Serratia_proteamaculans_YP_001477389
Yersinia_pestis_Angola_YP_001605806

FIG. 47 (Cont.)

```
                                            +--------+----------+--------+--------+--------+--------+--------+-----
                                            20       30         40       50       60       70       80       90
                                            +--------+----------+--------+--------+--------+--------+--------+-----
TesA_P_Domains_without_Signal_Peptide       SAAWPALLNDKWQSKTS---VVNASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFQPQQTEQTLRQILQDVK   96
ECoLi_1JOO                                  SAAWPALLNDKWQSKTS---VVNASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFQPQQTEQTLRQILQDVK   96
ECoLi_1JRL                                  SAAWPALLNDKWQSKTS---VVNASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFQPQQTEQTLRQILQDVK   96
ECoLi_0157_NP_286243                        SAAWPALLNDKWQSKTS---VVNASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFQPQQTEQTLRQILQDVK  122
Shigella_boydii_Sb227_YP_406934             SAAWPALLNDKWQSKTS---VVNASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFQPQQTEQTLRQILQDVK  122
ECoLi_0157_ZP_02799578                      SAAWPALLNDKWQSKTS---VVNASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFQPQQTEQTLRQILQDVK  121
ECoLid_ZP_02902430                          SAAWPALLNDKWQSKTS---VVNASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFQPQQTEQTLRQILQDVK  121
ECoLi_ZP_03081449                           SAAWPALLNDKWQSKTS---VVNASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFQPQQTEQTLRQILQDVK  111
Shigella_dysenteriae_YP_402105              SAAWPALLNDKWQSKTS---VVNASISSDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFQPQQTEQTLRQILQDVK  122
Citrobacter_koseri_YP_001454190             SAAWPALLNDKWQDKTP---VINASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFQPQQTEQTLRKILLDVK  111
marine_metagenome_ECJ13936                  SAAWPALLNDKWQSKTT---VVNASISGDTSQQALARLPALLKQHQPRWVLVELGGNDGLRGFAPQQTEQTLRTIVQDVK  132
ABH77568_Sequence_7411_from_patent          SAAWPALLNDKWQSRAS---VVNGSISGDTSQQGLSRLPALLKQHQPRWVLVELGGNDGLRGFQPQQTEQTLRTILQTIK  206
Enterobacter_cancerogenus_ZP_03281441       SAAWPALLNDKWQSQTT---VVNGSISGDTSQQGLSRLPALLKQHQPRWVLVELGGNDGLRGFQPQQTEHTLRTILQEIK  111
AAR53009_Sequence_12726_from_patent         NAAWPALLNEQWQAKTP---VVNASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFPPQQTEQTLRTIIKDIK  381
Enterobacter_YP_001175703                   TAAWPALLNDKWQTKTP---VLNASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFQPQQTEQTLRKIIQDIQ  122
Klebsiella_pneumoniae_YP_001334153          NAAWPALLNEQWQAKTP---VVNASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFPPQQTEQTLRTIIKDIK  111
Klebsiella_pneumoniae_YP_002240008          NAAWPALLNEKWQAKTP---VVNASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFPPQQTEQTLRTIIKDIK  121
Salmonella_enterica_NP_455101               SAAWPSLLNDKWQNKTS---VVNASISGDTSQQGLARLPALLQQHHPRWVVVELGGNDGLRGFAPAQTEQTLRKIIQTVK  121
Salmonella_typhimurium_NP_459501            SAAWPSLLNDKWQNKTS---VVNASISGDTSQQGLARLPALLQQHHPRWVVVELGGNDGLRGFAPAQTEQTLRKIIQTVK  121
Salmonella_enterica_YP_002225613            SAAWPSLLNDKWQNKTS---VVNASISGDTSQQGLARLPALLQQHHPRWVVVELGGNDGLRGFAPAQTEQTLRKIIQTVK  121
Salmonella_enterica_YP_215534               SAAWPSLLNDKWQNKTS---VVNASISGDTSQQGLARLPALLQQHHPRWVVVELGGNDGLRGFAPAQTEQTLRKIIQTVK  132
Salmonella_enterica_ZP_02344720             SAAWPSLLNDKWQNKTS---VVNASISGDTSQQGLARLPALLQQHHPRWVVVELGGNDGLRGFAPAQTEQTLRKIIQTVK  121
Salmonella_enterica_ZP_02683026             SAAWPSLLNDKWQNKTS---VVNASISGDTSQQGLARLPTLLQQHHPRWVVVELGGNDGLRGFAPAQTEQTLRKIIQTVK  121
Salmonella_enterica_ZP_03163359             SAAWPSLLNDKWQNKTS---VVNASISGDTSQQGLARLPALLQQHHPRWVVVELGGNDGLRGFAPAQTEQTLRKIIQTVK  121
Salmonella_enterica_ZP_03221362             SAAWPSLLNDKWQNKTS---VVNASISGDTSQQGLARLPALLQQHHPRWVVVELGGNDGLRGFAPAQTEQTLRKIIQTVK  121
Salmonella_enterica_YP_001571431            NAAWPSLLNDKWQNQTP---VVNASISGDTSLQGLTRLPALLQQHQPRWVLVELGGNDGLRGFAPAQTEQTLRKIIQAVK  111
Klebsiella_ACC78298                         NAAWPALLNEKWQAKTP---VVNASISGDTSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFPPQQTEQTLRTIIQTIK  186
Enterobacter_sakazakii_YP_001438839         DAAWPALLNDKWQQRDVR--VVNASISGDTAQQGLSRLPALLKQHQPRWVLIELGGNDGLRGFPPDTLSATLRKIIEQVK  133
Pectobacterium_atrosepticum_YP_049328       ANAWPTLLNTQWQTQKKGIAVVNASISGDTTAQGLARLPALLKQHQPRWVLIELGGNDGLRGFPAPNIEQDLAKIITLVK  141
Erwinia_tasmaniensis_YP_001908369           SAAWPALLNEKWQ-KSPA--IINGSISGDTTAQGLARLSALLEQHQPRWVLIELGGNDGLRGFPPQQVEQDLNQAIAQIQ  106
Yersinia_pestis_ZP_02223456                 AQAWPSLLDKKWQATPSLPKVVNASISGDTAAQGLARLPALLKQHQPRWVLIELGANDALRGFPTQDIQRDLSEIINQIT  104
Yersinia_pestis_CO92_NP_406570              AQAWPSLLDKKWQATPSLPKVVNASISGDTAAQGLARLPALLKQHQPRWVLIELGANDALRGFPTQDIQRDLSEIINQIT  126
Yersinia_pestis_KIM_NP_668426               AQAWPSLLDKKWQATPSLPKVVNASISGDTAAQGLARLPALLKQHQPRWVLIELGANDALRGFPTQDIQRDLSEIINQIT  136
Yersinia_pseudotuberculosis_YP_00140198     AQAWPSLLDKKWQATPSLPKVVNASISGDTAAQGLARLPALLKQHQPRWVLIELGANDALRGFPTQDIQRDLSEIINQIT  125
Serratia_proteamaculans_YP_001477389        AQAWPTLLADQWQKKPGDPQLVNASISGDTAAQGLARLPELLKQHQPRWVLIELGANDGLRGFPAQDLQRDLSQIITLVQ  109
Yersinia_pestis_Angola_YP_001605806         AQAWPSLLDKKWQATPSLPKVVNASISGDTAAQGLARLPALLKQHQPRWVLIELGANDALRGFPTQDIQRDLSEIINQIT  130
```

FIG. 47 (Cont.)

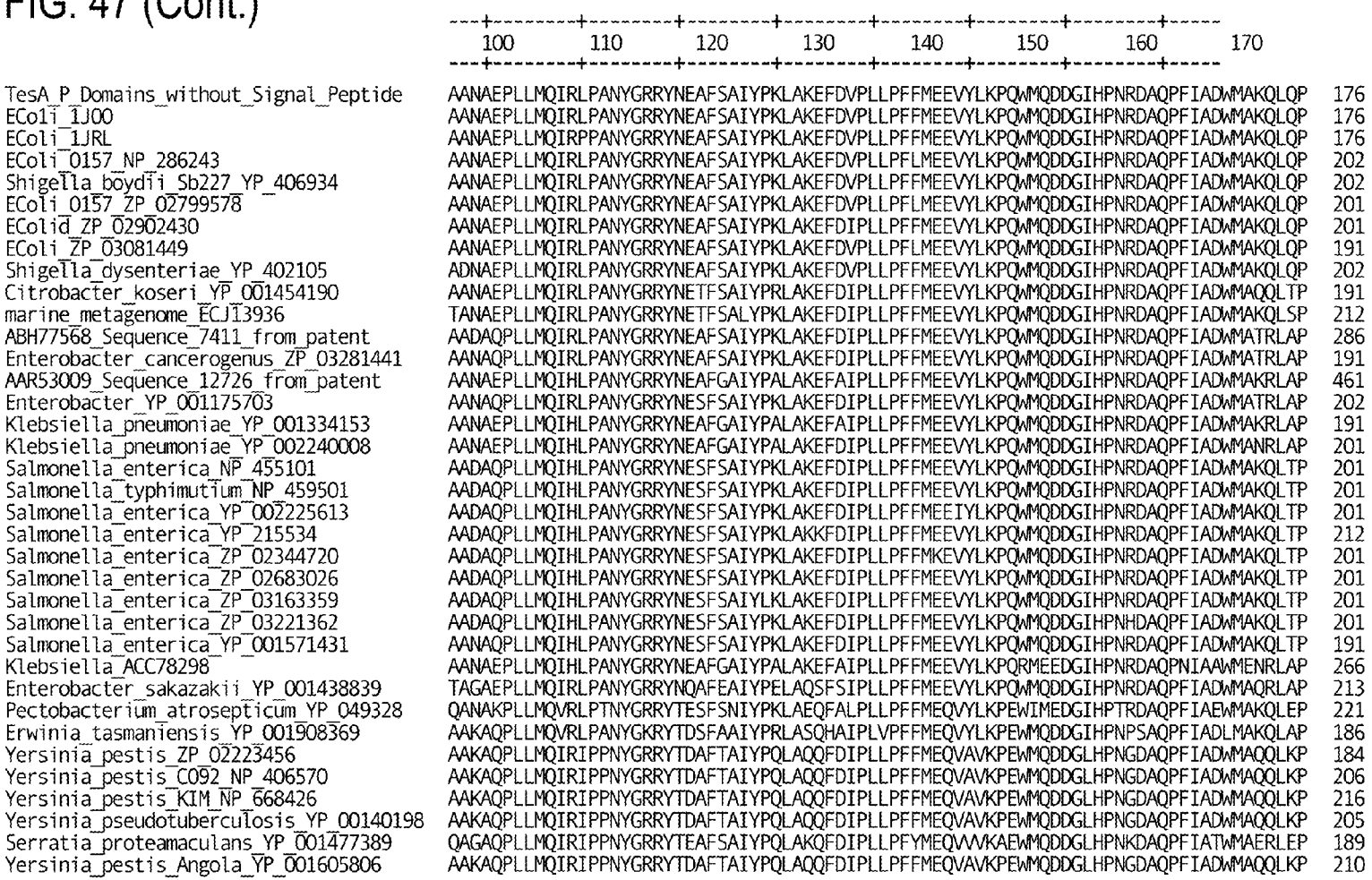

100 110 120 130 140 150 160 170
TesA_P_Domains_without_Signal_Peptide AANAEPLLMQIRLPANYGRRYNEAFSAIYPKLAKEFDVPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLQP 176
EColi_1J00 AANAEPLLMQIRLPANYGRRYNEAFSAIYPKLAKEFDVPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLQP 176
EColi_1JRL AANAEPLLMQIRPPANYGRRYNEAFSAIYPKLAKEFDVPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLQP 176
EColi_0157_NP_286243 AANAEPLLMQIRLPANYGRRYNEAFSAIYPKLAKEFDVPLLPFLMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLQP 202
Shigella_boydii_Sb227_YP_406934 AANAEPLLMQIRLPANYGRRYNEAFSAIYPKLAKEFDVPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLQP 202
EColi_0157_ZP_02799578 AANAEPLLMQIRLPANYGRRYNEAFSAIYPKLAKEFDVPLLPFLMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLQP 201
EColid_ZP_02902430 AANAEPLLMQIRLPANYGRRYNEAFSAIYPKLAKEFDIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLQP 201
EColi_ZP_03081449 AANAEPLLMQIRLPANYGRRYNEAFSAIYPKLAKEFDVPLLPFLMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLQP 191
Shigella_dysenteriae_YP_402105 ADNAEPLLMQIRLPANYGRRYNEAFSAIYPKLAKEFDVPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLQP 202
Citrobacter_koseri_YP_001454190 AANAEPLLMQIRLPANYGRRYNETFSAIYPRLAKEFDIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAQQLTP 191
marine_metagenome_ECJ13936 TANAEPLLMQIRLPANYGRRYNETFSALYPKLAKEFDIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLSP 212
ABH77568_Sequence_7411_from_patent AADAQPLLMQIRLPANYGRRYNEAFSAIYPKLAKEFDIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMATRLAP 286
Enterobacter_cancerogenus_ZP_03281441 AANAQPLLMQIRLPANYGRRYNEAFSAIYPKLAKEFDIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMATRLAP 191
AAR53009_Sequence_12726_from_patent AANAEPLLMQIHLPANYGRRYNEAFGAIYPALAKEFAIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKRLAP 461
Enterobacter_YP_001175703 AANAQPLLMQIRLPANYGRRYNESFSAIYPKLAKEFDIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMATRLAP 202
Klebsiella_pneumoniae_YP_001334153 AANAEPLLMQIHLPANYGRRYNEAFGAIYPALAKEFAIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKRLAP 191
Klebsiella_pneumoniae_YP_002240008 AANAEPLLMQIHLPANYGRRYNEAFGAIYPALAKEFDIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMANRLAP 201
Salmonella_enterica_NP_455101 AADAQPLLMQIHLPANYGRRYNESFSAIYPKLAKEFDIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLTP 201
Salmonella_typhimutium_NP_459501 AADAQPLLMQIHLPANYGRRYNESFSAIYPKLAKEFDIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLTP 201
Salmonella_enterica_YP_002225613 AADAQPLLMQIHLPANYGRRYNESFSAIYPKLAKEFDIPLLPFFMEEIYLKPQWMQDDGIHPNRDAQPFIADWMAKQLTP 201
Salmonella_enterica_YP_215534 AADAQPLLMQIHLPANYGRRYNESFSAIYPKLAKKFDIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLTP 212
Salmonella_enterica_ZP_02344720 AADAQPLLMQIHLPANYGRRYNESFSAIYPKLAKEFDIPLLPFFMKEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLTP 201
Salmonella_enterica_ZP_02683026 AADAQPLLMQIHLPANYGRRYNESFSAIYPKLAKEFDIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLTP 201
Salmonella_enterica_ZP_03163359 AADAQPLLMQIHLPANYGRRYNESFSAIYLKLAKEFDIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLTP 201
Salmonella_enterica_ZP_03221362 AADAQPLLMQIHLPANYGRRYNESFSAIYPKLAKEFDIPLLPFFMEEVYLKPQWMQDDGIHPNHDAQPFIADWMAKQLTP 201
Salmonella_enterica_YP_001571431 AANAQPLLMQIHLPANYGRRYNESFSAIYPKLAKEFDIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQLTP 191
Klebsiella_ACC78298 AANAEPLLMQIHLPANYGRRYNEAFGAIYPALAKEFAIPLLPFFMEEVYLKPQRMEEDGIHPNRDAQPNIAAWMENRLAP 266
Enterobacter_sakazakii_YP_001438839 TAGAEPLLMQIRLPANYGRRYNQAFEAIYPELAQSFSIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAQRLAP 213
Pectobacterium_atrosepticum_YP_049328 QANAKPLLMQVRLPTNYGRRYTESFSNIYPKLAEQFALPLLPFFMEQVYLKPEWIMEDGIHPTRDAQPFIAEWMAKQLEP 221
Erwinia_tasmaniensis_YP_001908369 AAKAQPLLMQVRLPANYGKRYTDSFAAIYPRLASQHAIPLVPFFMEQVYLKPEWMQDDGIHPNPSAQPFIADLMAKQLAP 186
Yersinia_pestis_ZP_02223456 AAKAQPLLMQIRIPPNYGRRYTDAFTAIYPQLAQQFDIPLLPFFMEQVAVKPEWMQDDGLHPNGDAQPFIADWMAQQLKP 184
Yersinia_pestis_C092_NP_406570 AAKAQPLLMQIRIPPNYGRRYTDAFTAIYPQLAQQFDIPLLPFFMEQVAVKPEWMQDDGLHPNGDAQPFIADWMAQQLKP 206
Yersinia_pestis_KIM_NP_668426 AAKAQPLLMQIRIPPNYGRRYTDAFTAIYPQLAQQFDIPLLPFFMEQVAVKPEWMQDDGLHPNGDAQPFIADWMAQQLKP 216
Yersinia_pseudotuberculosis_YP_00140198 AAKAQPLLMQIRIPPNYGRRYTDAFTAIYPQLAQQFDIPLLPFFMEQVAVKPEWMQDDGLHPNGDAQPFIADWMAQQLKP 205
Serratia_proteamaculans_YP_001477389 QAGAQPLLMQIRIPPNYGRRYTEAFSAIYPQLAKQFDIPLLPFYMEQVVVKAEWMQDDGLHPNKDAQPFIATWMAERLEP 189
Yersinia_pestis_Angola_YP_001605806 AAKAQPLLMQIRIPPNYGRRYTDAFTAIYPQLAQQFDIPLLPFFMEQVAVKPEWMQDDGLHPNGDAQPFIADWMAQQLKP 210

FIG. 47 (Cont.)

```
                                          ---+-
                                             180
                                          ---+-
TesA_P_Domains_without_Signal_Peptide     LVNHDS                182
EColi_1J00                                LVNHDSLEHHHHHH        190
EColi_1JRL                                LVNHDSLEHHHHHH        190
EColi_0157_NP_286243                      LVNHDS                208
Shigella_boydii_Sb227_YP_406934           LVNHDS                208
EColi_0157_ZP_02799578                    LVNHDS                207
EColid_ZP_02902430                        LVNHDS                207
EColi_ZP_03081449                         LVNHDS                197
Shigella_dysenteriae_YP_402105            LVNHDS                208
Citrobacter_koseri_YP_001454190           LVNHDS                197
marine_metagenome_ECJ13936                LVKHES                218
ABH77568_Sequence_7411_from_patent        LVNHDSSNS             295
Enterobacter_cancerogenus_ZP_03281441     LVKHDS                197
AAR53009_Sequence_12726_from_patent       LVNHDS                467
Enterobacter_YP_001175703                 LVKHDS                208
Klebsiella_pneumoniae_YP_001334153        LVNHDS                197
Klebsiella_pneumoniae_YP_002240008        LVNHDS                207
Salmonella_enterica_NP_455101             FLS                   204
Salmonella_typhimurium_NP_459501          FLS                   204
Salmonella_enterica_YP_002225613          FLS                   204
Salmonella_enterica_YP_215534             FLS                   215
Salmonella_enterica_ZP_02344720           FLS                   204
Salmonella_enterica_ZP_02683026           FLS                   204
Salmonella_enterica_ZP_03163359           FLS                   204
Salmonella_enterica_ZP_03221362           FLS                   204
Salmonella_enterica_YP_001571431          FLS                   194
Klebsiella_ACC78298                       LDKHVS                272
Enterobacter_sakazakii_YP_001438839       LVKHDS                219
Pectobacterium_atrosepticum_YP_049328     LVNHES                227
Erwinia_tasmaniensis_YP_001908369         LVKHEASRSVGNDG        200
Yersinia_pestis_ZP_02223456               LVVDPK                190
Yersinia_pestis_CO92_NP_406570            LVVDPK                212
Yersinia_pestis_KIM_NP_668426             LVVDPK                222
Yersinia_pseudotuberculosis_YP_00140198   LVVDPK                211
Serratia_proteamaculans_YP_001477389      LVKHESN               196
Yersinia_pestis_Angola_YP_001605806       LVVDSK                216
```

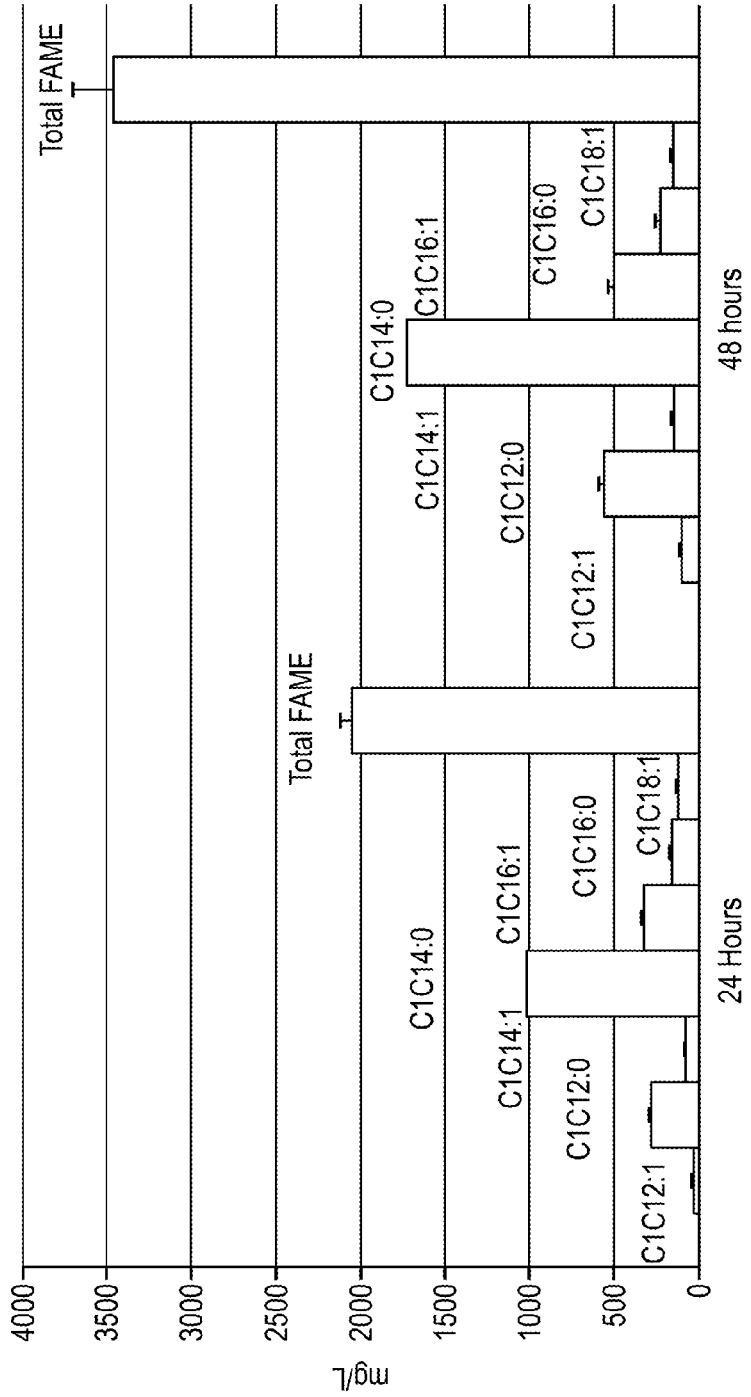

Total FAME
C1C14:0
C1C16:1
C1C16:0
C1C18:1
C1C14:1
C1C12:0
C1C12:1
48 hours
Total FAME
C1C14:0
C1C16:1
C1C16:0
C1C18:1
C1C14:1
C1C12:0
C1C12:1
24 Hours
4000
3500
3000
2500
2000
1500
1000
500
0
mg/L

FIG. 48

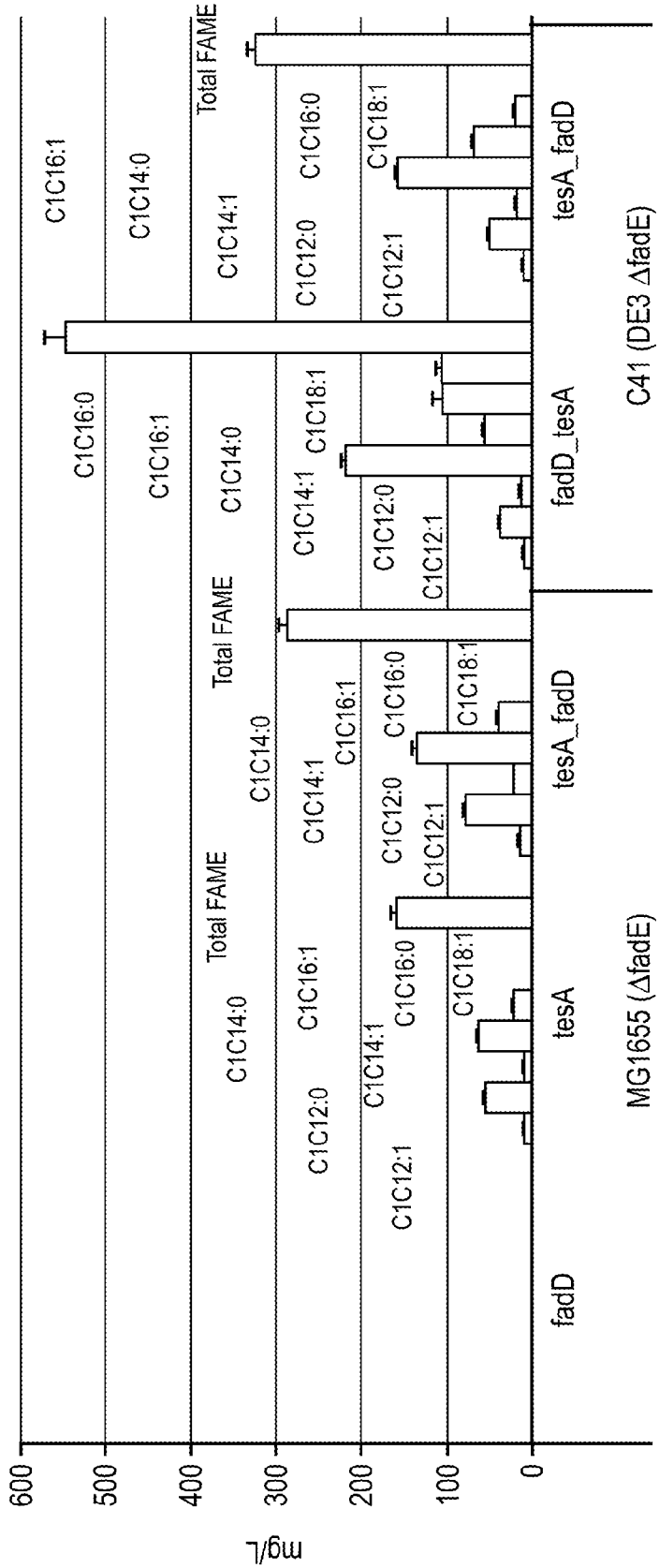

mg/L
600
500
400
300
200
100
0
Total FAME
C1C16:1
C1C16:0
C1C14:0
C1C16:1
C1C12:0
C1C14:1
C1C12:1
C1C16:0
C1C18:1
fadD
tesA
tesA_fadD
fadD_tesA
MG1655 (ΔfadE)
C41 (DE3 ΔfadE)

FIG. 49

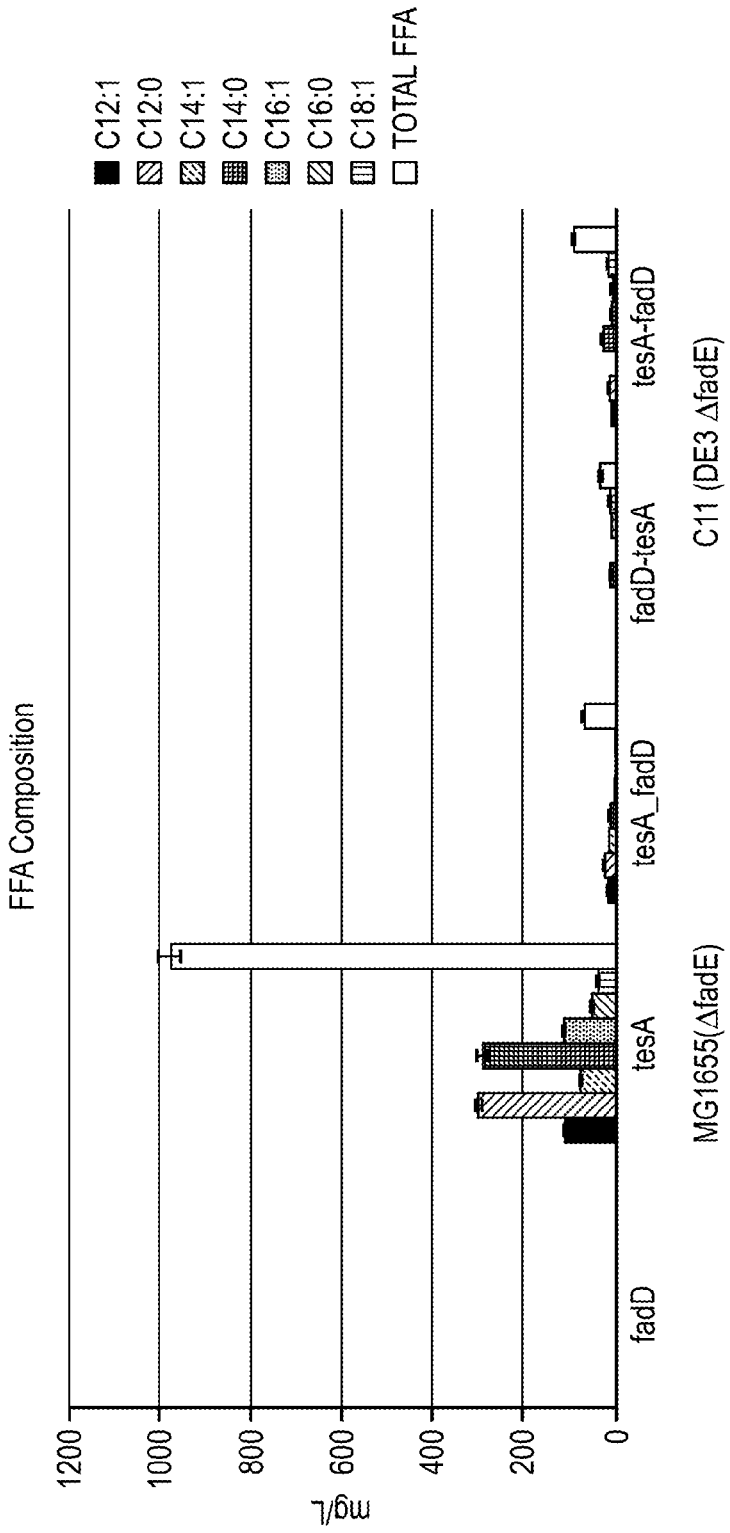
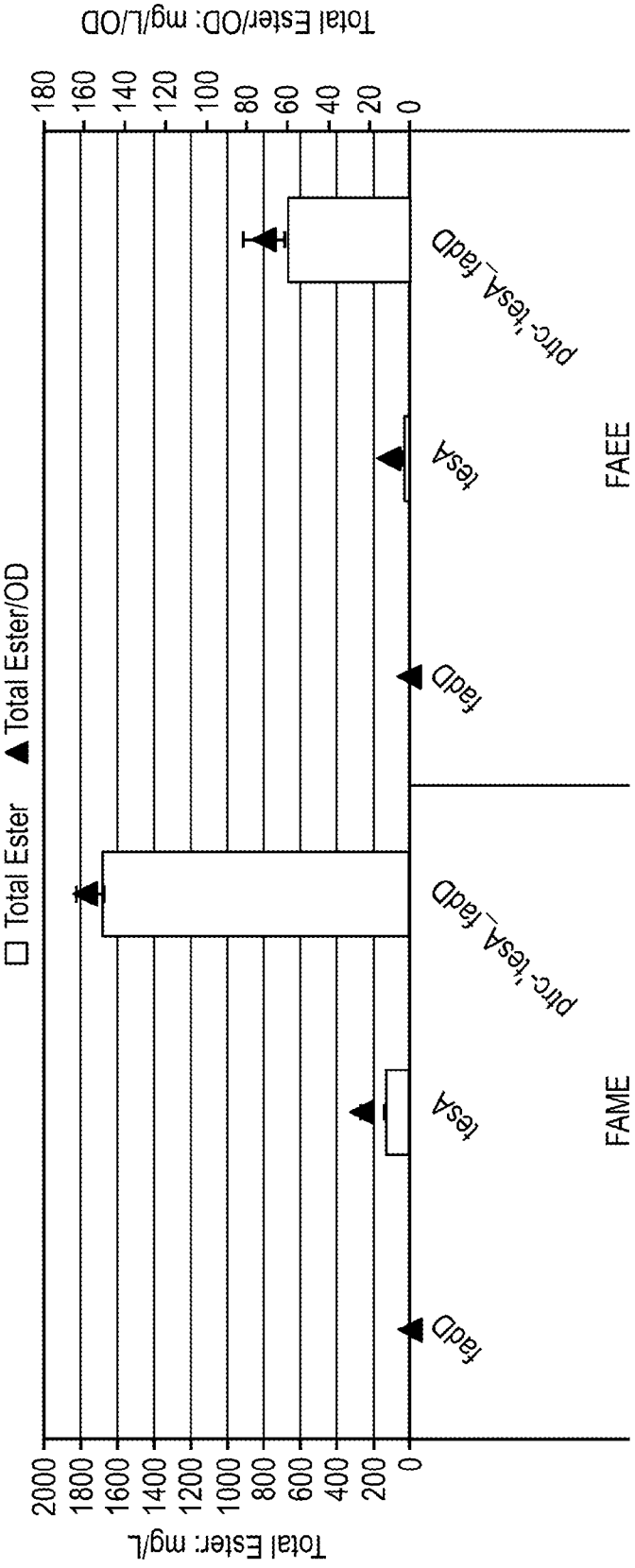

FFA Composition
C12:1
C12:0
C14:1
C14:0
C16:1
C16:0
C18:1
TOTAL FFA
mg/L
1200
1000
800
600
400
200
0
fadD
tesA
tesA_fadD
fadD-tesA
tesA-fadD
MG1655(ΔfadE)
C11 (DE3 ΔfadE)

FIG. 50

FIG. 51


Total Ester/OD: mg/L/OD
180
160
140
120
100
80
60
40
20
0
Total Ester: mg/L
2000
1800
1600
1400
1200
1000
800
600
400
200
0
Total Ester
Total Ester/OD
pltc-tesA_fadD
tesA
fadD
FAEE
FAME

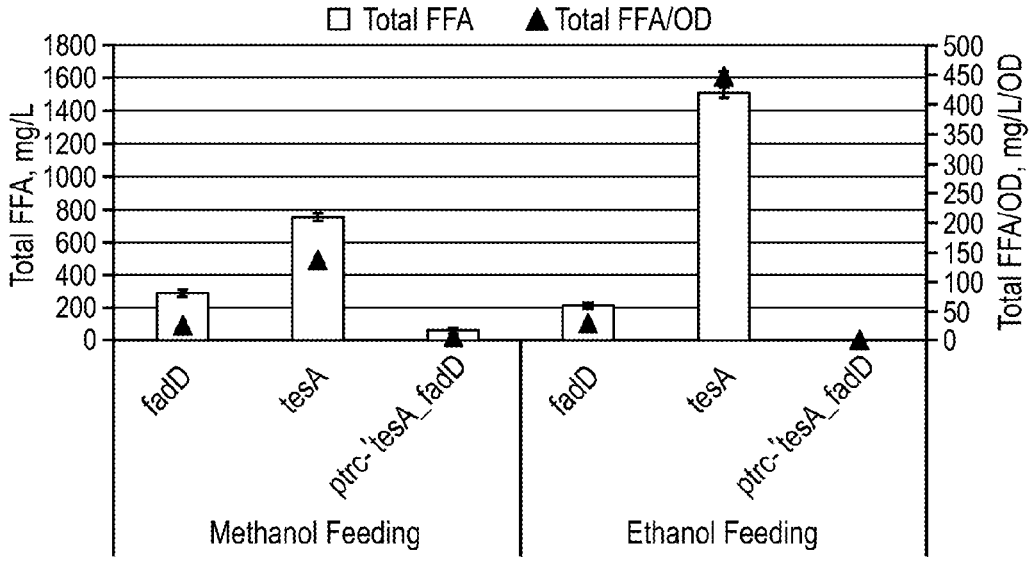

Total FFA
Total FFA/OD
Total FFA, mg/L
Total FFA/OD, mg/L/OD
1800
1600
1400
1200
1000
800
600
400
200
0
500
450
400
350
300
250
200
150
100
50
0
fadD
tesA
ptrc-'tesA_fadD
fadD
tesA
ptrc-'tesA_fadD
Methanol Feeding
Ethanol Feeding

FIG. 52

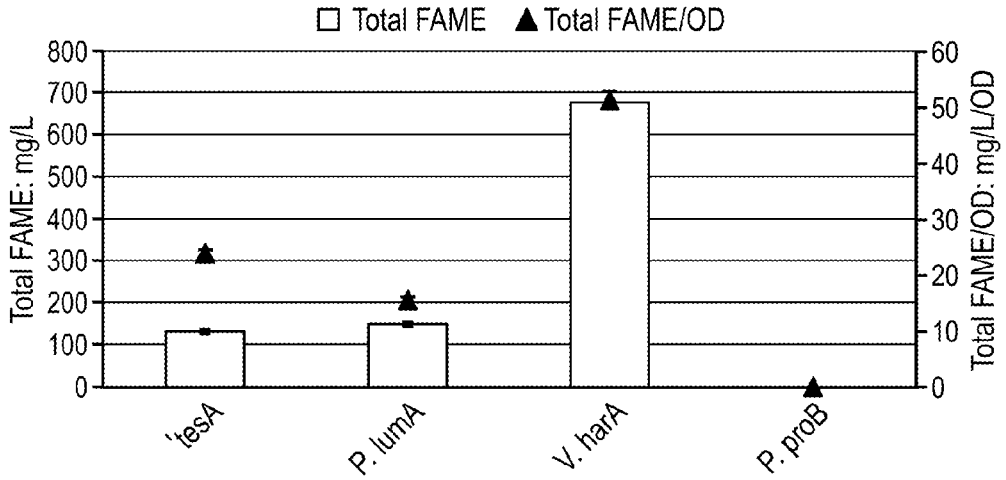

Total FAME
Total FAME/OD
Total FAME: mg/L
Total FAME/OD: mg/L/OD
800
700
600
500
400
300
200
100
0
60
50
40
30
20
10
0
'tesA
P. lumA
V. harA
P. proB

FIG. 53

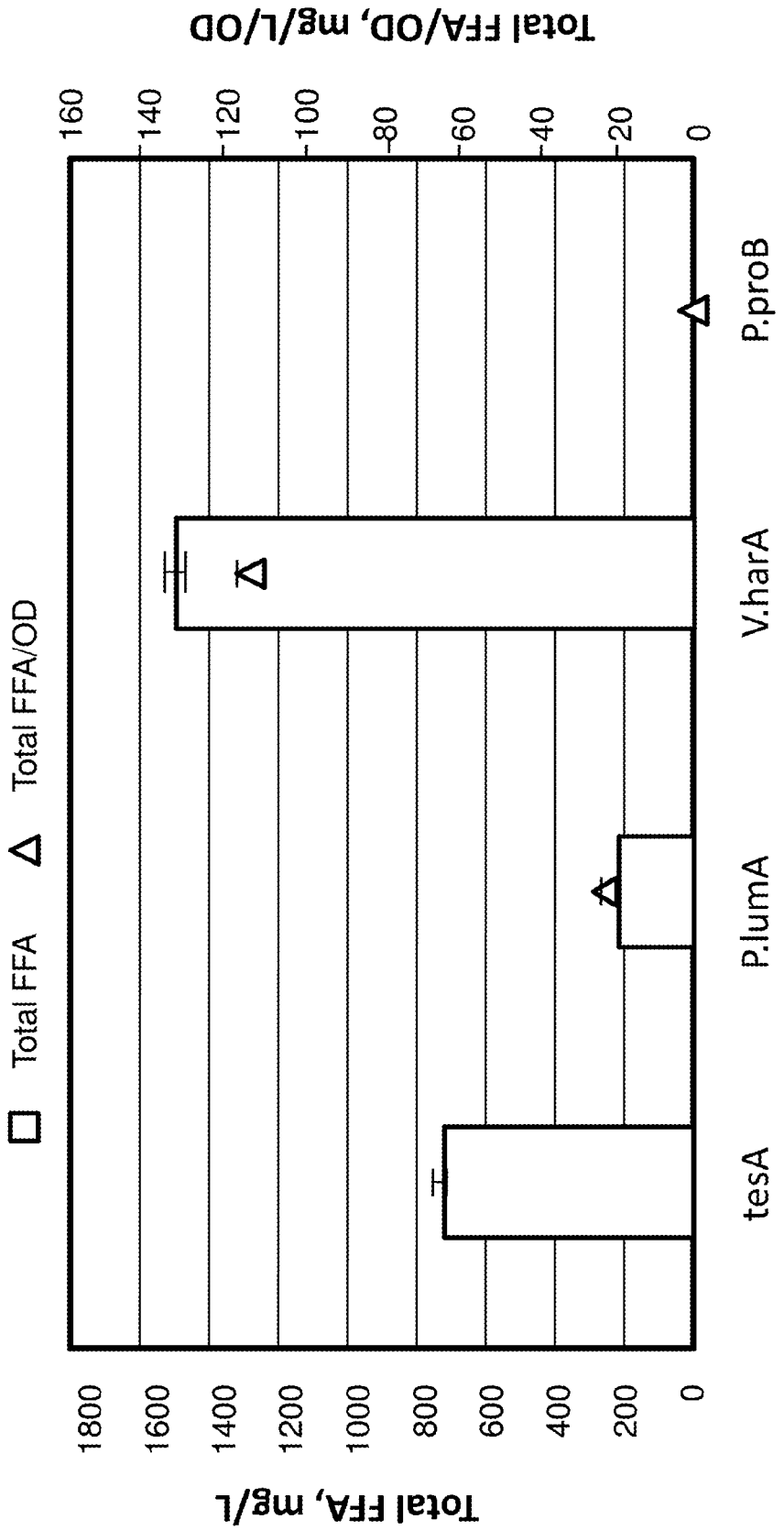

Total FFA, mg/L
1800
1600
1400
1200
1000
800
600
400
200
0
Total FFA/OD, mg/L/OD
160
140
120
100
80
60
40
20
0
Total FFA
Total FFA/OD
tesA
P.lumA
V.harA
P.proB

FIG. 54

FIG. 55

Residue	Mutation	Sequence alignment near region of interest	1 10
A1	A1S		
		E.coli_TesA_1U8U	**A**DTLLILGDSLSA
		gi|156977016|ref|YP_001447923.1	SEKLLVLGDSLSA
		gi|209809090|ref|YP_002264628.1	SQTLLILGDSLSA
		gi|59714227|ref|YP_207002.1	SQTLLILGDSLSA
		gi|197337441|ref|YP_002158710.1	SQTLLILGDSLSA
		gi|125620500|gb|EAZ48871.1	SKTLLVLGDSLSA
		gi|15601538|ref|NP_233169.1	SKTLLVLGDSLSA
		gi|121588086|ref|ZP_01677835.1	SKTLLVLGDSLSA
		gi|153827484|ref|ZP_01980151.1	SKTLLVLGDSLSA
		gi|163800656|ref|ZP_02194557.1	SEKLLVLGDSLSA
		gi|91226151|ref|ZP_01261041.1	SEKLLVLGDSLSA
		gi|28900726|ref|ZP_800381.1	SEKLLVLGDSLSA
		gi|729449|sp|Q07792.1|ESTE_VIBMI	SEKLLVLGDSLSA
		gi|90579358|ref|ZP_01235168.1	SQTLLVLGDSLSA
		gi|89072709|ref|ZP_01159274.1	SQTLLVLGDSLSA
		gi|78484894|ref|YP_390819.1	SQNLLVLGDSLSA
		gi|94500900|ref|ZP_01307426.1	SDKILVLGDSLSA
		gi|187478460|ref|YP_786484.1	SHTILVVGDSLSA

FIG. 55 Cont.

		gi|134094953|ref|YP_001100028.1	SKTILVLGDSLSA
		gi|152980543|ref|YP_001353227.1	SKTIVVLGDSLSA
		gi|86143029|ref|ZP_01061451.1	SNSILFFGDSLTA
L7	L7V, L7M		1 10
		E.coli_TesA_1U8U	ADTLLI**L**GDSLSAGYRMS
		gi|54309970|ref|YP_130990.1	GNTLLVVGDSLSAGYQMR
		gi|148548695|ref|YP_001268761.1	AGTLLVVGDSISAGFGLD
		gi|90412817|ref|ZP_01220817.1	GNTLLVVGDSLSAGYQMR
		gi|88859908|ref|ZP_01134547.1	--TILIVGDSLSAAYGLK
		gi|88703495|ref|ZP_01101211.1	---ILVVGDSISAAYGMS
		gi|192359766|ref|YP_001982095.1	---ILVVGDSLSAAYGID
		gi|163856534|ref|YP_001630831.1	--TLLVVGDSLSAEYGLA
		gi|187478460|ref|YP_786484.1	SHTILVVGDSLSAEYGLK
		gi|33597579|ref|NP_885222.1	--AVLVVGDSLSAEYGLR
		gi|33592804|ref|NP_880448.1	--AVLVVGDSLSAEYGLR
		gi|121604790|ref|YP_982119.1	--TVLIVGDSLSAEYGLK
		gi|91788891|ref|YP_549843.1	--TILIVGDSLSAEYGLK
		gi|124267005|ref|YP_001021009.1	---ILVVGDSLSAEYGLQ
		gi|171058584|ref|YP_001790933.1	---ILVVGDSLSAEYGLP
		gi|146220121|gb|ABQ11275.1	AKTILVVGDSLSAEYGLA
		gi|121594614|ref|YP_986510.1	APVILVVGDSLSAEYGLP
		gi|120611683|ref|YP_971361.1	--VVLVVGDSLSAEYGIA

FIG. 55 Cont.

		gi|198263408|gb|EDY87686.1	---NLLIVGDSLSAAYGIA
		gi|149377045|ref|ZP_01894796.1	----MIVGDSLSAAYGVQ
		gi|92114738|ref|YP_574666.1	ADTLLIVGDSLSAAHGIE
		gi|153874618|ref|ZP_02002768.1	--TLLIVGDSLSAAYGIA
		gi|21241630|ref|NP_641185.1	----ILVVGDSLSAAHNIP
		gi|78046442|ref|YP_362617.1	---VLVVGDSLSAAHNIP
		gi|188992969|ref|YP_001904979.1	AAPILVVGDSLSAAHNIP
		gi|21230252|ref|NP_636169.1	AAPILVVGDSLSAAHNIP
		gi|166710711|ref|ZP_02241918.1	----ILVVGDSLSAAHNIP
		gi|58583387|ref|YP_202403.1	---ILVVGDSLSAAHNIP
		gi|152996229|ref|YP_001341064.1	ASTLLVMGDSLSAAYNLR
		gi|71908327|ref|YP_285914.1	AKTILIMGDSLSAGYGIR
		gi|149928382|ref|ZP_01916622.1	---ILVMGDSLSAAYGLP
		gi|126667344|ref|ZP_01738317.1	ANTLLVMGDSLSAAYGVP
D9	D9N		1 10
		E.coli_TesA_1U8U	ADTLLILG**D**SLSAGYRMS
		gi|82542988|ref|YP_406934.1	ADTLLILGNSLSAGYRMS
		gi|193215472|ref|YP_001996671.1	--TILFFGNSITAGMGLR

FIG. 55 Cont.

G14	G14S		1 10 20
		E.coli_TesA_1U8U	ADTLLILGDSLSA**G**YRMSASAAWP
		gi|149907876|ref|ZP_01896544.1	---ILLLGDSLSASYGMTQNEGWV
		gi|120598433|ref|YP_963007.1	AAKVLILGDSLGASYGMSEQLGWV
		gi|124550111|ref|ZP_01707934.1	AAKVLILGDSLGASYGMSEQLGWV
		gi|126174896|ref|YP_001051045.1	AAKVLILGDSLGASYGMAEQSGWV
		gi|160875896|ref|YP_001555212.1	AAKVLILGDSLGASYGMAEQSGWV
		gi|153001225|ref|YP_001366906.1	AAKVLILGDSLGASYGMAEQSGWV
		gi|149117668|ref|ZP_01844343.1	AAKVLILGDSLGASYGMAEQSGWV
		gi|24374455|ref|NP_718498.1	AAKVLILGDSLGASYGMSEQLGWV
		gi|117919985|ref|YP_869177.1	AAKVLILGDSLGASYGMSEQVGWV
		gi|114047048|ref|YP_737598.1	AAKVLILGDSLGASYGMSEQIGWV
		gi|113969820|ref|YP_733613.1	AAKVLILGDSLGASYGMSEQLGWV
		gi|119774622|ref|YP_927362.1	AETILILGDSLSASYGMEENQGWI
		gi|60893017|gb|AAX37297.1	ANPILILGDSLSASYGMEQDQGWV
		gi|127513331|ref|YP_001094528.1	ANPILILGDSLSASYGMEQDKGWV
		gi|212634759|ref|YP_002311284.1	AAPILILGDSLSASYGMPENEGWV
		gi|167624526|ref|YP_001674820.1	AAPILILGDSLSASYGMPEDQGWV
		gi|157961485|ref|YP_001501519.1	AAPILILGDSLSASYGMPEDQGWV
		gi|170727240|ref|YP_001761266.1	AAPILILGDSLSASYGVDEDQGWV
		gi|157374835|ref|YP_001473435.1	AAPILILGDSLSASYGVDEDKGWV
		gi|163749678|ref|ZP_02156924.1	AAPLILILGDSLSASYGIDEDKGWV

FIG. 55 Cont.

		gi|77163958|ref|YP_342483.1	----ILILGDSLSASYGLSLEQGWV
		gi|207088375|gb|EDZ65647.1	----ILILGDSLSASYGLSLEQGWV
R16	R16G		1 10 20
		E.coli_TesA_1U8U	ADTLLILGDSLSAGYRMSAS
		gi|148548659|ref|YP_001268761.1	AGTLLVVGDSISAGFGLDSR
		gi|114772942|ref|ZP_01450253.1	--TVLILGDSLSAAYGLIQE
		gi|109899221|ref|YP_662476.1	----LLILGDSLSAGYGLTQA
		gi|196157105|ref|YP_002126594.1	--VLLILGDSLSAAYGLQQH
		gi|71280033|ref|YP_269028.1	-DKILLIGDSLSAGYGLEQA
		gi|88859908|ref|ZP_01134547.1	--TILIVGDSLSAAYGLKQS
		gi|77360818|ref|YP_340393.1	-NTILILGDSLSAAYGLKQE
		gi|119472458|ref|ZP_01614557.1	-NTILILGDSLSAAYGLQQE
		gi|194369063|ref|ABF57909.2	-NTILILGDSLSAAYGLQQE
		gi|149907876|ref|ZP_01896544.1	----ILLLGDSLSASYGMTQN
		gi|120598433|ref|YP_963007.1	AAKVLILGDSLGASYGMSEQ
		gi|124550111|ref|ZP_01707934.1	AAKVLILGDSLGASYGMSEQ
		gi|126174896|ref|YP_001051045.1	AAKVLILGDSLGASYGMAEQ
		gi|160875896|ref|YP_001555212.1	AAKVLILGDSLGASYGMAEQ
		gi|153001225|ref|YP_001366906.1	AAKVLILGDSLGASYGMAEQ
		gi|149117668|ref|ZP_01844343.1	AAKVLILGDSLGASYGMAEQ
		gi|24374455|ref|NP_718498.1	AAKVLILGDSLGASYGMSEQ
		gi|117919985|ref|YP_869177.1	AAKVLILGDSLGASYGMSEQ

FIG. 55 Cont.

	gi|114047048|ref|YP_737598.1		AAKVLILGDSLGASYGMSEQ
	gi|113969820|ref|YP_733613.1		AAKVLILGDSLGASYGMSEQ
	gi|91793720|ref|YP_563371.1		AATILVLGDSLSAGYGIDEH
	gi|114563734|ref|YP_751247.1		AATILILGDSLSAGYGMPED
	gi|119774622|ref|YP_927362.1		AETILILGDSLSASYGMEEN
	gi|60893017|gb|AAX37297.1		ANPILILGDSLSASYGMEQD
	gi|127513331|ref|YP_001094528.1		ANPILILGDSLSASYGMEQD
	gi|212634759|ref|YP_002311284.1		AAPILILGDSLSASYGMPEN
	gi|167624526|ref|YP_001674820.1		AAPILILGDSLSASYGMPED
	gi|157961485|ref|YP_001501519.1		AAPILILGDSLSASYGMPED
	gi|170727240|ref|YP_001761266.1		AAPILILGDSLSASYGVDED
	gi|157374835|ref|YP_001473435.1		AAPILILGDSLSASYGVDED
	gi|163749678|ref|ZP_02156924.1		AAPILILGDSLSASYGIDED

FIG. 55 Cont.

S20	S20G		20
		E.coli_TesA_1U8U	GYRMSA**S**AAWPALLND
		gi|74316704|ref|YP_314444.1	GYGLAAGQGWVDRLRA
		gi|145589121|ref|YP_001155718.1	EYGLSRGTGWVKLLET
		gi|30249426|ref|NP_841496.1	GYGLPPGTGWVNLLER
		gi|34499190|ref|NP_903405.1	GYGLAPGQGWAALLAR
		gi|119897957|ref|YP_933170.1	GYGLKNGEAWPTLLQT
		gi|169182148|ref|ZP_02842667.1	GYGLERGQEWPTLLQT
		gi|163856534|ref|YP_001630831.1	EYGLARGTGWVPLLAR
		gi|187478460|ref|YP_786484.1	EYGLKRGAGWVPLLAQ
		gi|33597579|ref|NP_885222.1	EYGLRRGSGWVPMLAQ
		gi|33592804|ref|NP_880448.1	EYGLRRGSGWVPMLAQ
		gi|118051335|ref|ZP_01519884.1	EYGLTRGKGWVQLLQQ
		gi|121604790|ref|YP_982119.1	EYGLRRGTGWVPLLEK
		gi|91788891|ref|YP_549843.1	EYGLKRGTGWVPLLEK
		gi|124267005|ref|YP_001021009.1	EYGLQRGSGWVALLEK
		gi|171058584|ref|YP_001790933.1	EYGLPRGSGWVALLEA
		gi|146220121|gb|ABQ11275.1	EYGLARGTGWVALLDQ
		gi|121594614|ref|YP_986510.1	EYGLPRGTGWVALLDK
		gi|121610344|ref|YP_998151.1	EYGLARGTGWVALLEQ
		gi|160899469|ref|YP_001565051.1	EYGLARGTGWVALLQK
		gi|120611683|ref|YP_971361.1	EYGIARGTGWVALLEK
		gi|153888470|ref|ZP_02009612.1	GYGLAQGTGWVALLDR
		gi|187928944|ref|YP_001899431.1	GYGLAQGTGWVALLDR
		gi|17546436|ref|NP_519838.1	GYGLAQGTGWVTLLGN

FIG. 55 Cont.

		gi|207724196|ref|YP_002254594.1 gi|83749049|ref|ZP_00946056.1 gi|207743056|ref|YP_002259448.1 gi|134094953|ref|YP_001100028.1 gi|152980543|ref|YP_001353227.1 gi|94310819|ref|YP_584029.1 gi|73541078|ref|YP_295598.1 gi|113867511|ref|YP_726000.1	GYGLAQGTGWVALLGN GYGLAQGTGWVALLGN GYGLAQGTGWVALLGN EYGLARGEGWVNLLQK EYGLARGEGWVSLLQK EYGIARGTGWVSLLQD EYGIARGSGWVSLLQQ EYGIARGAGWVTLLQD
A25	A25V	E.coli_TesA_1U8U gi|54309970|ref|YP_130990.1 gi|90412817|ref|ZP_01220817.1 gi|182677824|ref|YP_001831970.1 gi|154245703|ref|YP_001416661.1 gi|115522331|ref|YP_779242.1 gi|211958502|gb|EEA93702.1 gi|83594979|ref|YP_428731.1	20 30 ASAAWP**A**LLNDKWQS AEQSWPVLLQPALKH AEQSWPVLLQPALKH AQAAFPVVLEKALRN ASAAFPVQLEAALKA ASGAFPVKLQKALKE PEDAFPVKLEKALQE PETAFPVQLEAALRA
N39	N39A	E.coli_TesA_1U8U gi|167645243|ref|YP_001682906.1	40 SKISVV**N**ASISGDTS VLAKVRAAGVSGDTS
I42	I42S	E.coli_TesA_1U8U	40 50

FIG. 55 Cont.

		gi|149200040|ref|ZP_01877066.1	SVVNASISGDTSQQGL KVINAGSSGSTSAGGM
D45	D45Q, D45S, D45A		40 50
		E.coli_TesA_1U8U	NASISGDTSQQGLAR
		gi|71280033|ref|YP_269028.1	NTAISGQTTDNALLK
		gi|88859908|ref|ZP_01134547.1	NVSVSGQTTGNALLT
		gi|94500900|ref|ZP_01307426.1	NASISGQTTSEGLRQ
		gi|90023084|ref|YP_528911.1	NASISGATTNAGLQR
		gi|91762028|ref|ZP_01263993.1	DGSVSGSTSAGGLNR
		gi|71083551|ref|YP_266270.1	DGSVSGSTSAGGLNR
		gi|42521961|ref|NP_967341.1	NAGVSGSTTASGLSR
		gi|149200040|ref|ZP_01877066.1	NAGSSGSTSAGGMSK
Q48	Q48W		40 50
		E.coli_TesA_1U8U	NASISGDTSQQGLARLP
		gi|82703094|ref|YP_412660.1	NNSISGETAWGGRNRIE
Q49	Q49A, Q49G, Q49D, Q49S		40 50
		E.coli_TesA_1U8U	ASISGDTSQQGLARLPA
		gi|148548659|ref|YP_001268761.1	ASISGDTSAGGQARLPA
		gi|114772924|ref|ZP_01450253.1	ASISGETTDGGLARLAR
		gi|109899221|ref|YP_662476.1	AAISGETTDGALARLPR
		gi|196157105|ref|YP_002126594.1	AAVSGETTDGGLARFPR
		gi|77360818|ref|YP_340393.1	ASISGETTGGALRRVDA

FIG. 55 Cont.

	gi|119472458|ref|ZP_01614557.1	ASISGETSGGALRRLDA
	gi|194369063|gb|ABF57909.2	ASISGETSGGALRRLDA
	gi|149907876|ref|ZP_01896544.1	ASISGETTAGGLSRLPG
	gi|120598433|ref|YP_963007.1	GSVSGETTAGGLRRLPA
	gi|124550111|ref|ZP_01707934.1	GSVSGETTAGGLRRLPA
	gi|126174896|ref|YP_001051045.1	GSVSGETTAGGLRRLPA
	gi|160875896|ref|YP_001555212.1	GSVSGETTAGGLRRLPA
	gi|153001225|ref|YP_001366906.1	GSVSGETTAGGLRRLPA
	gi|149117668|ref|ZP_01844343.1	GSVSGETTAGGLRRLPA
	gi|24374455|ref|NP_718498.1	GSVSGETTAGGLRRLPA
	gi|117919985|ref|YP_869177.1	GSVSGETTAGGLRRLPA
	gi|114047048|ref|YP_737598.1	GSVSGETTAGGLRRLPA
	gi|113969820|ref|YP_733613.1	GSVSGETTAGGLRRLPA
	gi|91793720|ref|YP_563371.1	GSVSGETTAGALRRLPS
	gi|114563734|ref|YP_751247.1	GSVSGETTAGGLRRLPS
	gi|119774622|ref|YP_927362.1	AAVSGETSAGGLRRLPA
	gi|60893017|gb|AAX37297.1	GSVSGETSAGGLRRLPG
	gi|127513331|ref|YP_001094528.1	GSVSGETSAGGLRRLPA
	gi|42521961|ref|NP_967341.1	AGVSGSTTASGLSRMKW
	gi|88806192|ref|ZP_01121710.1	AGLSGETTASGANRLDW
	gi|116620953|ref|YP_823109.1	MGVSGDTTQDGLARLSM
	gi|162147014|ref|YP_001601475.1	GGVSGDTSADALARLDW
	gi|90023084|ref|YP_528911.1	ASISGATTNAGLQRMPA
	gi|85710420|ref|ZP_01041484.1	AGVSGDTSAAGRDRLEF
	gi|94497924|ref|ZP_01304489.1	AGVSGDTTTAGRARLAF
	gi|103486193|ref|YP_615754.1	AGVSGDTSAAGRQRLTY

FIG. 55 Cont.

G50	G50A, G50T, G50L		50
		E.coli_TesA_1U8U	DTSQQ**G**LARLPAL
		gi|109899221|ref|YP_662476.1	ETIDGALARLPRL
		gi|71280033|ref|YP_269028.1	QTIDNALLKIDAW
		gi|88859908|ref|ZP_01134547.1	QTITGNALLTLNEH
		gi|77360818|ref|YP_340393.1	ETITGGALRRVDAL
		gi|119472458|ref|ZP_01614557.1	ETSGGALRRLDAL
		gi|194369063|gb|ABF57909.2	ETSGGALRRLDAL
		gi|119475890|ref|ZP_01616242.1	ETIDGALSRLPTL
		gi|207724196|ref|YP_002254594.1	DTTAGARARLPAV
		gi|114321556|ref|YP_743239.1	DTTRQALNRLAPL
		gi|77163958|ref|YP_342483.1	ETTRGALARLDSL
		gi|207088375|gb|EDZ65647.1	ETTRGALARLDSL
		gi|194364429|ref|YP_002027039.1	ETTAGALTRLPGL
		gi|190572845|ref|YP_001970690.1	ETTAGALTRLPAL
		gi|21241603|ref|NP_641185.1	ETTSGALTRLPGL
		gi|78046442|ref|YP_362617.1	ETTSGALTRLPGL
		gi|188992969|ref|YP_001904979.1	ETTSGALTRLPGL
		gi|21230252|ref|NP_636169.1	ETTSGALTRLPGL
		gi|166710711|ref|ZP_02241918.1	ETTSGALTRLPGL
		gi|58583387|ref|YP_202403.1	ETTSGALTRLPGL
		gi|188575357|ref|YP_001912286.1	ETTSGALTRLPGL
		gi|15029382|gb|AAK81865.1|AF395191_1	ETTSGALARLPKL
		gi|50084257|ref|YP_045767.1	ETTSGALARLPKL
		gi|169796818|ref|YP_001714611.1	ETTSGALARLPKL

FIG. 55 Cont.

		gi|126641035|ref|YP_001084019.1	ETTSGALARLPKL
		gi|193076712|gb|ABO11417.2	ETTSGALARLPKL
		gi|169633925|ref|YP_001707661.1	ETTSGALARLPKL
		gi|184157266|ref|YP_001845605.1	ETTSGALARLPKL
		gi|51243931|ref|YP_063815.1	EVSAQTLARASDI
		gi|148651904|ref|YP_001278997.1	ETSTGLVNRLDWV
		gi|71066667|ref|YP_265394.1	ETSTGLVNRLDWV
		gi|93007258|ref|YP_581695.1	ETSTGLVNRLDWV
E69	E69Q		70
		E.coli_TesA_1U8U	PRWVLV**E**LGGNDGLR
		gi|121998847|ref|YP_001003634.1	PEIVLLQLGGNDGLR
		gi|114321556|ref|YP_743239.1	PEVLVVQLGGNDGLR
L70	L70T		70
		E.coli_TesA_1U8U	RWVLVE**L**GGNDGLRG
		gi|51243931|ref|YP_063815.1	DIVILETGANDGLRG
		gi|39997510|ref|NP_953461.1	DIVILVTGANDGLRG
		gi|148651904|ref|YP_001278997.1	DITILTTGANDAMRG
G72	G72A		70
		E.coli_TesA_1U8U	VLVELG**G**NDGLRGF
		gi|156977016|ref|YP_001447923.1	VLIELGANDGLRGF
		gi|54309970|ref|YP_130990.1	VIIELGANDGLRGF
		gi|37527678|ref|NP_931022.1	VLIELGANDGLRGF
		gi|209809090|ref|YP_002264628.1	VLIELGANDGLRGF

FIG. 55 Cont.

		gi|59714227|ref|YP_207002.1	VLIELGANDGLRGF
		gi|197337441|ref|YP_002158710.1	VLIELGANDGLRGF
		gi|125620500|gb|EAZ48871.1	VLIELGANDGLRGF
		gi|15601538|ref|NP_233169.1	VLIELGANDGLRGF
		gi|121588086|ref|ZP_01677835.1	VLIELGANDGLRGF
		gi|153827484|ref|ZP_01980151.1	VLIELGANDGLRGF
		gi|163800656|ref|ZP_02194557.1	VLIELGANDGLRGF
		gi|91226151|ref|ZP_01261041.1	VLIELGANDGLRGF
		gi|28900726|ref|NP_800381.1	VLIELGANDGLRGF
		gi|729449|sp|Q07792|ESTE_VIBMI	VLIELGANDGLRGF
		gi|90412817|ref|ZP_01220817.1	VIIELGANDGLRGF
		gi|90579358|ref|ZP_01235168.1	VLIELGANDGLRGF
		gi|89072709|ref|ZP_01159274.1	VLIELGANDGLRGF
		gi|157369400|ref|YP_001477389.1	VLIELGANDGLRGF
		gi|165927624|ref|ZP_02223456.1	VLIELGANDALRGF
		gi|22125003|ref|NP_668426.1	VLIELGANDALRGF
		gi|162420602|ref|YP_001605806.1	VLIELGANDALRGF
		gi|153949498|ref|YP_001401981.1	VLIELGANDALRGF
		gi|16123257|ref|NP_406570.1	VLIELGANDALRGF
		gi|77958377|ref|ZP_00822411.1	VLIELGANDGLRGF
G75	G75A		70 80
		E.coli_TesA_1U8U	ELGGND**G**LRGFQPQQT
		gi|165927624|ref|ZP_02223456.1	ELGANDALRGFPTQDI
		gi|22125003|ref|NP_668426.1	ELGANDALRGFPTQDI
		gi|162420602|ref|YP_001605806.1	ELGANDALRGFPTQDI

FIG. 55 Cont.

		gi|153949498|ref|YP_001401981.1	ELGANDALRGFPTQDI
		gi|16123257|ref|NP_406570.1	ELGANDALRGFPTQDI
		gi|74316704|ref|YP_314444.1	ELGGNDALRGTPPAQI
		gi|78484894|ref|YP_390819.1	ELGANDALRGQSLQAT
		gi|145589121|ref|YP_001155718.1	ELGANDALRGLTIEQT
		gi|152996229|ref|YP_001341064.1	ELGANDALRGYPLDQT
		gi|163856534|ref|YP_001630831.1	ELGPNDALRGLSLKMT
		gi|187478460|ref|YP_786484.1	ELGSNDALRGLPLNMT
		gi|33597579|ref|NP_885222.1	ELGSNDALRGLALDMT
		gi|33592804|ref|NP_880448.1	ELGSNDALRGLALDMT
		gi|118051335|ref|ZP_01519884.1	ELGGNDALRGLALQST
		gi|121604790|ref|YP_982119.1	ELGGNDALRGLPLDMT
		gi|91788891|ref|YP_549843.1	ELGGNDALRGLPLDMT
		gi|124267005|ref|YP_001021009.1	ELGGNDALRGLPLAMT
		gi|171058584|ref|YP_001709333.1	ELGGNDALRGLPLAMT
		gi|146220121|gb|ABQ11275.1	ELGANDALRGLSLKAT
		gi|121594614|ref|YP_986510.1	ELGGNDALRGLPLAST
		gi|121610344|ref|YP_998151.1	ELGGNDALRGLPLKSI
		gi|160899469|ref|YP_001565051.1	ELGGNDALRGLPLQST
		gi|120611683|ref|YP_971361.1	ELGGNDALRGLPLQGT
		gi|186475782|ref|YP_001857252.1	ELGANDALRGVPLSTT
L76	L76I, L76F, L76M		70 80
		E.coli_TesA_1U8U	ELGGNDG**L**RGFQPQQ
		gi|71066667|ref|YP_265394.1	TIGANDAIRGIDVAT
		gi|93007258|ref|YP_581695.1	TIGANDAIRGIDVAT

FIG. 55 Cont.

		gi|71280033|ref|YP_269028.1	ELGGNDGIRGFPVKL
		gi|78357184|ref|YP_388633.1	ELGVNDTFMGLEYEE
		gi|46580334|ref|YP_011142.1	ELGANDSFIGIEPDE
		gi|120602288|ref|YP_966688.1	ELGANDSFIGIEPDE
		gi|148651904|ref|YP_001278997.1	TTGANDAMRGIDVAT
		gi|51892159|ref|YP_074850.1	ELGANDGMQARPVAE
		gi|116327860|ref|YP_797580.1	ELGANDSMRGISPDQ
		gi|45657291|ref|YP_001377.1	ELGANDSMRGISPDQ
		gi|24215621|ref|NP_712742.1	ELGANDSMRGIFPDQ
R77	R77L		70 80
		E.coli_TesA_1U8U	ELGGNDGL**R**GFQPQQT
		gi|197103612|ref|YP_002128989.1	ALGGNDLLLGAEPREV
F79	F79M		80
		E.coli_TesA_1U8U	GLRG**F**QPQQTEQT
		gi|90023084|ref|YP_528911.1	GLQGMPVAGITRN
		gi|152988620|ref|YP_001347669.1	GLRGMAPAQLQQN
		gi|116050859|ref|YP_790318.1	GLRGMAPAQLQQN
		gi|107102405|ref|ZP_01366323.1	GLRGMAPAQLQQN
		gi|15598052|ref|NP_251546.1	GLRGMAPAQLQQN
		gi|49082664|gb|AAT50732.1	GLRGMAPAQLQQN
		gi|77460235|ref|YP_349742.1	GLRGMPPTQLQQN
Q80	Q80S		80
		E.coli_TesA_1U8U	GLRGF**Q**PQQTEQT

FIG. 55 Cont.

		gi|188026282|ref|ZP_02997874.1	GLQGLSVKQMENT
		gi|212706885|ref|ZP_03315013.1	GLQGLSVEQLEIT
		gi|212711255|ref|ZP_03319383.1	GLQGLSVEQLAIT
		gi|114772942|ref|ZP_01450253.1	GLQGHSIKKLKNN
		gi|109899221|ref|YP_662476.1	GLQGHSVSKMRDN
		gi|119774622|ref|YP_927362.1	GLRGFSPTELKKN
		gi|60893017|gb|AAX37297.1	GLRGFSPKQLKTN
		gi|127513331|ref|YP_001094528.1	GLRGFSPKQLKNN
		gi|78484894|ref|YP_390819.1	ALRGQSLQATQRN
		gi|94500900|ref|ZP_01307426.1	GLRGLSISAMKSN
		gi|82703094|ref|YP_412660.1	GLRGASIGSIRDN
		gi|30249426|ref|NP_841496.1	GLQGRSITSIYEN
		gi|149928382|ref|ZP_01916622.1	GLRGLSLDTMKDN
		gi|163856534|ref|YP_001630831.1	ALRGLSLKMTEQN
		gi|153888470|ref|ZP_02009612.1	ALRGLSLASSEAN
		gi|187928944|ref|YP_001899431.1	ALRGLSLASSEGN
		gi|17546436|ref|NP_519838.1	ALRGLSLSASEAN
		gi|20724196|ref|YP_002254594.1	ALRGLSLSASEAN
		gi|83749049|ref|ZP_00946056.1	ALRGLSLSASEAN
		gi|207743056|ref|YP_002259448.1	ALRGLSLSASEAN
		gi|134094953|ref|YP_001100028.1	ALRGLSLAATQEN
		gi|152980543|ref|YP_001353227.1	ALRGLSLIATQQN
		gi|73541078|ref|YP_295598.1	ALRGLSLQVTESN
		gi|77163958|ref|YP_342483.1	GLRGLSLTEMRRN
Q82	Q82P, Q82F		80

FIG. 55 Cont.

		E.coli_TesA_1U8U	GLRGFQPQQTEQTL
		gi|50120161|ref|YP_049328.1	GLRGFPAPNIEQDL
		gi|89093794|ref|ZP_01166740.1	GLRGTPPFAIKRNL
		gi|198263408|gb|EDY87686.1	GLRGFPPPITKNNL
Q83	Q83A		80 90
		E.coli_TesA_1U8U	RGFQPQQTEQTLRQ
		gi|89093794|ref|ZP_01166740.1	TGTPPFAIKRNLSR
		gi|78484894|ref|YP_390819.1	RGQSLQATQRNLQT
		gi|94500900|ref|ZP_01307426.1	RGLSISAMKSNLNS
		gi|146220121|gb|ABQ11275.1	RGLSLKATEANLDQ
		gi|167562421|ref|ZP_02355337.1	RGVPLTATESNLRE
		gi|167569605|ref|ZP_02362479.1	RGVPLTATENNLRE
		gi|167893816|ref|ZP_02481218.1	RGVPLAATEGNLRE
		gi|134277643|ref|ZP_01764358.1	RGVPLAATEGNLRE
		gi|167738130|ref|ZP_02410904.1	RGVPLAATEGNLRE
		gi|194505954|ref|YP_002035524.1	RGVPLAATEGNLRE
		gi|76810223|ref|YP_333863.1	RGVPLAATEGNLRE
		gi|161355201|ref|ZP_02101081.1	RGVPLAATEGNLRE
		gi|167902268|ref|ZP_02489473.1	RGVPLAATEGNLRE
		gi|194570836|ref|YP_002105836.1	RGVPLAATEGNLRE
		gi|53719047|ref|YP_108033.1	RGVPLAATEGNLRE
		gi|126453719|ref|YP_001066613.1	RGVPLAATEGNLRE
		gi|126441228|ref|YP_001059345.1	RGVPLAATEGNLRE
		gi|53723658|ref|YP_103103.1	RGVPLAATEGNLRE
		gi|124384223|ref|YP_001029293.1	RGVPLAATEGNLRE

FIG. 55 Cont.

		gi|67642011|ref|ZP_00440774.1	RGVPLAATEGNLRE
		gi|167836274|ref|ZP_02463157.1	RGVPLAATESNLRE
		gi|167581585|ref|ZP_02374459.1	RGVPLAATESNLRE
		gi|83720994|ref|YP_442651.1	RGVPLAATESNLRE
		gi|167619702|ref|ZP_02388333.1	RGVPLAATESNLRE
Q86	Q86A, Q86T		80 90
		E.coli_TesA_1U8U	FQPQQTE**Q**TLRQI
		gi|59714227|ref|YP_207002.1	FPPQKINANLEKI
		gi|197337441|ref|YP_002158710.1	FPPQKINANLEEI
		gi|156934923|ref|YP_001438839.1	FPPDTLSATLRKI
		gi|77360818|ref|YP_340393.1	FPVSKLQANLTEL
		gi|119472458|ref|ZP_01614557.1	FPVKKMQANLTSL
		gi|88703495|ref|ZP_01101211.1	YPTSKLEANLSFM
		gi|90416813|ref|ZP_01224743.1	QPLALMKANLQAM
		gi|171058584|ref|YP_001790933.1	LPLAMTEANLLAM
		gi|146220121|gb|ABQ11275.1	LSLKATEANLDQM
		gi|153888470|ref|ZP_02009612.1	LSLASSEANMKAM
		gi|17546436|ref|NP_519838.1	LSLSASEANLKAM
		gi|207724196|ref|YP_002254594.1	LSLSASEANLKAM
		gi|83749049|ref|ZP_00946056.1	LSLSASEANLKAM
		gi|207743056|ref|YP_002259448.1	LSLSASEANLKAM
		gi|94310819|ref|YP_584029.1	FPLQTTEANLRTI
		gi|113867511|ref|YP_726000.1	LPLQTTEANLRNI
		gi|194289548|ref|YP_002005455.1	LPLHTTEANLRNI
		gi|53804283|ref|YP_113859.1	LPPAALKANLGAM

FIG. 55 Cont.

		gi|46580334|ref|YP_011142.1	IEPDEVAANLDAI
		gi|197103612|ref|YP_002128989.1	AEPREVRANLDAI
		gi|167645243|ref|YP_001682906.1	IEPRVTKANLRAI
		gi|84684212|ref|ZP_01012114.1	IPLNSIEANLEQI
		gi|206686219|gb|EDZ46701.1	LEPQEARANLTRI
		gi|206680133|gb|EDZ44620.1	IDPVSSRANLESI
		gi|114764037|ref|ZP_01443276.1	LPPETSRANLEGI
		gi|126725548|ref|ZP_01741390.1	IDPQVSRANIRGI
		gi|120602288|ref|YP_966688.1	IEPDEVAANLDAI
		gi|167624526|ref|YP_001674820.1	FPPKQLKTNLTKI
		gi|60893017|gb|AAX37297.1	FSPKQLKTNLAEM
		gi|186454892|ref|ZP_02965207.1	IPVAATRTNLQTI
		gi|194369063|gb|ABE57909.2	FPVKKMQTNLTAL
T87	T87H		90
			QTEQ**T**LRQILQD
		E.coli_TesA_1U8U	LLQKHLTELVTK
		gi|71280033|ref|YP_269028.1	EIRSHLGQIVRL
		gi|88813651|ref|ZP_01128881.1	DSEKHLAQSIEY
		gi|42521961|ref|NP_967341.1	
V95	V95L		90 100
			QILQD**V**KAANAEP
		E.coli_TesA_1U8U	AILQILTAQDVPV
		gi|78357184|ref|YP_388633.1	AILSLLAGHGIPA
		gi|46580334|ref|YP_011142.1	EMVRTLKERNVTV
		gi|39997510|ref|NP_953461.1	TAIKRLQDQGSVV
		gi|148651904|ref|YP_001278997.1	

FIG. 55 Cont.

	gi|71066667|ref|YP_265394.1	TAVKRLQDNDSVV
	gi|93007258|ref|YP_581695.1	TAVKRLODNDSVV
	gi|51892159|ref|YP_074850.1	GIIARLQEEGVAV
	gi|167645243|ref|YP_001682906.1	AILQSLRSRRISA
	gi|197103612|ref|YP_002128989.1	AIVRRLKARGVRV
	gi|162147014|ref|YP_001601475.1	AILDRLRQAHVPV
	gi|182677824|ref|YP_001831970.1	EILTRLRQRRIKA
	gi|154245703|ref|YP_001416661.1	EIVQRLKGRGITV
	gi|170747446|ref|YP_001753706.1	AIIERLKARGIPV
	gi|170743566|ref|YP_001772221.1	AIVARLRGRGIPV
	gi|163700508|ref|ZP_02119362.1	AIIARLKERGIPV
	gi|118592340|ref|ZP_01549732.1	EIVRRLTDRGITV
	gi|90421721|ref|YP_530091.1	QIVKKLKARNIAV
	gi|86747410|ref|YP_483906.1	EIVKRLKARNIAV
	gi|39933272|ref|NP_945548.1	EILKRLKARNLPV
	gi|192288623|ref|YP_001989228.1	EILKRLKARNLPV
	gi|167367448|ref|ZP_02301590.1	EILKRLKARNLPV
	gi|92116169|ref|YP_575898.1	EILKRLKARDIAV
	gi|27375570|ref|NP_767099.1	DIVQRLKARGIPV
	gi|146337546|ref|YP_001202594.1	EIVKRLKARGIAV
	gi|148251997|ref|YP_001236582.1	EIVQRLKARGIAV
	gi|90421109|ref|ZP_01229011.1	QILAKLQARDQAA
	gi|114705373|ref|ZP_01438281.1	KILEQLNERGQTV
	gi|13473671|ref|NP_105239.1	EMLARLKQRKIAV
	gi|211958502|gb|EEA93702.1	AMLARLSSRDIPV
	gi|163757370|ref|ZP_02164459.1	AMITRLKERGIAV

FIG. 55 Cont.

		gi|190893785|ref|YP_001980327.1	QMIGRLKQRGIAV
A100	A100V		100
		E.coli_TesA_1U8U	KAANAEPLLM
		gi|114772942|ref|ZP_01450253.1	QSANVQVAIQ
		gi|167624526|ref|YP_001674820.1	KAQQVTILLS
		gi|157374835|ref|YP_001473435.1	QAKDVEVLLS
		gi|78357184|ref|YP_388633.1	TAQDVPVLLM
		gi|51243931|ref|YP_063815.1	ADNDVVVVLA
		gi|39997510|ref|NP_953461.1	KERNVTVVLG
		gi|51892159|ref|YP_074850.1	QEEGVAVLLA
		gi|42521961|ref|NP_967341.1	QSQKVKVILG
		gi|198256435|gb|EDY80743.1	KYPEVKIVLA
		gi|186454892|ref|ZP_02965207.1	KKKDVKIIVA
		gi|116327860|ref|YP_797580.1	KKKNVKILLV
		gi|197103612|ref|YP_002128989.1	KARGVRVVLA
		gi|126739740|ref|ZP_01755431.1	RQEQVEVLLI
		gi|126725548|ref|ZP_01741390.1	AAKEVPVLLA
		gi|110678555|ref|YP_681562.1	AAQSVEVLLV
		gi|126730043|ref|ZP_01745855.1	EENDVEVLLI
		gi|85707175|ref|ZP_01038244.1	EAQGVEVLLV
		gi|149203588|ref|ZP_01880557.1	QANEVEVLLV
		gi|149915746|ref|ZP_01904271.1	RSRDVEVLLV
		gi|83950569|ref|ZP_00959302.1	EAREVPVLLV
		gi|84502882|ref|ZP_01000995.1	RAKGVEMLVI

FIG. 55 Cont.

		gi|198268949|gb|EDY93219.1	QDAGVDVLLV
		gi|198252001|gb|EDY76315.1	VDAGVEVLLV
		gi|84514338|ref|ZP_01001702.1	QQAGVAMLLV
		gi|126733689|ref|ZP_01749436.1	QDAGVEMLLV
		gi|162147014|ref|YP_001601475.1	RQAHVPVLLS
		gi|195970122|ref|NP_387325.1	KERGVAVLLA
		gi|163795307|ref|ZP_02189274.1	RSHRVPVLLA
M105	M105C, M105V		100 110
		E.coli_TesA_1U8U	NAEPLL**M**QIRLPA
		gi|54309970|ref|YP_130990.1	DAKPMLVQIKVPP
		gi|90412817|ref|ZP_01220817.1	DAKPMLVQIKVPP
		gi|30249426|ref|NP_841496.1	NATPLLVGMQLPP
		gi|34499190|ref|NP_903405.1	KAKVLLVGMALPP
		gi|119897957|ref|YP_933170.1	GAKVLLVGMRMPP
		gi|163856534|ref|YP_001630831.1	GARVLIVGMQIPP
		gi|187478460|ref|YP_786484.1	GAKVLIVGMQIPP
		gi|33597579|ref|NP_885222.1	GASVLVVGMQIPP
		gi|33592804|ref|NP_880448.1	GASVLVVGMQIPP
		gi|118051335|ref|ZP_01519884.1	GAQVLLVGMQVPP
		gi|121604790|ref|YP_982119.1	GAKVLLVGMQVPP
		gi|91788891|ref|YP_549843.1	GAKVLLVGMQVPP
		gi|171058584|ref|YP_001790933.1	GAAVMLVGMQVPP
		gi|146220121|gb|ABQ11275.1	GAKVLLVGQQVPP

FIG. 55 Cont.

		gi|121594614|ref|YP_986510.1	GARVLLVGVQVPP
		gi|160899469|ref|YP_001565051.1	GAKVLLVGMQVPP
		gi|120611683|ref|YP_971361.1	GAKVLIVGMQVPP
		gi|186475782|ref|YP_001857252.1	HAKVLLVGMYVPP
		gi|209521452|ref|ZP_03270160.1	HAKVVLVGMYVPP
		gi|170692416|ref|ZP_02883579.1	HAKVVLVGMYVPP
		gi|187923902|ref|YP_001895544.1	HAKVVLVGMYVPP
		gi|91783526|ref|YP_558732.1	HAKVVLVGMYVPP
		gi|167562421|ref|ZP_02355337.1	RAQVLLVGMYVPP
		gi|115522331|ref|YP_779242.1	NIPVLLCGMYAPP
		gi|90421721|ref|YP_530091.1	NIAVFLCGMYAPP
		gi|92116169|ref|YP_575898.1	DIAVLLCGMYAPP
		gi|27375570|ref|NP_767099.1	GIPVMLCGMLAPP
		gi|146337546|ref|YP_001202594.1	GIAVMLCGMLAPP
		gi|148251997|ref|YP_001236582.1	GIAVMLCGMLAPP
Q106	Q106R, Q106S		100 110
		E.coli_TesA_1U8U	AEPLLM**Q**IRLPANY
		gi|149907876|ref|ZP_01896544.1	IPVYVMSIRIPPNY
		gi|119503149|ref|ZP_01625233.1	ASVLLLSMEIPPNF
		gi|77163958|ref|YP_342483.1	AQVLLVRMRLPPNY
		gi|207088375|gb|EDZ65647.1	AQVLLVRMRLPPNY
		gi|124007358|ref|ZP_01692092.1	IKILLVRMEAPPNL
R108	R108S, R108D,		110

FIG. 55 Cont.

	R108Y	E.coli_TesA_1U8U	LLMQI**R**LPANY
		gi|77360818|ref|YP_340393.1	ALMEIYIPPNY
		gi|119472458|ref|ZP_01614557.1	ALMEIYIPPNY
		gi|194369063|gb|ABF57909.2	ALMEIYIPPNY
		gi|186475782|ref|YP_001857252.1	LLVGMYVPPNY
		gi|209521452|ref|ZP_03270160.1	VLVGMYVPPNY
		gi|170692416|ref|ZP_02883579.1	VLVGMYVPPNY
		gi|187923902|ref|YP_001895544.1	VLVGMYVPPNY
		gi|91783526|ref|YP_558732.1	VLVGMYVPPNY
		gi|167562421|ref|ZP_02355337.1	LLVGMYVPPNY
		gi|167569605|ref|ZP_02362479.1	LLVGMYVPPNY
		gi|167893816|ref|ZP_02481218.1	LLVGMYVPSNY
		gi|134277643|ref|ZP_01764358.1	LLVGMYVPSNY
		gi|167738130|ref|ZP_02410904.1	LLVGMYVPSNY
		gi|194505954|ref|YP_002035524.1	LLVGMYVPSNY
		gi|76810223|ref|YP_333863.1	LLVGMYVPSNY
		gi|161355201|ref|ZP_02101081.1	LLVGMYVPSNY
		gi|167902268|ref|ZP_02489473.1	LLVGMYVPSNY
		gi|194364429|ref|YP_002027039.1	LLLGIDVPPNY
		gi|190572845|ref|YP_001970690.1	LLLGIDVPPNY
		gi|21241603|ref|NP_641185.1	LLLGIDVPPNY
		gi|78046442|ref|YP_362617.1	LLLGIDVPPNY
		gi|188992969|ref|YP_001904979.1	LLLGIDVPPNY
		gi|21230252|ref|NP_636169.1	LLLGIDVPPNY
		gi|166710711|ref|ZP_02241918.1	LLLGIDMPPNY

FIG. 55 Cont.

		gi|58583387|ref|YP_202403.1	LLLGIDVPPNY
		gi|198268949|gb|EDY93219.1	LLVGLDAPSNY
		gi|198252001|gb|EDY76315.1	LLVGLDAPSNY
		gi|188575357|ref|YP_001912286.1	LLLGIDVPPNY
		gi|149203588|ref|ZP_01880557.1	LLVGLSAPGNY
		gi|126733689|ref|ZP_01749436.1	LLVGLSVGANY
L109	L109M		110
		E.coli_TesA_1U8U	MQIR**L**PANYGRRY
		gi|119897957|ref|YP_933170.1	VGMPMPPNYGTSY
		gi|169182148|ref|ZP_02842667.1	IGMRMPPNYGPAY
		gi|56479332|ref|YP_160921.1	IGMQMPPNYGPPY
		gi|166710711|ref|ZP_02241918.1	LGIDMPPNYGPAY
		gi|146282380|ref|YP_001172533.1	LGMRMPPNLGQRY
		gi|15029382|gb|AAK81865.1|AF395191_1	LGMKMPPNYGTAY
		gi|39997510|ref|NP_953461.1	GGMKMVANLGRDY
		gi|42521961|ref|NP_967341.1	GGLYMPPNYGKDY
		gi|182411899|ref|YP_001816965.1	AGMMMPPSMGPDY
		gi|198256435|gb|EDY80743.1	AGMQMPPNLGEDY
		gi|186454892|ref|ZP_02965207.1	AGMQMPPNMGEEY
N112	N112A		110
		E.coli_TesA_1U8U	MQIRLPA**N**YGRRYN
		gi|46580334|ref|YP_011142.1	MGWQATMADTPDYA
		gi|120602288|ref|YP_966688.1	MGWQATMADTPDYA

FIG. 55 Cont.

Y113	Y113I		110 120
		E.coli_TesA_1U8U	RLPAN**Y**GRRYNEAF
		gi|167645243|ref|YP_001682906.1	GAPPLIGATYAREF
R115	R115N, R115S, R115E, R115G, R115A		110 120
		E.coli_TesA_1U8U	PANYG**R**RYNEAF
		gi|89093794|ref|ZP_01166740.1	PSNYGAAYNKQF
		gi|118051335|ref|ZP_01519884.1	PPNYGATYTEQF
		gi|146220121|gb|ABQ11275.1	PPNYGADYNQRF
		gi|121610344|ref|YP_998151.1	PPNYGAAYADRF
		gi|121594614|ref|YP_986510.1	PPNYGANYTRQF
		gi|194364429|ref|YP_002027039.1	PPNYGAGYRQRL
		gi|92114738|ref|YP_574666.1	PPNYGAAYTDAF
		gi|146307581|ref|YP_001188946.1	PPNYGARYTSAF
		gi|149276542|ref|ZP_01882686.1	PPNMGAEYATEF
		gi|167645243|ref|YP_001682906.1	PPLIGATYAREF
		gi|114772942|ref|ZP_01450253.1	PTNYGARYNRMF
		gi|91788891|ref|YP_549843.1	PPNYGGAYGAGF
		gi|53804283|ref|YP_113859.1	PPNYGGRYAEAF
		gi|197103612|ref|YP_002128989.1	PPLLSGAWASAF
		gi|119774622|ref|YP_927362.1	PTNYGGRYAKAF
		gi|119503149|ref|ZP_01625233.1	PPNFGSRYTTLF
		gi|90023084|ref|YP_528911.1	PPNFGSRYTQPF

FIG. 55 Cont.

		gi|121604790|ref|YP_982119.1	PPNYGSAYAATF
		gi|160899469|ref|YP_001565051.1	PPNYGSGYTRQF
		gi|120611683|ref|YP_971361.1	PPNYGSDYTRRF
		gi|71066667|ref|YP_265394.1	YDNLGSDYVKSF
		gi|93007258|ref|YP_581695.1	YDNLGSDYVKSF
		gi|134094953|ref|YP_001100028.1	PPNYGSDYTKQF
		gi|209904237|ref|ZP_03278741	PPNYGNHFTERF
		gi|198256435|gb|EDY80743.1	PPNLGEDYTKEF
		gi|114705373|ref|ZP_01438281.1	PPNMGEDYAERF
		gi|186454892|ref|ZP_02965207.1	PPNMGEEYNKAY
Y117	Y117L, Y117W		110 120
		E.coli_TesA_1U8U	PANYGRR**Y**NEAFSA
		gi|69935214|ref|ZP_00630194.1	PDHDDP-LRRDWAG
		gi|197103612|ref|YP_002128989.1	PPLLSGAWASAFDE
E119	E119R, E119K		120
		E.coli_TesA_1U8U	GRRYN**E**AFSAIYP
		gi|88703495|ref|ZP_01101211.1	GPRYTRSFRESFE
		gi|149928382|ref|ZP_01916622.1	GPAYARRFGDTFP
		gi|171058584|ref|YP_001790933.1	GQAYSRDFAGLFG
		gi|121594614|ref|YP_986510.1	GANYTRQFAEVFE
		gi|160899469|ref|YP_001565051.1	GSGYTRQFEQLFA
		gi|120611683|ref|YP_971361.1	GSDYTRRFENVFP
		gi|152980543|YP_001353227.1	GTDYTRQFAELYP

FIG. 55 Cont.

		gi|149377045|ref|ZP_01894796.1	GQRYTRAFADIYP
		gi|91775603|ref|YP_545359.1	GPKYTREFIASYT
		gi|146282380|ref|YP_001172533.1	GQRYTRAFADAFD
		gi|69935214|ref|ZP_00630194.1	DP-LRRDWAGIWP
		gi|114772942|ref|ZP_01450253.1	GARYNRMFISAFS
		gi|71280033|ref|YP_269028.1	GQRYRKMFTDSYT
		gi|77360818|ref|YP_340393.1	GPRYSKMFTDSFT
		gi|119472458|ref|ZP_01614557.1	GPRYSKMFTDSFS
		gi|194369063|gb|ABF57909.2	GPRYSKMFTSSFT
		gi|149907876|ref|ZP_01896544.1	GPRYSKMFTDVFT
		gi|91793720|ref|YP_563371.1	GPRYSKAFNQVYH
		gi|114563734|ref|YP_751247.1	GPRYAKSFTQIYH
		gi|119774622|ref|YP_927362.1	GGRYAKAFADVYQ
		gi|127513331|ref|YP_001094528.1	GPRYAKQFTQVYQ
		gi|170727240|ref|YP_001761266.1	GPRYAKMFNQVYA
		gi|119475890|ref|ZP_01616242.1	GTRYTKMFYESYG
		gi|89093794|ref|ZP_01166740.1	GAAYNKQFSEIYP
		gi|134094953|ref|YP_001100028.1	GSDYTKQFSALFP
		gi|66045308|ref|YP_235149.1	GPRYTKAFEEVYS
		gi|15029382|gb|AAK81865.1|AF395191_1	GTAYSKAFENNYK
F121	F121L, F121Y		120 130
		E.coli_TesA_1U8U	RYNEA**F**SAIYPKLAK
		gi|78484894|ref|YP_390819.1	AYDQMLQQTFKQVAT

FIG. 55 Cont.

		gi|194364429|ref|YP_002027039.1		GYRQRLAAAYKALAT
		gi|190572845|ref|YP_001970690.1		AYRQRLAAAYRALAT
		gi|212416031ref|NP_641185.1		AYRERLKATYADLSK
		gi|78046442|ref|YP_362617.1		AYRERLKATYADLST
		gi|188992969|ref|YP_001904979.1		AYRERLKATYADLSK
		gi|212302521ref|NP_636169.1		AYRERLKATYADLSK
		gi|166710711|ref|ZP_02241918.1		AYRERLKATYADLAK
		gi|58583387|ref|YP_202403.1		AYRERLKATYADLSK
		gi|188575357|ref|YP_001912286.1		AYRERLKATYADLSK
		gi|51243931|ref|YP_063815.1		AYMQRYNRIYSQLEE
		gi|186454892|ref|ZP_02965207.1		EYNKAYRETFPEVAK
S122	S122F, S122G, S122V, S122Y, S122E, S122I	E.coli_TesA_1U8U	120 130	YNEAFSAIYPKLAK
		gi|209809090|ref|YP_002264628.1		YSQAFGSLYPKISE
		gi|59714227|ref|YP_207002.1		YSQAFGSLYPKLSE
		gi|186461326|gb|ACC78298.1		YNEAFGAIYPALAK
		gi|206576527|ref|YP_002240008.1		YNEAFGAIYPALAK
		gi|156977016|ref|YP_001447923.1		YSDMFYDIYPKLAE
		gi|125620500|gb|EAZ48871.1		YSDAFYQIYPSLAE
		gi|156015381ref|NP_233169.1		YSDAFYQIYPSLAE
		gi|121588086|ref|ZP_01677835.1		YSDAFYQIYPSLAE
		gi|153827484|ref|ZP_01980151.1		YSDAFYQIYPSLAE
		gi|156934923|ref|YP_001438839.1		YNQAFEAIYPELAW
		gi|188026282|ref|ZP_02997874.1		YTSSFENVYPALAQ

FIG. 55 Cont.

		gi|212706885|ref|ZP_03315013.1	YTSSFEKVYPTLAE
		gi|119897957|ref|YP_933170.1	YTTRFEAAFADVAR
		gi|91775603|ref|YP_545359.1	YTREFIASYTELAK
		gi|114772942|ref|ZP_01450253.1	YNRMFISAFSDVAD
		gi|149928382|ref|ZP_01916622.1	YARRFGDTFPDVAR
		gi|90023084|ref|YP_528911.1	YTQPFFEQYSSLAK
		gi|152996229|ref|YP_001341064.1	YTQMFFNLYKDIAS
		gi|153888470|ref|ZP_02009612.1	YSERFFAMFGKLAQ
		gi|187928944|ref|YP_001899431.1	YSERFFAMFGKLAQ
		gi|113867511|ref|YP_726000.1	YTEKFVSLYPKLAG
		gi|194289548|ref|YP_002005455.1	YTEKFVSLYPRLAG
		gi|114321556|ref|YP_743239.1	YNQRFEALFHELAE
		gi|77163958|ref|YP_342483.1	YTERFEQLFTDLKD
		gi|207088375|gb|EDZ65647.1	YTERFEQLFTDLKD
		gi|53804283|ref|YP_113859.1	YAEAFERVYQELAE
		gi|66045308|ref|YP_235149.1	YTKAFEEVYSNLAE
A123	A123T		120 130
		E.coli_TesA_1U8U	YNE**A**FSAIYPKLAKE
		gi|167624526|ref|YP_001674820.1	YASQISTVYKELATE
		gi|157961485|ref|YP_001501519.1	YASQISTVYKELAEE
		gi|163757370|ref|ZP_02164459.1	YEAKFNTIYPDLAKK
Y125	Y125F		120 130

FIG. 55 Cont.

E.coli_TesA_1U8U	EAFSAIYPKLAKEF
gi|114772942|ref|ZP_01450253.1	RMFISAFSDVADEF
gi|196157105|ref|YP_002126594.1	QMFTQNFSKVADEQ
gi|88859908|ref|ZP_01134547.1	SLFTAVFSETTQKT
gi|77360818|ref|YP_340393.1	KMFTDSFTQVSKNT
gi|119472458|ref|ZP_01614557.1	KMFTDSFSQISEET
gi|149907876|ref|ZP_01896544.1	KMFTSSFTQISEDT
gi|194369063|gb|ABF57909.2	KMFTDVFTQVGSEK
gi|88703495|ref|ZP_01101211.1	RSFRESFERAATDT
gi|78484894|ref|YP_390819.1	QMLQQTFKQVATQN
gi|94500900|ref|ZP_01307426.1	QMFKQAFADVAEQQ
gi|71908327|ref|YP_285914.1	ADFHSSFTSIAQAK
gi|119897957|ref|YP_933170.1	TRFEAAFADVARER
gi|169182148|ref|ZP_02842667.1	QRFAEVFANVAAEK
gi|56479332|ref|YP_160921.1	QRFEQTFADVAREH
gi|149928382|ref|ZP_01916622.1	RRFGDTFPDVARKQ
gi|163856534|ref|YP_001630831.1	QRFAAVFPAVAKAE
gi|187478460|ref|YP_786484.1	ERFAKVFQNVAEKE
gi|33597579|ref|NP_885222.1	QRFAQVFPAVAEQE
gi|33592804|ref|NP_880448.1	QRFAQVFPAVAEQE
gi|118051335|ref|ZP_01519884.1	EQFAGMFKKVADTQ
gi|121604790|ref|YP_982119.1	ATFSGLFAKVAKEE
gi|91788891|ref|YP_549843.1	AGFAGLFPKVARAE
gi|124267005|ref|YP_001021009.1	EDFAALFGKVARAE

FIG. 55 Cont.

		gi|171058584|ref|YP_001790933.1	REFAGLFGKVAQRE
		gi|121594614|ref|YP_986510.1	RQFAEVFENVAQER
		gi|121610344|ref|YP_998151.1	DRFAALFTTVAQAR
		gi|160899469|ref|YP_001565051.1	RQFEQLFAKVAQEQ
F140	F140M		130 140
		E.coli_TesA_1U8U	LAKEFDVPLLPF**F**MEEVYL
		gi|94500900|ref|ZP_01307426.1	VAEQQGVAFIPFMLKPLMN
		gi|152996229|ref|YP_001341064.1	IASKYNIAYLPFMLENVAL
		gi|88798847|ref|ZP_01114429.1	LASTYNLPFLPFMLEGVAE
		gi|149928382|ref|ZP_01916622.1	VARKQKVPLVPFMLEGFAL
		gi|134094953|ref|YP_001100028.1	LAQETKSSLVPFMLQGVAE
		gi|152980543|ref|YP_001353227.1	IAKETKSALVPFMLKDVAD
		gi|198263408|gb|EDY87686.1	LAQQHDVALVPFMLEDIYQ
		gi|149200040|ref|ZP_01877066.1	LAEKNKIELIPFMLEEVAG
		gi|206686219|gb|EDZ46701.1	LAAEFGAVLHPGMAAEAGG
		gi|94497924|ref|ZP_01304489.1	LAHKYDAALYPFMLDGVLG
M141	M141P, M141A, M141L, M141M, M141G		140
		E.coli_TesA_1U8U	FDVPLLPFF**M**EEVYL-KP
		gi|156977016|ref|YP_001447923.1	QQVALMPFFLEHVII-KP
		gi|54309970|ref|YP_130990.1	LATPLLPFFLEQIIL-KQ
		gi|148548659|ref|YP_001268761.1	KQVPLVPFFLEGVGG-VP
		gi|209809090|ref|YP_002264628.1	HDIPLVPFFLEHVII-KP
		gi|59714227|ref|YP_207002.1	HAIPLLPFFLEQVIV-KP

FIG. 55 Cont.

		gi|197337441|ref|YP_002158710.1	HAIPLLPFFLEQVIV-KP
		gi|125620500|gb|EAZ48871.1	FSIPLIPFFLEQVIL-KP
		gi|15601538|ref|NP_233169.1	FSIPLIPFFLEQVIL-KP
		gi|121588086|ref|ZP_01677835.1	FSIPLIPFFLEQVIL-KP
		gi|153827484|ref|ZP_01980151.1	FSIPLIPFFLEQVIL-KP
		gi|163800656|ref|ZP_02194557.1	QQVNLIPFFLEQVIV-KP
		gi|146279956|ref|YP_001170114.1	YEADLEANFLDEPDA-RQ
		gi|91226151|ref|ZP_01261041.1	QQVALMPFFLEHVVT-KP
		gi|28900726|ref|ZP_800381.1	QQVQLMPFFLEHVIT-KP
		gi|119897957|ref|YP_933170.1	RKVRLVPFLFDGFAD-KP
		gi|84684212|ref|ZP_01012114.1	HDMIFMPYIFQGMMS-RT
		gi|206680133|ref|EDZ44620.1	YDTLYVQDFFDGTVD-RP
		gi|145589121|ref|YP_001155718.1	EHIQLLPFFFNGLAT-NK
		gi|78357184|ref|YP_388633.1	HRVMLHPFFPEGVAA-NP
		gi|85707175|ref|ZP_01038244.1	YDTLFMPFFAGLGEG-DP
		gi|206686219|ref|EDZ46701.1	FGAVLHPGMAAEAGG-DP
		gi|149203588|ref|ZP_01880557.1	YGAFYAPFFAGLGGG-DP
		gi|126739740|ref|ZP_01755431.1	YEAIFHPVVGEDPAA-AR
E142	E142C		130 140
		E.coli_TesA_1U8U	KLAKEFDVPLLPFFM**E**EVYL
		gi|74316704|ref|YP_314444.1	EVARSEKVTHVPCFVCEVGV
Y145	Y145E, Y145M, Y145T,		140 150
		E.coli_TesA_1U8U	DVPLLPFFMEEV**Y**L-KPQ

FIG. 55 Cont.

Y145D, Y145L, Y145A	gi|37527678|ref|NP_931022.1		QIPLLPFYMEQVAI-KPE
	gi|165927624|ref|ZP_02223456.1		DIPLLPFFMEQVAV-KPE
	gi|22125003|ref|NP_668426.1		DIPLLPFFMEQVAV-KPE
	gi|162420602|ref|YP_001605806.1		DIPLLPFFMEQVAV-KPE
	gi|153949498|ref|YP_001401981.1		DIPLLPFFMEQVAV-KPE
	gi|16123257|ref|NP_406570.1		DIPLLPFFMEQVAV-KPE
	gi|77958377|ref|ZP_00822411.1		GIPLVPFFMEQVAV-KPE
	gi|77979334|ref|ZP_00834753.1		SIPLVPFFMEHVAV-KPE
	gi|123443264|ref|YP_001007238.1		NIPLVPFFMEAVAV-KPQ
	gi|77974242|ref|ZP_00829783.1		GIPLVPFFMEQVAV-KPE
	gi|197286014|ref|YP_002151886.1		DIPLVPFFMEQVAV-KPE
	gi|114772942|ref|ZP_01450253.1		ALELIPFYMEQIAD--KPE
	gi|109899221|ref|YP_662476.1		DVPLVPFFLADIAL-NPE
	gi|196157105|ref|YP_002126594.1		DVTLLPFFLADIAL-NNE
	gi|71280033|ref|YP_269028.1		DIATIPFFLEEIAL-HQE
	gi|163757370|ref|ZP_02164459.1		GAHLMAYFMTDVAI-DSS
	gi|84684212|ref|ZP_01012114.1		DVVFYPFFLDGVTG-NPS
	gi|126733689|ref|ZP_01749436.1		DMIFMPYIFQGMMS-RTD
	gi|84514338|ref|ZP_01001702.1		DIALYADFMQEGM---S-E
	gi|94500900|ref|ZP_01307426.1		DVPLYHD--MFAGMRVTPA
	gi|167562421|ref|ZP_02355337.1		GVAFIPFMLKPLMN-KDK
	gi|167569605|ref|ZP_02362479.1		RVPLVPFLLAGIEN-KPD
	gi|186475782|ref|YP_001857252.1		RVPLVPFLLAGIED-KPD
	gi|77465602|ref|YP_355105.1		GADLEPNFLDEPDA-RQR
	gi|126464041|ref|YP_001045154.1		GADLEPNFLDEPDA-RQR

FIG. 55 Cont.

		gi|146279956|ref|YP_001170114.1	EADLEANFLDEPDE-RQR
		gi|94497924|ref|ZP_01304489.1	DAALYPFMLDGVLG-DRT
M151	M151V, M151I		130 140 150
		E.coli_TesA_1U8U	AKEFDVPLLPFFMEEVYL-KPQW**M**QDDG
		gi|50120161|ref|YP_049328.1	AEQFALPLLPFFMEQVYL-KPEWIMEDG
		gi|209809090|ref|YP_002264628.1	SEKHDIPLVPFFLEHVII-KPEWIMKDG
		gi|212706885|ref|ZP_03315013.1	AEKNQIPLLPFFMESVIT-KPEWIQPDG
		gi|212711255|ref|ZP_03319383.1	AEKNQLPLIPFFMESVIT-KPEWIQPDG
		gi|88859908|ref|ZP_01134547.1	TQKTNTTLMPFFMLAVAG-NPELIQNDN
		gi|90416813|ref|ZP_01224743.1	SEAEDVLLIPFQLEELSV-TEGMIQEDG
		gi|153874618|ref|ZP_02002768.1	AAEYDIPLVPFFLDKVAL-NPALIQVDG
		gi|37527678|ref|NP_931022.1	AEYNQIPLLPFYMEQVAI-KPEWVQQDG
		gi|94500900|ref|ZP_01307426.1	AEQQGVAFIPFMLKPLMM-KDKYVQDDG
		gi|196195006|gb|EDX89965.1	AQSTSAPWVPFFLDGVIE-QG-WVQDDG
		gi|154245703|ref|YP_001416661.1	AAAEGVLLYPFFLDGVAG-ERALVQPDG
Q152	Q152L		130 140 150
		E.coli_TesA_1U8U	KEFDVPLLPFFMEEVYL-KPQWM**Q**DDGI
		gi|71280033|ref|YP_269028.1	DQTGAHLMAYFMTDVAI-DSSLMLNDNL
		gi|169182148|ref|ZP_02842667.1	AEKKVPLVPFLMDGFAD-RPELFLPDGI
		gi|78357184|ref|YP_388633.1	ARHRVMLHPFFPEGVAA-NPALSLPDGI
		gi|46580334|ref|YP_011142.1	AKHGTPLYADTLAGIWG-EDRMTLHDGL
		gi|120602288|ref|YP_966688.1	AKHGTPLYADTLAGIWG-EDRMTLHDGL
		gi|119713520|gb|ABL97573.1	EKHSLIFMPFLLEEVAL-QKALLLPDYK

FIG. 55 Cont.

		gi|42521961|ref|NP_967341.1	KKYKLTFIPFILDKVAG-NPKYNLADGI
		gi|149200040|ref|ZP_01877066.1	EKNKIELIPFMLEEVAG-HAKMNLPDGI
		gi|126647348|ref|ZP_01719853.1	EEKDVELIPFLLQDVGG-IKELNLPDGI
		gi|193215472|ref|YP_001996671.1	KENRAQLIPFLLEGVGG-QPNLNLPDGI
		gi|182677824|ref|YP_001831970.1	QQFDVPFYPFFLDGVAG-NPALELPDRV
		gi|170747446|ref|YP_001753706.1	ERYGLTLYPFFLDGIIG-DRAQHLDDMI
		gi|170743566|ref|YP_001772221.1	ERYGLVLYPFFLDGVAG-NRGLTLADGL
		gi|163700508|ref|ZP_02119362.1	ERHGLMLYPFFLDGVAT-DRSLTLPDGL
		gi|118592340|ref|ZP_01549732.1	KAHDALFYPFFLEGVAL-NPDLNLSDGM
		gi|13473671|ref|NP_105239.1	KKYDVALYPFFLDGVAG-QPGMQLEDGL
		gi|211958502|gb|EEA93702.1	EKHDALLYPFFLDGVAA-EPKLNLGDGM
		gi|163757370|ref|ZP_02164459.1	KKHDVVFYPFFLDGVTG-NPSLLLSDGM
		gi|190893785|ref|YP_001980327.1	EKHGVRLYDFFLDGVAL-DAGLKLDDGM
		gi|167357739|ref|ZP_02292403.1	EKHGLPLYAFFLDGVAL-EAGLKLDDGM
		gi|116254256|ref|YP_770094.1	EKHGLPLYAFFLDGVAL-EAGLKLEDGM
		gi|150398267|ref|YP_001328734.1	KEHDTVFYPFFLDGVVT-EAGLKLEDGM
		gi|195970122|ref|NP_387325.2	KEHNLVFYPFFLDGVVT-EVGLKLDDGM
D153	D153K		130 140 150
		E.coli_TesA_1U8U	AKEFDVPLLPFFMEEVYL-KPQWMQ**D**DGI
		gi|209809090|ref|YP_002264628.1	SEKHDIPLVPFFLEHVII-KPEWIMKDGL
		gi|59714227|ref|YP_207002.1	SEKHAIPLLPFFLEQVIV-KPEWMMKDGL
		gi|197337441|ref|YP_002158710.1	SEKHAIPLLPFFLEQVIV-KPEWMMKDGL
		gi|90579358|ref|ZP_01235168.1	SKDTNVPLLPFFLIDIIV-KPELMMKDGL
		gi|89072709|ref|ZP_01159274.1	SEDTNVPLLPFFLIDIIV-KPELMMKDGL

FIG. 55 Cont.

		gi|183220370|ref|YP_001838366.1	AKEENVPLVPFILEKVAT-IRKLNQKDGI
		gi|116327860|ref|YP_797580.1	AKEENLPLVPFFLNGVAG-VKKLNQKDGI
		gi|45657291|ref|YP_001377.1	AKEENLILVPFFLDGVAG-IKNLNQKDGI
		gi|85707157|ref|ZP_01038244.1	SEAYDTLFMPFFAGLGEG-DPSTLQKDGI
		gi|24215621|ref|NP_712742.1	AKEENLILVPFFLDGVAG-IKNLNQKDGI
I156	I156V		150 160
		E.coli_TesA_1U8U	KPQWMQDDG**I**HPNRDAQ
		gi|121998847|ref|YP_001003634.1	RDGMMQDDGVHPTAKAQ
		gi|15029382|gb|AAK81865.1|AF395191_1	NKSLMQKDLVHPNGKAQ
		gi|182677824|ref|YP_001831970.1	NPALELPDRVHPNQEGV
P158	P158A		150 160
		E.coli_TesA_1U8U	KPQWMQDDGIH**P**NRDAQPFI
		gi|69935214|ref|ZP_00630194.1	LPAMLQPDGLHASAKGVGLI
N159	N159V, N159T, N159G		160
		E.coli_TesA_1U8U	DDGIHP**N**RDAQPF
		gi|50120161|ref|YP_049328.1	EDGIHPTRDAQPF
		gi|209809090|ref|YP_002264628.1	KDGLHPTPEAQPW
		gi|90579358|ref|ZP_01235168.1	KDGLHPTAQAQPL
		gi|89072709|ref|ZP_01159274.1	KDGLHPTAQAQPL
		gi|188026282|ref|ZP_02997874.1	QDGIHPTVEAQPS
		gi|212706885|ref|ZP_03315013.1	PDGIHPTAEAQPS
		gi|212711255|ref|ZP_03319383.1	PDGIHPTEQAQPT

FIG. 55 Cont.

		gi|114772942|ref|ZP_01450253.1	NDGIHPTAEAQPM
		gi|88703495|ref|ZP_01101211.1	QDGIHPTVEAQPM
		gi|119503149|ref|ZP_01625233.1	SDGIHPTAGAQSL
		gi|90416813|ref|ZP_01224743.1	EDGLHPTAMAQPI
		gi|121998847|ref|YP_001003634.1	DDGVHPTAKAQPE
		gi|82703094|ref|YP_412660.1	ADGIHPTARAQEK
		gi|30249426|ref|NP_841496.1	ADGIHPTIQAQEK
		gi|88798847|ref|ZP_01114429.1	ADGLHPTAAAQPI
		gi|90023084|ref|YP_528911.1	ADGLHPTAEAQPI
		gi|56479332|ref|YP_160921.1	SDGIHPTAEAQEL
		gi|192359766|ref|YP_001982095.1	RDGIHPTEEAQPL
		gi|171058584|ref|YP_001790933.1	PDRIHPTAWAHP-
		gi|146220121|gb|ABQ11275.1	PDRIHPTAAAHPT
		gi|121594614|ref|YP_986510.1	PDRIHPTAQAHPR
		gi|160899469|ref|YP_001565051.1	ADRIHPTAKAQPR
		gi|186475782|ref|YP_001857252.1	SDQIHPTQRAQPL
		gi|134295954|ref|YP_001119689.1	SDQMHPGEQAQRV
		gi|83749049|ref|ZP_00946056.1	EDRIHPVAAAQPT
		gi|207724196|ref|YP_002254594.1	EDRIHPVAAAQPT
		gi|207743056|ref|YP_002259448.1	EDRIHPVAAAQPT
R160	R160A, R160G, R160S, R160D		160
		E.coli_TesA_1U8U	DDGIHPN**R**DAQPFI
		gi|153949498|ref|YP_001401981.1	DDGLHPNGDAQPFI
		gi|22125003|ref|NP_668426.1	DDGLHPNGDAQPFI

FIG. 55 Cont.

		gi|165927624|ref|ZP_02223456.1	DDGLHPNGDAQPFI
		gi|16123257|ref|NP_406570.1	DDGLHPNGDAQPFI
		gi|150398267|ref|YP_001328734.1	EDGMHPNGEGIAVM
		gi|211958502|gb|EEA93702.1	GDGMHPTGEGVSII
		gi|195970122|ref|NP_387325.1	DDGMHPNGGGVGVM
		gi|162420602|ref|YP_001605806.1	DDGLHPNGDAQPFI
		gi|77962143|ref|ZP_00825967.1	DDGLHPNAEAQPFI
		gi|90579358|ref|ZP_01235168.1	KDGLHPTAQAQPLI
		gi|77958377|ref|ZP_00822411.1	DDGLHPNAEAQPFI
		gi|77979334|ref|ZP_00834753.1	DDGLHPNAAAQPFI
		gi|77974242|ref|ZP_00829783.1	DDGLHPNAEAQPFI
		gi|212706885|ref|ZP_03315013.1	PDGIHPTAEAQPSI
		gi|123443264|ref|YP_001007238.1	DDGLHPNAQAQPFI
		gi|89072709|ref|ZP_01159274.1	KDGLHPTAQAQPLI
		gi|54309970|ref|YP_130990.1	NDGLHPKSDAQPWI
		gi|94310819|ref|YP_584029.1	TDRIHPTSAAQPTL
		gi|149915746|ref|ZP_01904271.1	PDGIHPNSEGVERI
		gi|183220370|ref|YP_001838366.1	KDGIHPTDAGHKLV
Q163	Q163S		160
		E.coli_TesA_1U8U	DDGIHPNRDA**Q**PFI
		gi|213023388|ref|ZP_03337835.1	DDGIHPNATRSPFM
F165	F165M		160 170
		E.coli_TesA_1U8U	NRDAQP**F**IADWMAK

FIG. 55 Cont.

		gi|114772942|ref|ZP_01450253.1	TAEAQPMIAEFMLT
		gi|109899221|ref|YP_662476.1	NAKAQPMIAKSMQA
		gi|88703495|ref|ZP_01101211.1	TVEAQPMITDIVQP
I166	I166L		160 170
		E.coli_TesA_1U8U	LIHPNRDAQPF▌ADWMAKQL
		gi|77360818|ref|YP_340393.1	LHPNKTAQPILRDEMYNTI
		gi|119503149|ref|ZP_01625233.1	IHPTAGAQSLLLENVLPYA
		gi|89093794|ref|ZP_01166740.1	IHPSAEGQPYLLNTVWPHL
		gi|145589121|ref|YP_001155718.1	IHPNEKAQNIL--------
		gi|88798847|ref|ZP_01114429.1	LHPTAAAQPILLD------
		gi|83647632|ref|YP_436067.1	IHPNAKGQPQLVENVLPHL
		gi|163856534|ref|YP_001630831.1	IHPNEQAQPLLLDNVWAAL
		gi|187478460|ref|YP_786484.1	IHPNEMAQPALLNNVWPGL
		gi|33597579|ref|NP_885222.1	IHPNEDAQPALLDNVWPVL
		gi|33592804|ref|NP_880448.1	IHPNENAQPALLDNVWPLL
		gi|146220121|gb|ABQ11275.1	IHPTAAAHPTLLDNVWVEL
		gi|186475782|ref|YP_001857252.1	IHPTQRAQPLLLDNVWPAL
		gi|209521452|ref|ZP_03270160.1	IHPTQQAQPVLLNNVWPAV
		gi|187923902|ref|YP_001895544.1	IHPTQQAQPVLLNNVWPAV
		gi|91783526|ref|YP_558732.1	IHPTQQAQPVLLNNVWPAV
		gi|167562421|ref|ZP_02355337.1	IHPTQAAQRRLLDNVWPAL
		gi|167569605|ref|ZP_02362479.1	IHPTQAAQRRLLDNVWPAL
		gi|167893816|ref|ZP_02481218.1	IHPTQAAQRQLLDNVWPAL
		gi|134277643|ref|ZP_01764358.1	IHPTQAAQRQLLDNVWPAL

FIG. 55 Cont.

		gi|167738130|ref|ZP_02410904.1	IHPTQAAQRQLLDNVWPAL
		gi|194505954|ref|YP_002035524.1	IHPTQAAQRQLLDNVWPAL
		gi|76810223|ref|YP_333863.1	IHPTQAAQRQLLDNVWPAL
		gi|161355201|ref|ZP_02101081.1	IHPTQAAQRQLLDNVWPAL
		gi|167902268|ref|ZP_02489473.1	IHPTQAAQRQLLDNVWPAL
		gi|194570836|ref|YP_002105836.1	IHPTQAAQRQLLDNVWPAL
		gi|53719047|ref|YP_108033.1	IHPTQAAQRQLLDNVWPAL
		gi|126453719|ref|YP_001066613.1	IHPTQAAQRQLLDNVWPAL
		gi|126441228|ref|YP_001059345.1	IHPTQAAQRQLLDNVWPAL
		gi|53723658|ref|YP_103103.1	IHPTQAAQRQLLDNVWPAL
		gi|124384223|ref|YP_001029293.1	IHPTQAAQRQLLDNVWPAL
A167	A167T		160 170
		E.coli_TesA_1U8U	IHPNRDAQPFI**A**DWM
		gi|114563734|ref|YP_751247.1	IHPNEQAQDTITLIM
		gi|88703495|ref|ZP_01101211.1	IHPTVEAQPMITDIV

FIG. 56

dbj|AP007255.1
dbj|AP008229.1
dbj|AP008232.1
dbj|AP009384.1
dbj|BA000007.2
dbj|BA000032.2
dbj|BA000038.2
dbj|BAAW01000080.1
dbj|BAAW01003851.1
dbj|BAAW01008327.1
dbj|BAAW01012499.1
dbj|BAAW01015319.1
dbj|BAAX01023606.1
emb|AJ537556.1|UNK537556
emb|AL499619.1|LMFLCHR16
emb|AL499622.1|LMFLCHR32
emb|AL590842.1
emb|AL627267.1
emb|AL646052.1
emb|AL954747.1
emb|AM039952.1
emb|AM167904.1
emb|AM260479.1
emb|AM286415.1
emb|AM286690.1
emb|AM406670.1
emb|AM902716.1
emb|BX571871.1
emb|BX571965.1
emb|BX572593.1
emb|BX640416.1
emb|BX640432.1
emb|BX640446.1
emb|BX936398.1
emb|BX950851.1
emb|CAD61204.1
emb|CR378672.1
emb|CR543861.1
emb|CR954246.1
emb|CT573326.1
emb|CU207211.1
emb|CU234118.1
emb|X71116.1|VMP1662
gb|AAAA02045720.1
gb|AACV01025855.1
gb|AACV01026072.1
gb|AACV01029939.1
gb|AACY020000130.1
gb|AACY020014506.1
gb|AACY020022286.1
gb|AACY020022355.1
gb|AACY020039259.1
gb|AACY020045251.1
gb|AACY020046419.1
gb|AACY020047385.1
gb|AACY020055714.1
gb|AACY020063599.1
gb|AACY020074167.1
gb|AACY020074366.1
gb|AACY020093792.1
gb|AACY020108764.1
gb|AACY020111063.1
gb|AACY020111064.1
gb|AACY020134856.1
gb|AACY020145333.1
gb|AACY020145771.1
gb|AACY020184726.1
gb|AACY020237026.1
gb|AACY020242275.1
gb|AACY020259651.1
gb|AACY020262079.1
gb|AACY020281768.1
gb|AACY020291995.1
gb|AACY020301750.1
gb|AACY020307221.1
gb|AACY020329402.1
gb|AACY020351844.1
gb|AACY020355833.1
gb|AACY020365173.1
gb|AACY020368816.1
gb|AACY020373791.1
gb|AACY020376764.1
gb|AACY020385476.1
gb|AACY020397913.1
gb|AACY020399540.1
gb|AACY020412418.1
gb|AACY020413074.1
gb|AACY020413415.1
gb|AACY020421995.1
gb|AACY020440166.1
gb|AACY020442826.1
gb|AACY020448939.1
gb|AACY020462670.1
gb|AACY020484856.1
gb|AACY020500357.1
gb|AACY020501970.1
gb|AACY020503987.1
gb|AACY020508107.1
gb|AACY020520332.1
gb|AACY020525877.1
gb|AACY020527033.1
gb|AACY020528033.1
gb|AACY020529987.1
gb|AACY020536168.1
gb|AACY020538235.1
gb|AACY020539054.1
gb|AACY020548368.1
gb|AACY020551059.1
gb|AACY020557224.1
gb|AACY020559781.1
gb|AACY020561170.1
gb|AACY020561311.1
gb|AACY020577147.1
gb|AACY020597815.1
gb|AACY020603183.1
gb|AACY020608825.1
gb|AACY020629299.1
gb|AACY020714154.1
gb|AACY020727996.1
gb|AACY020759226.1
gb|AACY020784436.1
gb|AACY020834700.1
gb|AACY020839834.1
gb|AACY020868630.1

FIG. 56 Cont.

gb|AACY020917183.1
gb|AACY020958566.1
gb|AACY020990569.1
gb|AACY021019213.1
gb|AACY021020329.1
gb|AACY021023140.1
gb|AACY021026108.1
gb|AACY021059895.1
gb|AACY021060006.1
gb|AACY021070713.1
gb|AACY021076206.1
gb|AACY021115796.1
gb|AACY021166167.1
gb|AACY021245686.1
gb|AACY021260329.1
gb|AACY021268388.1
gb|AACY021275321.1
gb|AACY021288062.1
gb|AACY021314456.1
gb|AACY021334178.1
gb|AACY021344027.1
gb|AACY021383177.1
gb|AACY021451602.1
gb|AACY021583045.1
gb|AACY021586453.1
gb|AACY021608834.1
gb|AACY021641112.1
gb|AACY021691881.1
gb|AACY021705793.1
gb|AACY021712936.1
gb|AACY021721493.1
gb|AACY021739391.1
gb|AACY021784434.1
gb|AACY021819907.1
gb|AACY021848317.1
gb|AACY021853587.1
gb|AACY021891459.1
gb|AACY021899606.1
gb|AACY021919551.1
gb|AACY021938954.1
gb|AACY021947911.1
gb|AACY021963896.1
gb|AACY021984021.1
gb|AACY022040971.1
gb|AACY022045015.1
gb|AACY022065493.1
gb|AACY022078953.1
gb|AACY022105658.1
gb|AACY022129745.1
gb|AACY022140162.1
gb|AACY022151412.1
gb|AACY022158644.1
gb|AACY022178276.1
gb|AACY022209206.1
gb|AACY022212959.1
gb|AACY022218518.1
gb|AACY022219522.1
gb|AACY022231109.1
gb|AACY022242656.1
gb|AACY022277008.1
gb|AACY022282671.1
gb|AACY022329894.1
gb|AACY022348615.1
gb|AACY022377715.1
gb|AACY022380265.1
gb|AACY022465251.1
gb|AACY022510303.1
gb|AACY022575717.1
gb|AACY022607847.1
gb|AACY022636395.1
gb|AACY022672162.1
gb|AACY022685318.1
gb|AACY022706774.1
gb|AACY022710910.1
gb|AACY022761432.1
gb|AACY022779517.1
gb|AACY022786809.1
gb|AACY022792439.1
gb|AACY022794397.1
gb|AACY022850370.1
gb|AACY022879954.1
gb|AACY022895438.1
gb|AACY022931408.1
gb|AACY022939397.1
gb|AACY022975187.1
gb|AACY023000354.1
gb|AACY023011187.1
gb|AACY023028940.1
gb|AACY023036979.1
gb|AACY023064011.1
gb|AACY023073442.1
gb|AACY023081853.1
gb|AACY023088523.1
gb|AACY023101395.1
gb|AACY023108227.1
gb|AACY023127322.1
gb|AACY023150083.1
gb|AACY023151385.1
gb|AACY023214217.1
gb|AACY023220721.1
gb|AACY023225833.1
gb|AACY023293937.1
gb|AACY023309868.1
gb|AACY023317959.1
gb|AACY023341349.1
gb|AACY023344504.1
gb|AACY023397471.1
gb|AACY023419945.1
gb|AACY023423908.1
gb|AACY023459087.1
gb|AACY023466994.1
gb|AACY023470806.1
gb|AACY023471792.1
gb|AACY023472351.1
gb|AACY023474031.1
gb|AACY023483626.1
gb|AACY023512718.1
gb|AACY023518449.1
gb|AACY023573915.1
gb|AACY023574575.1
gb|AACY023575256.1
gb|AACY023580795.1
gb|AACY023597741.1
gb|AACY023600467.1
gb|AACY023629708.1
gb|AACY023630954.1

FIG. 56 Cont.

gb|AACY023638464.1
gb|AACY023647630.1
gb|AACY023649900.1
gb|AACY023659331.1
gb|AACY023667824.1
gb|AACY023676429.1
gb|AACY023685825.1
gb|AACY023793978.1
gb|AACY023794579.1
gb|AACY023802343.1
gb|AACY023803322.1
gb|AACY023804625.1
gb|AACY023810273.1
gb|AACY023812347.1
gb|AACY023824210.1
gb|AACY023824449.1
gb|AACY023825258.1
gb|AACY023825339.1
gb|AACY023828022.1
gb|AACY023831940.1
gb|AACY023837606.1
gb|AACY023837743.1
gb|AACY023841556.1
gb|AACY023874455.1
gb|AACY023876717.1
gb|AACY023882676.1
gb|AACY023908767.1
gb|AACY023929341.1
gb|AACY023947565.1
gb|AACY023964925.1
gb|AACY023970962.1
gb|AACY023972056.1
gb|AACY023974977.1
gb|AACY023980237.1
gb|AACY023984499.1
gb|AACY024025458.1
gb|AACY024034457.1
gb|AACY024063931.1
gb|AACY024085821.1
gb|AACY024096204.1
gb|AACY024096594.1
gb|AAFX01005675.1
gb|AAFX01011167.1
gb|AAFX01025782.1
gb|AAFX01038468.1
gb|AAFX01066401.1
gb|AAFX01106490.1
gb|AAFX01116872.1
gb|AAHY01746239.1
gb|AAK16084.1|AF288082_2
gb|AAK81865.1|AF395191_1
gb|AAMB02000002.1
gb|AAQ28697.1
gb|AAR43890.1
gb|AAR53009.1
gb|AASG02022698.1
gb|AASG02023246.1
gb|AASZ01000785.1
gb|AAT50732.1
gb|AATN01000167.1
gb|AATN01000814.1
gb|AATN01001106.1
gb|AATO01000008.1
gb|AATO01001850.1
gb|AATO01003739.1
gb|AATO01010104.1
gb|AAVS01000036.1
gb|AAVT01000002.1
gb|AAVV01000002.1
gb|AAX37297.1
gb|ABDH01009660.1
gb|ABDH01051283.1
gb|ABEF01005448.1
gb|ABEF01038687.1
gb|ABEF01040384.1
gb|ABEF01048738.1
gb|ABEF01052460.1
gb|ABF57909.2
gb|ABH77568.1
gb|ABO11417.2
gb|ABOK01442679.1
gb|ABOK01586584.1
gb|ABQ11275.1
gb|ABZ56880.1
gb|ACC78298.1
gb|AE003853.1
gb|AE004091.2
gb|AE005174.2
gb|AE005673.1
gb|AE005674.1
gb|AE008719.1
gb|AE009952.1
gb|AE011715.1
gb|AE012177.1
gb|AE013598.1
gb|AE014073.1
gb|AE014299.1
gb|AE014613.1
gb|AE015451.1
gb|AE016796.1
gb|AE016825.1
gb|AE016853.1
gb|AE017042.1
gb|AE017220.1
gb|AE017282.2
gb|AE017340.1
gb|AF288082.1|AF288082
gb|AF395190.2
gb|AY658457.1
gb|AY833091.1
gb|BZ549080.1
gb|CD439532.1
gb|CF322583.1
gb|CL669240.1
gb|CO742357.1
gb|CP000010.1
gb|CP000026.1
gb|CP000034.1
gb|CP000036.1
gb|CP000050.1
gb|CP000058.1
gb|CP000075.1
gb|CP000076.1
gb|CP000086.1
gb|CP000089.1

FIG. 56 Cont.

gb|CP000090.1
gb|CP000094.1
gb|CP000103.1
gb|CP000109.2
gb|CP000112.1
gb|CP000115.1
gb|CP000116.1
gb|CP000124.1
gb|CP000127.1
gb|CP000151.1
gb|CP000155.1
gb|CP000250.1
gb|CP000266.1
gb|CP000267.1
gb|CP000269.1
gb|CP000282.1
gb|CP000283.1
gb|CP000284.1
gb|CP000285.1
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gb|CP000304.1
gb|CP000305.1
gb|CP000308.1
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gb|CP000319.1
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gb|CP000380.1
gb|CP000388.1
gb|CP000438.1
gb|CP000440.1
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gb|CP000447.1
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gb|CP000555.1
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gb|CP000570.1
gb|CP000572.1
gb|CP000606.1
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gb|CP000647.1
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gb|CP000668.1
gb|CP000680.1
gb|CP000681.1
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gb|CP000720.1
gb|CP000744.1
gb|CP000749.1
gb|CP000753.1
gb|CP000783.1
gb|CP000790.1
gb|CP000821.1
gb|CP000822.1
gb|CP000826.1
gb|CP000851.1
gb|CP000868.1
gb|CP000880.1
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gb|CP000886.1
gb|CP000891.1
gb|CP000901.1
gb|CP000908.1
gb|CZ545523.1
gb|DQ771288.1
gb|DQ775969.1
gb|DU774646.1
gb|DU780221.1
gb|DX074846.1
gb|EAZ48871.1
gb|EBB00196.1
gb|EBB00995.1
gb|EBB14613.1
gb|EBB44352.1
gb|EBB65340.1
gb|EBB86785.1
gb|EBC00015.1
gb|EBC61260.1
gb|EBC67157.1
gb|EBC78525.1
gb|EBC80168.1
gb|EBC89014.1
gb|EBD12471.1
gb|EBD44387.1
gb|EBD83454.1
gb|EBE34945.1
gb|EBE46909.1
gb|EBE51481.1
gb|EBF18406.1
gb|EBF25038.1
gb|EBF35305.1
gb|EBF42247.1
gb|EBF46989.1
gb|EBF47131.1
gb|EBF48585.1
gb|EBF48999.1
gb|EBF70249.1
gb|EBF74014.1
gb|EBF84055.1
gb|EBF86466.1
gb|EBF88229.1
gb|EBG02140.1
gb|EBG03131.1
gb|EBH92870.1
gb|EBI09735.1

FIG. 56 Cont.

gb|EBI25014.1
gb|EBI40029.1
gb|EBI56927.1
gb|EBI60584.1
gb|EBI75401.1
gb|EBJ53471.1
gb|EBJ62451.1
gb|EBJ63565.1
gb|EBJ64666.1
gb|EBK67121.1
gb|EBK79457.1
gb|EBL34868.1
gb|EBL54355.1
gb|EBL57875.1
gb|EBL69503.1
gb|EBL86174.1
gb|EBM55815.1
gb|EBM63919.1
gb|EBN11937.1
gb|EBO21799.1
gb|EBO27566.1
gb|EBO70247.1
gb|EBO84406.1
gb|EBP12605.1
gb|EBQ43581.1
gb|EBQ56471.1
gb|EBR96977.1
gb|EBS05704.1
gb|EBS21319.1
gb|EBS29947.1
gb|EBS52576.1
gb|EBS87208.1
gb|EBS97371.1
gb|EBT20408.1
gb|EBT33808.1
gb|EBT66016.1
gb|EBU12431.1
gb|EBU22544.1
gb|EBU77869.1
gb|EBV49315.1
gb|EBV56371.1
gb|EBV65046.1
gb|EBV84832.1
gb|EBW51301.1
gb|EBX02078.1
gb|EBX43817.1
gb|EBX78437.1
gb|EBY36073.1
gb|EBY78830.1
gb|EBY98532.1
gb|EBZ04862.1
gb|EBZ09819.1
gb|EBZ17831.1
gb|ECA00284.1
gb|ECA11464.1
gb|ECA76985.1
gb|ECB56272.1
gb|ECB74738.1
gb|ECB77773.1
gb|ECC13206.1
gb|ECC26498.1
gb|ECC37977.1
gb|ECC47879.1
gb|ECC73123.1
gb|ECC78215.1
gb|ECC91531.1
gb|ECD18906.1
gb|ECE14473.1
gb|ECE44114.1
gb|ECE87400.1
gb|ECF24361.1
gb|ECF30240.1
gb|ECF37835.1
gb|ECF93596.1
gb|ECF98523.1
gb|ECG10921.1
gb|ECG16969.1
gb|ECG23088.1
gb|ECG38755.1
gb|ECG70380.1
gb|ECH02658.1
gb|ECI03908.1
gb|ECI15831.1
gb|ECJ11841.1
gb|ECJ13936.1
gb|ECJ68205.1
gb|ECK39698.1
gb|ECK49422.1
gb|ECK84801.1
gb|ECL48993.1
gb|ECL92086.1
gb|ECM04375.1
gb|ECM61983.1
gb|ECM77528.1
gb|ECM90949.1
gb|ECM91670.1
gb|ECN07633.1
gb|ECN11725.1
gb|ECN27086.1
gb|ECN63461.1
gb|ECN88937.1
gb|ECO63169.1
gb|ECP23021.1
gb|ECP37860.1
gb|ECP43062.1
gb|ECP53348.1
gb|ECQ61864.1
gb|ECR76976.1
gb|ECS36544.1
gb|ECS77197.1
gb|ECS89566.1
gb|ECS93972.1
gb|ECT11214.1
gb|ECT28045.1
gb|ECU27475.1
gb|ECU27569.1
gb|ECU50903.1
gb|ECV05661.1
gb|ECV09153.1
gb|ECV17481.1
gb|ECV30343.1
gb|ECV59558.1
gb|ECV66424.1
gb|ECV92255.1
gb|ECW21397.1
gb|ECW27586.1
gb|ECW34552.1

FIG. 56 Cont.

gb|ECW51884.1
gb|ECW86476.1
gb|ECX03181.1
gb|ECX07607.1
gb|ECX51959.1
gb|ECY15974.1
gb|ECY51053.1
gb|ECY65264.1
gb|ECY72008.1
gb|ECZ13704.1
gb|ECZ32055.1
gb|ECZ32791.1
gb|ECZ63045.1
gb|ECZ95526.1
gb|EDA15220.1
gb|EDA34659.1
gb|EDA43162.1
gb|EDA65955.1
gb|EDA75330.1
gb|EDB33474.1
gb|EDB63930.1
gb|EDC11631.1
gb|EDC18259.1
gb|EDC79853.1
gb|EDC86032.1
gb|EDE13368.1
gb|EDF12274.1
gb|EDF13440.1
gb|EDG04054.1
gb|EDG10020.1
gb|EDG47637.1
gb|EDG96629.1
gb|EDH45122.1
gb|EDH65891.1
gb|EDH68511.1
gb|EDH71634.1
gb|EDH86342.1
gb|EDI26270.1
gb|EDI26458.1
gb|EDI44671.1
gb|EDI82121.1
gb|EDJ18110.1
gb|EDJ33361.1
gb|EDJ60226.1
gb|EDX89965.1
gb|EDY87686.1
gb|EDZ46701.1
gb|EDZ65647.1
gb|EJ085421.1
gb|EJ099644.1
gb|EJ137266.1
gb|EJ146674.1
gb|EJ191501.1
gb|EJ212903.1
gb|EJ225122.1
gb|EJ227792.1
gb|EJ245549.1
gb|EJ266991.1
gb|EJ278016.1
gb|EJ329588.1
gb|EJ334720.1
gb|EJ391923.1
gb|EJ426203.1
gb|EJ434827.1
gb|EJ471737.1
gb|EJ477947.1
gb|EJ484731.1
gb|EJ498664.1
gb|EJ500550.1
gb|EJ555922.1
gb|EJ564676.1
gb|EJ640224.1
gb|EJ645847.1
gb|EJ650695.1
gb|EJ662911.1
gb|EJ664069.1
gb|EJ665938.1
gb|EJ667820.1
gb|EJ669120.1
gb|EJ703050.1
gb|EJ721950.1
gb|EJ730460.1
gb|EJ770502.1
gb|EJ777637.1
gb|EJ785431.1
gb|EJ788765.1
gb|EJ815775.1
gb|EJ851744.1
gb|EJ873052.1
gb|EJ879757.1
gb|EJ902539.1
gb|EJ931567.1
gb|EJ937131.1
gb|EJ972947.1
gb|EJ990165.1
gb|EJ999222.1
gb|EK000110.1
gb|EK000629.1
gb|EK023293.1
gb|EK065797.1
gb|EK078447.1
gb|EK093951.1
gb|EK109020.1
gb|EK123650.1
gb|EK133187.1
gb|EK180280.1
gb|EK196880.1
gb|EK222554.1
gb|EK257255.1
gb|EK313225.1
gb|EK325827.1
gb|EK441511.1
gb|EK492959.1
gb|EK507776.1
gb|EK508176.1
gb|EK529306.1
gb|EK539522.1
gb|EK543851.1
gb|EK576280.1
gb|EK601818.1
gb|EK616119.1
gb|EK621481.1
gb|EK623494.1
gb|EK628542.1
gb|EK639369.1
gb|EK645136.1
gb|EK666683.1

FIG. 56 Cont.

gb|EK670222.1
gb|EK670523.1
gb|EK673679.1
gb|EK682200.1
gb|EK691103.1
gb|EK692669.1
gb|EK725644.1
gb|EK743461.1
gb|EK771460.1
gb|EK791447.1
gb|EK806766.1
gb|EK818832.1
gb|EK834533.1
gb|EK835979.1
gb|EK837640.1
gb|EK843333.1
gb|EK859387.1
gb|EK885080.1
gb|EK889609.1
gb|EK890943.1
gb|EK903712.1
gb|EK918170.1
gb|EK935500.1
gb|EK947561.1
gb|EK951364.1
gb|EK960146.1
gb|EK960826.1
gb|EK967818.1
gb|EK981215.1
gb|EK983743.1
gb|EK984099.1
gb|EK989854.1
gb|EK990735.1
gb|EK991845.1
gb|ER010920.1
gb|ER032330.1
gb|ER049290.1
gb|ER052609.1
gb|ER096625.1
gb|ER127282.1
gb|ER130376.1
gb|ER131376.1
gb|ER161971.1
gb|ER162312.1
gb|ER176379.1
gb|ER177550.1
gb|ER195612.1
gb|ER200449.1
gb|ER206437.1
gb|ER211547.1
gb|ER212475.1
gb|ER214473.1
gb|ER214855.1
gb|ER242449.1
gb|ER253849.1
gb|ER262881.1
gb|ER350440.1
gb|ER382137.1
gb|ER390228.1
gb|ER423386.1
gb|ER429221.1
gb|ER442323.1
gb|ER442792.1
gb|ER471256.1
gb|ER482389.1
gb|ER509480.1
gb|ER566372.1
gb|ER576118.1
gb|ER613314.1
gb|ER615495.1
gb|FH365651.1
pdb|1J00|A
pdb|1JRL|A
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ref|NP_251546.1
ref|NP_286243.1
ref|NP_406570.1
ref|NP_420568.1
ref|NP_455101.1
ref|NP_459501.1
ref|NP_519838.1
ref|NP_636169.1
ref|NP_641185.1
ref|NP_668426.1
ref|NP_712742.1
ref|NP_718498.1
ref|NP_744467.1
ref|NP_762242.1
ref|NP_792087.1
ref|NP_800381.1
ref|NP_841496.1
ref|NP_880448.1
ref|NP_885222.1
ref|NP_889542.1
ref|NP_903405.1
ref|NP_931022.1
ref|NP_936828.1
ref|NP_945548.1
ref|NW_001083568.1
ref|NZ_AAAU03000001.1
ref|NZ_AACX01000017.1
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ref|NZ_AAHN02000001.1
ref|NZ_AAHO01000021.1
ref|NZ_AAHR02000004.1
ref|NZ_AAHS03000025.1
ref|NZ_AAHV02000013.1
ref|NZ_AAHW02000002.1
ref|NZ_AAIQ02000012.1
ref|NZ_AAIR02000006.1
ref|NZ_AAKH02000182.1
ref|NZ_AAKI02000073.1
ref|NZ_AAKJ02000066.1
ref|NZ_AAKK02000006.1
ref|NZ_AAKL01000052.1
ref|NZ_AAKV01000034.1
ref|NZ_AAKW01000024.1
ref|NZ_AAKX01000089.1
ref|NZ_AAKY01000063.1
ref|NZ_AALC01000018.1
ref|NZ_AALD01000017.1
ref|NZ_AALE01000009.1
ref|NZ_AALF01000005.1
ref|NZ_AAMM02000007.1
ref|NZ_AAMR01000030.1
ref|NZ_AAMX01000013.1
ref|NZ_AAMY01000001.1

FIG. 56 Cont.

ref|NZ_AAND01000039.1
ref|NZ_AANX02000019.1
ref|NZ_AAOA01000001.1
ref|NZ_AAOE01000009.1
ref|NZ_AAOF01000028.1
ref|NZ_AAOH01000005.1
ref|NZ_AAOJ01000002.1
ref|NZ_AAOU01000004.1
ref|NZ_AAOW01000010.1
ref|NZ_AAPH01000018.1
ref|NZ_AAPI01000005.1
ref|NZ_AAPJ01000011.1
ref|NZ_AAPS01000016.1
ref|NZ_AAQN01000001.1
ref|NZ_AAQW01000001.1
ref|NZ_AATR01000024.1
ref|NZ_AATY01000043.1
ref|NZ_AAUB01000051.1
ref|NZ_AAUJ01000003.1
ref|NZ_AAUR01000070.1
ref|NZ_AAUS01000048.1
ref|NZ_AAUT01000048.1
ref|NZ_AAUU01000083.1
ref|NZ_AAVS01000036.1
ref|NZ_AAVT01000002.1
ref|NZ_AAVV01000002.1
ref|NZ_AAWD01000202.1
ref|NZ_AAWE01000074.1
ref|NZ_AAWF01000084.1
ref|NZ_AAWG01000076.1
ref|NZ_AAWP01000238.1
ref|NZ_AAWQ01000062.1
ref|NZ_AAWQ01000361.1
ref|NZ_AAWY01000065.1
ref|NZ_AAXY01000012.1
ref|NZ_AAYR01000001.1
ref|NZ_AAYS01000016.1
ref|NZ_AAYT01000001.1
ref|NZ_AAYU01000018.1
ref|NZ_AAYV01000012.1
ref|NZ_AAYX01000001.1
ref|NZ_AAZP01000003.1
ref|NZ_AAZW01000032.1
ref|NZ_ABAN01000007.3
ref|NZ_ABAO01000003.1
ref|NZ_ABAT01000020.1
ref|NZ_ABAU01000083.1
ref|NZ_ABBD01000590.1
ref|NZ_ABBE01000454.1
ref|NZ_ABBF01000179.1
ref|NZ_ABBG01000111.1
ref|NZ_ABBH01000617.1
ref|NZ_ABBI01000494.1
ref|NZ_ABBJ01000389.1
ref|NZ_ABBK01000366.1
ref|NZ_ABBL01000369.1
ref|NZ_ABBM01000232.1
ref|NZ_ABBN01000303.1
ref|NZ_ABBO01000334.1
ref|NZ_ABBP01000274.1
ref|NZ_ABBQ01000228.1
ref|NZ_ABBR01000205.1
ref|NZ_ABBZ01001487.1
ref|NZ_ABCD01000001.1
ref|NZ_ABCH01000016.1
ref|NZ_ABCP01000022.1
ref|NZ_ABCQ01000002.1
ref|NZ_ABCT01000025.1
ref|NZ_ABDZ01000018.1
ref|NZ_ABEI01000007.1
ref|NZ_ABEJ01000025.1
ref|NZ_ABEL01000001.1
ref|NZ_ABEW01000005.1
ref|NZ_ABEX01000002.1
ref|NZ_ABFF01000003.1
ref|NZ_ABFG01000003.1
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ref|YP_001029293.1
ref|YP_001051045.1
ref|YP_001059345.1
ref|YP_001066613.1
ref|YP_001084019.1
ref|YP_001094528.1
ref|YP_001100028.1
ref|YP_001119689.1
ref|YP_001140725.1
ref|YP_001155718.1
ref|YP_001172533.1
ref|YP_001175703.1
ref|YP_001188046.1
ref|YP_001202594.1
ref|YP_001236582.1
ref|YP_001268761.1
ref|YP_001334153.1
ref|YP_001341064.1
ref|YP_001347669.1
ref|YP_001353227.1
ref|YP_001366906.1
ref|YP_001377.1
ref|YP_001401981.1
ref|YP_001438839.1
ref|YP_001447923.1
ref|YP_001454190.1
ref|YP_001473435.1
ref|YP_001477389.1
ref|YP_001501519.1
ref|YP_001526681.1
ref|YP_001555212.1
ref|YP_001565051.1
ref|YP_001571431.1
ref|YP_001579540.1
ref|YP_001605806.1
ref|YP_001630831.1
ref|YP_001641436.1
ref|YP_001668159.1
ref|YP_001674820.1
ref|YP_001707661.1
ref|YP_001714611.1
ref|YP_001748633.1
ref|YP_001761266.1
ref|YP_001765225.1
ref|YP_001790933.1
ref|YP_001808536.1
ref|YP_001831970.1
ref|YP_001845605.1

FIG. 56 Cont.

ref|YP_001857252.1
ref|YP_001899431.1
ref|YP_001904979.1
ref|YP_001908369.1
ref|YP_001912286.1
ref|YP_001927109.1
ref|YP_001946344.1
ref|YP_001970690.1
ref|YP_001982095.1
ref|YP_001989228.1
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ref|YP_002093983.1
ref|YP_002098168.1
ref|YP_002105836.1
ref|YP_002126594.1
ref|YP_002151886.1
ref|YP_002158710.1
ref|YP_002210388.1
ref|YP_002225613.1
ref|YP_002231119.1
ref|YP_002240008.1
ref|YP_002254594.1
ref|YP_002259448.1
ref|YP_002264628.1
ref|YP_002299265.1
ref|YP_045767.1
ref|YP_049328.1
ref|YP_103103.1
ref|YP_108033.1
ref|YP_113859.1
ref|YP_130990.1
ref|YP_156150.1
ref|YP_202403.1
ref|YP_207002.1
ref|YP_215534.1
ref|YP_235149.1
ref|YP_261370.1
ref|YP_274258.1
ref|YP_285914.1
ref|YP_295598.1
ref|YP_314444.1
ref|YP_317035.1
ref|YP_333863.1
ref|YP_340393.1
ref|YP_342483.1
ref|YP_349742.1
ref|YP_362617.1
ref|YP_369458.1
ref|YP_386909.1
ref|YP_388633.1
ref|YP_390819.1
ref|YP_402105.1
ref|YP_406934.1
ref|YP_412660.1
ref|YP_423690.1
ref|YP_436067.1
ref|YP_442651.1
ref|YP_483906.1
ref|YP_523672.1
ref|YP_528911.1
ref|YP_530091.1
ref|YP_545359.1
ref|YP_549843.1
ref|YP_563371.1
ref|YP_567671.1
ref|YP_574666.1
ref|YP_584029.1
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ref|YP_625997.1
ref|YP_662476.1
ref|YP_693120.1
ref|YP_726000.1
ref|YP_733613.1
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ref|YP_747911.1
ref|YP_751247.1
ref|YP_773797.1
ref|YP_779242.1
ref|YP_786484.1
ref|YP_790318.1
ref|YP_835563.1
ref|YP_857963.1
ref|YP_869177.1
ref|YP_927362.1
ref|YP_933170.1
ref|YP_944260.1
ref|YP_958323.1
ref|YP_963007.1
ref|YP_971361.1
ref|YP_982119.1
ref|YP_986510.1
ref|ZP_00415149.1
ref|ZP_00440774.1
ref|ZP_00822411.1
ref|ZP_00825967.1
ref|ZP_00829783.1
ref|ZP_00834753.1
ref|ZP_00946056.1
ref|ZP_00991723.1
ref|ZP_01043473.1
ref|ZP_01044690.1
ref|ZP_01066638.1
ref|ZP_01101211.1
ref|ZP_01114429.1
ref|ZP_01128881.1
ref|ZP_01134547.1
ref|ZP_01159274.1
ref|ZP_01166740.1
ref|ZP_01220817.1
ref|ZP_01224743.1
ref|ZP_01229011.1
ref|ZP_01235168.1
ref|ZP_01261041.1
ref|ZP_01366323.1
ref|ZP_01450253.1
ref|ZP_01519884.1
ref|ZP_01614557.1
ref|ZP_01616242.1
ref|ZP_01625233.1
ref|ZP_01677835.1
ref|ZP_01707934.1
ref|ZP_01738317.1
ref|ZP_01764358.1
ref|ZP_01814897.1

FIG. 56 Cont.

ref|ZP_01844343.1
ref|ZP_01867911.1
ref|ZP_01894796.1
ref|ZP_01896544.1
ref|ZP_01916622.1
ref|ZP_01980151.1
ref|ZP_01993202.1
ref|ZP_02002768.1
ref|ZP_02009612.1
ref|ZP_02055185.1
ref|ZP_02101081.1
ref|ZP_02156924.1
ref|ZP_02194557.1
ref|ZP_02223456.1
ref|ZP_02241918.1
ref|ZP_02301590.1
ref|ZP_02344720.2
ref|ZP_02355337.1
ref|ZP_02362479.1
ref|ZP_02374459.1
ref|ZP_02379324.1
ref|ZP_02388333.1
ref|ZP_02410904.1
ref|ZP_02463157.1
ref|ZP_02481218.1
ref|ZP_02489473.1
ref|ZP_02683026.2
ref|ZP_02799578.2
ref|ZP_02842667.1
ref|ZP_02883579.1
ref|ZP_02892970.1
ref|ZP_02902430.1
ref|ZP_02911087.1
ref|ZP_02946716.1
ref|ZP_02997848.1
ref|ZP_03026190.1
ref|ZP_03081449.1
ref|ZP_03163359.1
ref|ZP_03221362.1
ref|ZP_03278741.1
ref|ZP_03281441.1
sp|Q07792|ESTE_VIBMI

FIG. 57A

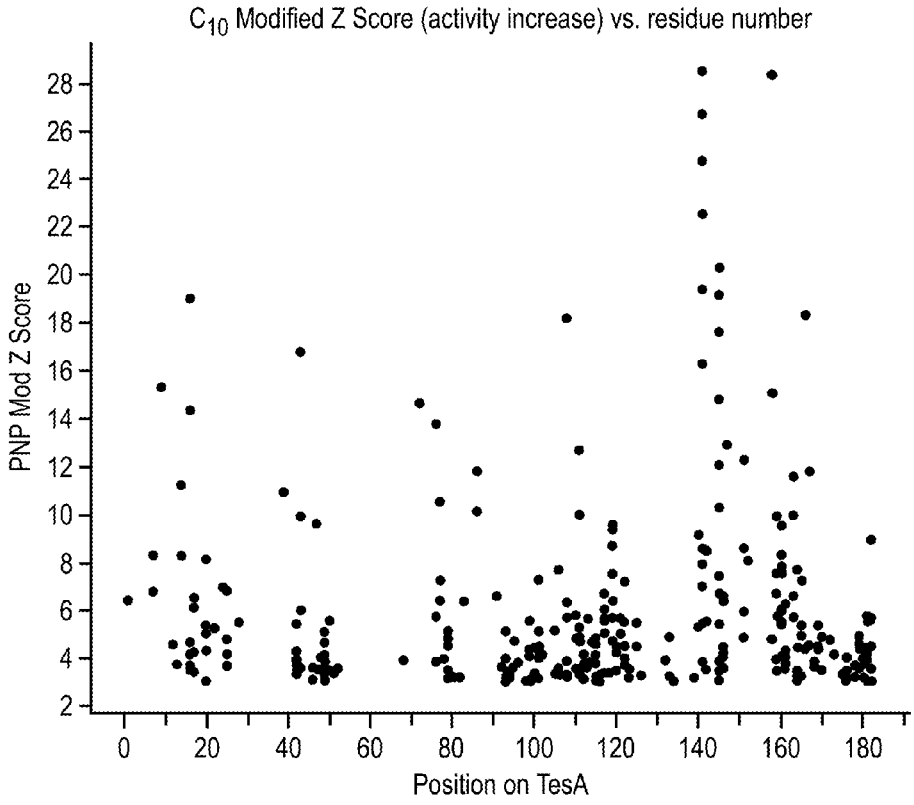

C_{10} Modified Z Score (activity increase) vs. residue number
PNP Mod Z Score
28
26
24
22
20
18
16
14
12
10
8
6
4
2
0
20
40
60
80
100
120
140
160
180
Position on TesA

FIG. 57B

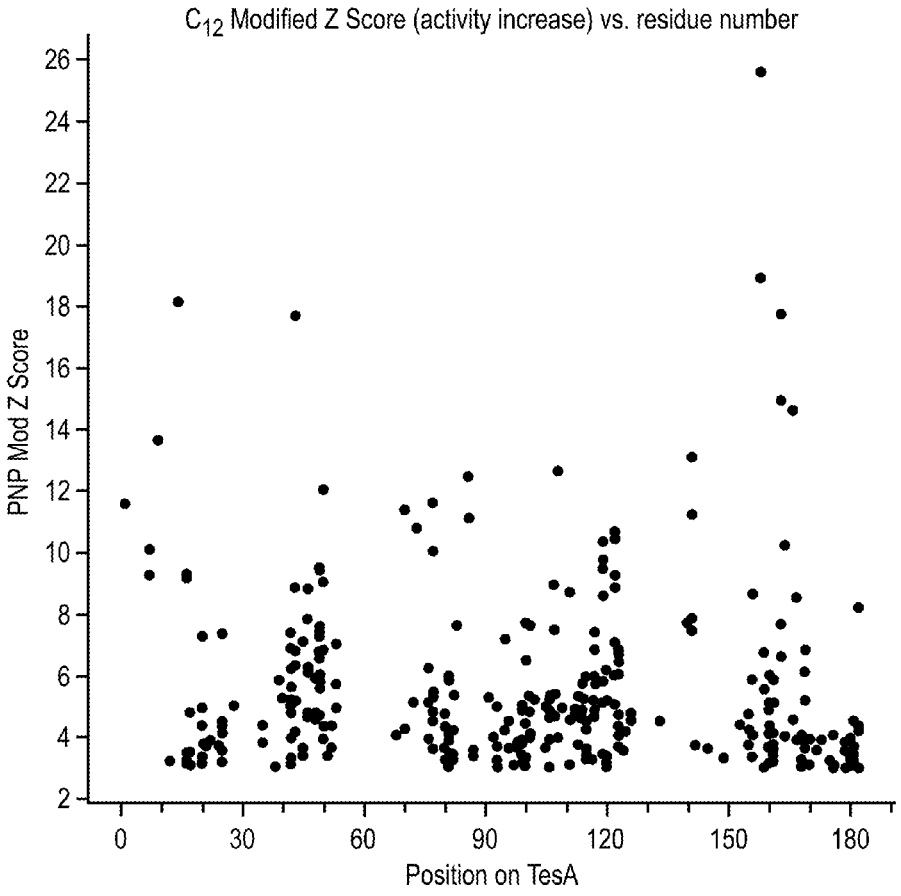

C_{12} Modified Z Score (activity increase) vs. residue number
PNP Mod Z Score
26
24
22
20
18
16
14
12
10
8
6
4
2
0
30
60
90
120
150
180
Position on TesA

FIG. 57C

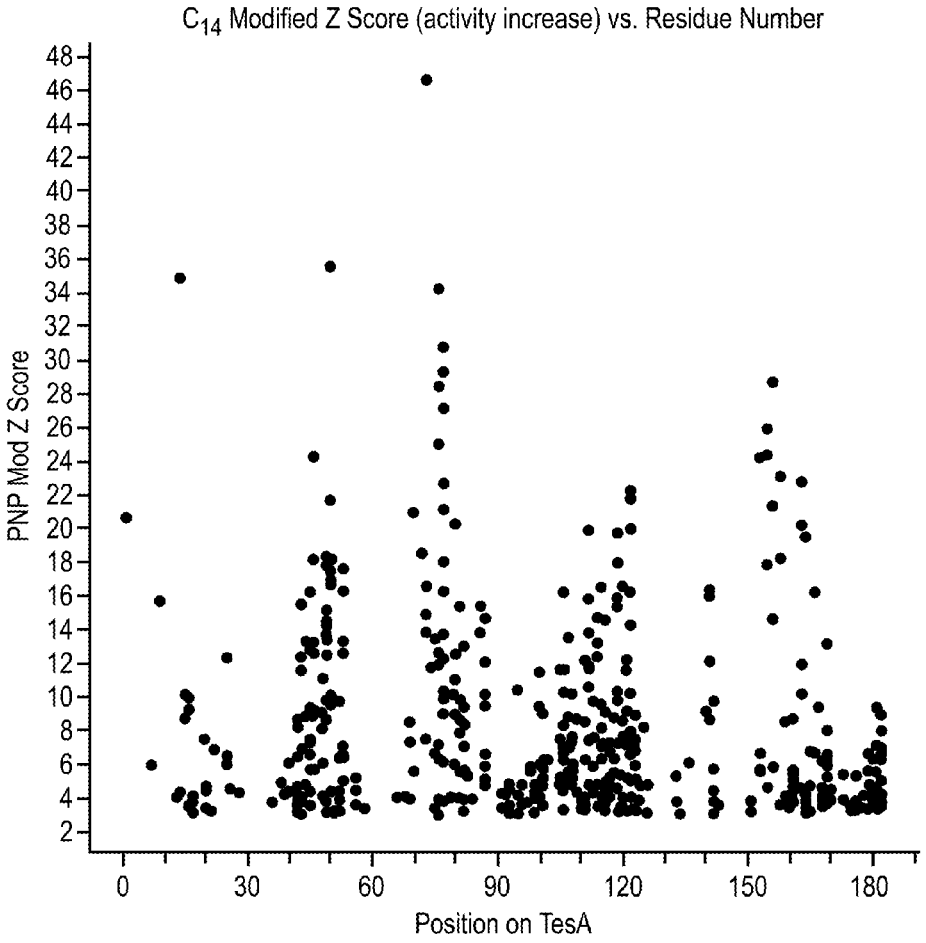

C_{14} Modified Z Score (activity increase) vs. Residue Number
PNP Mod Z Score
48
46
44
42
40
38
36
34
32
30
28
26
24
22
20
18
16
14
12
10
8
6
4
2
0
30
60
90
120
150
180
Position on TesA

FIG. 57D

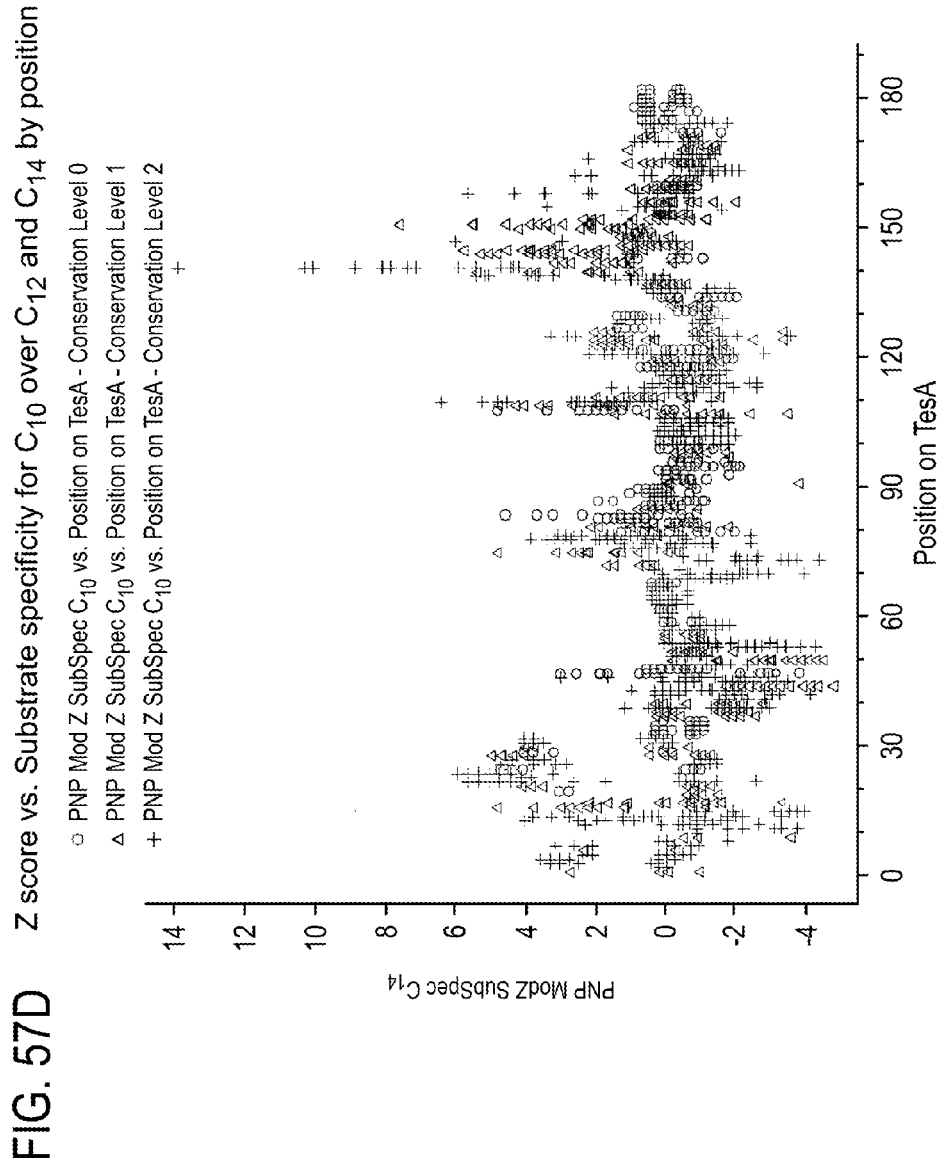

Z score vs. Substrate specificity for C_{10} over C_{12} and C_{14} by position
PNP Mod Z SubSpec C_{10} vs. Position on TesA - Conservation Level 0
PNP Mod Z SubSpec C_{10} vs. Position on TesA - Conservation Level 1
PNP Mod Z SubSpec C_{10} vs. Position on TesA - Conservation Level 2
PNP ModZ SubSpec C_{14}
14
12
10
8
6
4
2
0
-2
-4
0
30
60
90
120
150
180
Position on TesA

FIG. 57E

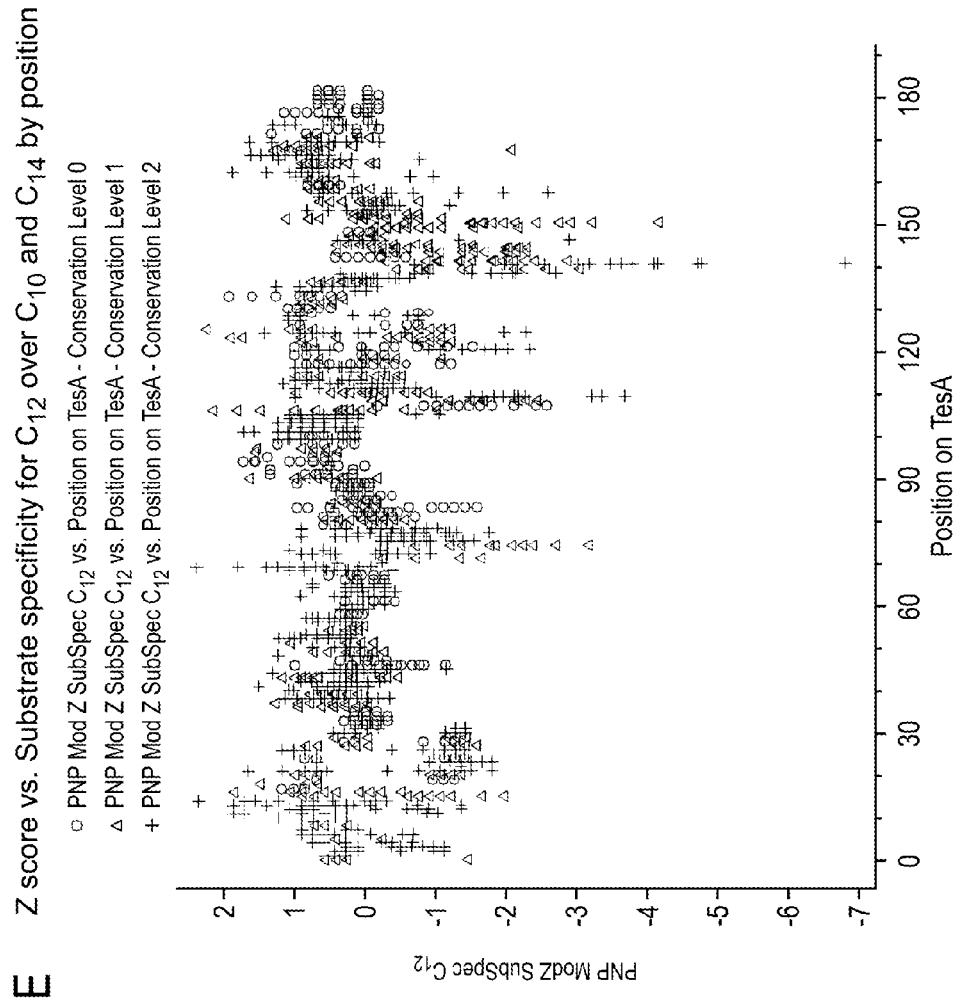

Z score vs. Substrate specificity for C_{12} over C_{10} and C_{14} by position
○ PNP Mod Z SubSpec C_{12} vs. Position on TesA - Conservation Level 0
△ PNP Mod Z SubSpec C_{12} vs. Position on TesA - Conservation Level 1
+ PNP Mod Z SubSpec C_{12} vs. Position on TesA - Conservation Level 2
PNP ModZ SubSpec C_{12}
2
1
0
-1
-2
-3
-4
-5
-6
-7
0
30
60
90
120
150
180
Position on TesA

FIG. 57F

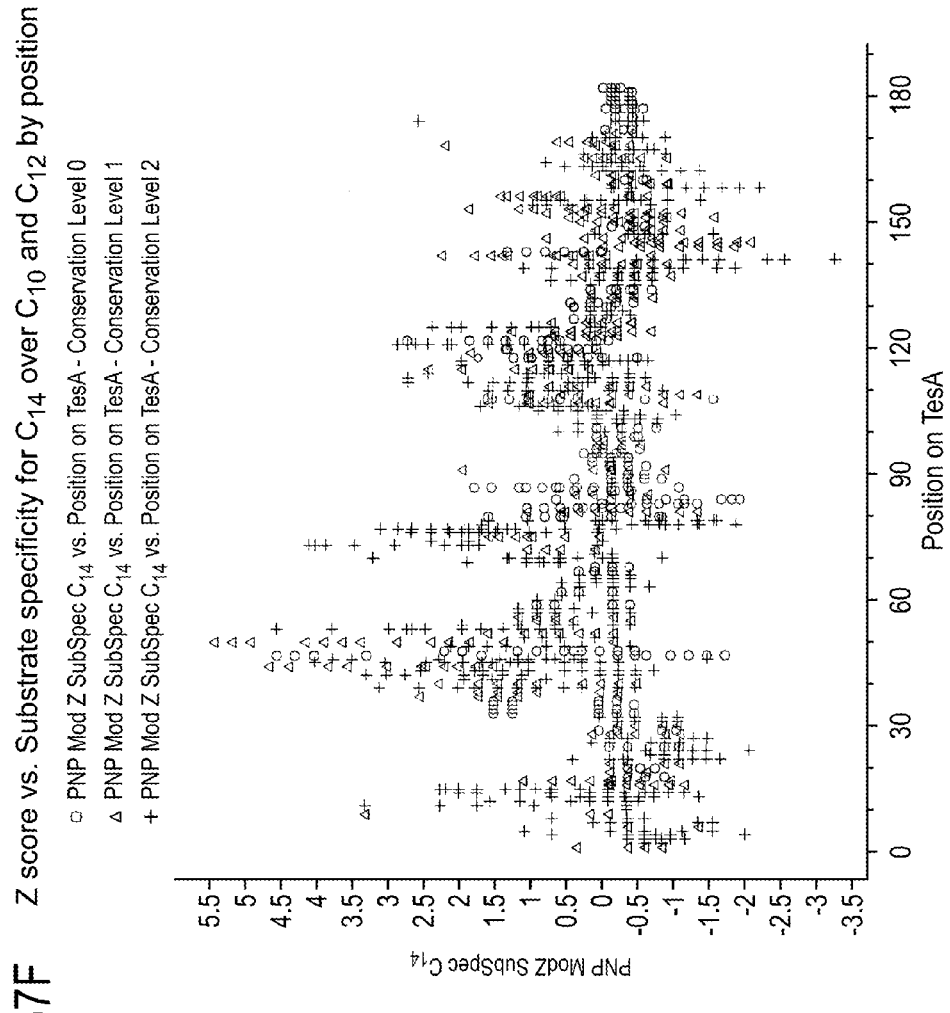

Z score vs. Substrate specificity for C_{14} over C_{10} and C_{12} by position
PNP Mod Z SubSpec C_{14} vs. Position on TesA - Conservation Level 0
PNP Mod Z SubSpec C_{14} vs. Position on TesA - Conservation Level 1
PNP Mod Z SubSpec C_{14} vs. Position on TesA - Conservation Level 2
PNP ModZ SubSpec C_{14}
5.5
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
-2.5
-3
-3.5
0
30
60
90
120
150
180
Position on TesA

FIG. 58

Met Ala Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr
Arg Met Ser Ala Ser Ala Ala Trp Pro Ala Leu Leu Asn Asp Lys Trp
Gln Ser Lys Thr Ser Val Val Asn Ala Ser Ile Ser Gly Asp Thr Ser
Gln Gln Gly Leu Ala Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro
Arg Trp Val Leu Val Glu Leu Gly Gly Asn Asp Gly Leu Arg Gly Phe
Gln Pro Gln Gln Thr Glu Gln Thr Leu Arg Gln Ile Leu Gln Asp Val
Lys Ala Ala Asn Ala Glu Pro Leu Leu Met Gln Ile Arg Leu Pro Ala
Asn Tyr Gly Arg Arg Tyr Asn Glu Ala Phe Ser Ala Ile Tyr Pro Lys
Leu Ala Lys Glu Phe Asp Val Pro Leu Leu Pro Phe Phe Met Glu Glu
Val Tyr Leu Lys Pro Gln Trp Met Gln Asp Asp Gly Ile His Pro Asn
Arg Asp Ala Gln Pro Phe Ile Ala Asp Trp Met Ala Lys Gln Leu Gln
Pro Leu Val Asn His Asp Ser (SEQ ID NO:31)

FIG. 59

ATGGCGGACACGTTATTGATTCTGGGTGATAGCCTGAGCGCCGGGTATCGAATGTCTGCCAGCG
CGGCCTGGCCTGCCTTGTTGAATGATAAGTGGCAGAGTAAAACGTCGGTAGTTAATGCCAGCAT
CAGCGGCGACACCTCGCAACAAGGACTGGCGCGCCTTCCGGCTCTGCTGAAACAGCATCAGCCG
CGTTGGGTGCTGGTTGAACTGGGCGGCAATGACGGTTTGCGTGGTTTTCAGCCACAGCAAACCG
AGCAAACGCTGCGCCAGATTTTGCAGGATGTCAAAGCCGCCAACGCTGAACCATTGTTAATGCA
AATACGTCTGCCTGCAAACTATGGTCGCCGTTATAATGAAGCCTTTAGCGCCATTTACCCCAAA
CTCGCCAAAGAGTTTGATGTTCCGCTGCTGCCCTTTTTTATGGAAGAGGTCTACCTCAAGCCAC
AATGGATGCAGGATGACGGTATTCATCCCAACCGCGACGCCCAGCCGTTTATTGCCGACTGGAT
GGCGAAGCAGTTGCAGCCTTTAGTAAATCATGACTCATAA (SEQ ID NO:32)

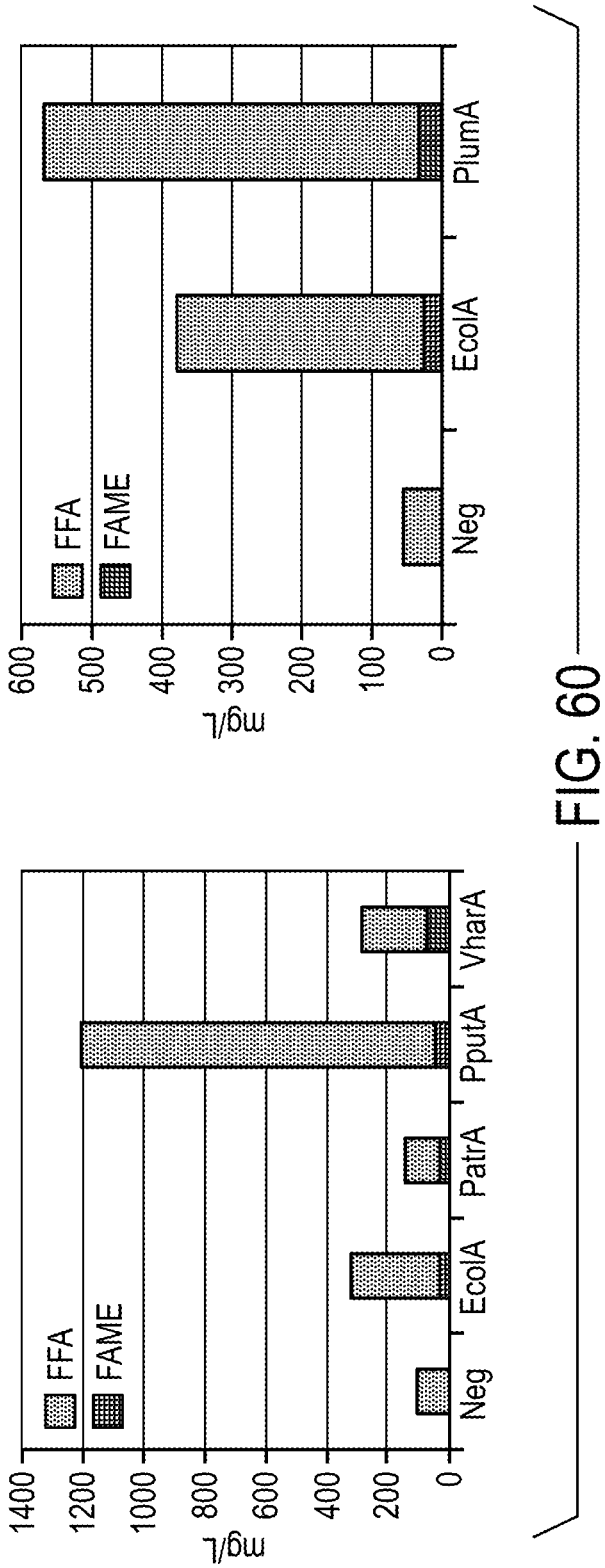

mg/L
1400
1200
1000
800
600
400
200
0
FFA
FAME
Neg
EcolA
PatrA
PputA
VharA
mg/L
600
500
400
300
200
100
0
FFA
FAME
Neg
EcolA
PlumA

FIG. 60

FIG. 61

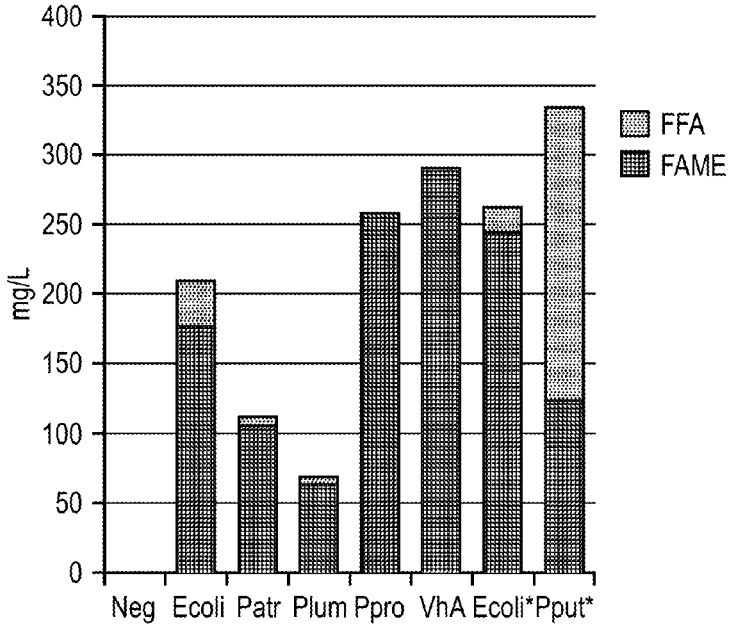

400
350
300
250
200
150
100
50
0
mg/L
FFA
FAME
Neg
Ecoli
Patr
Plum
Ppro
VhA
Ecoli*
Pput*

FIG. 62

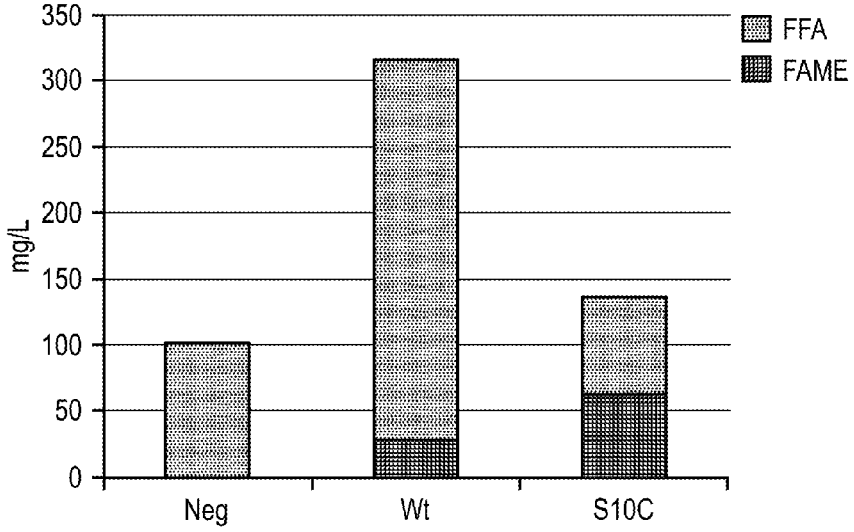

350
300
250
200
150
100
50
0
mg/L
FFA
FAME
Neg
Wt
S10C

FIG. 63

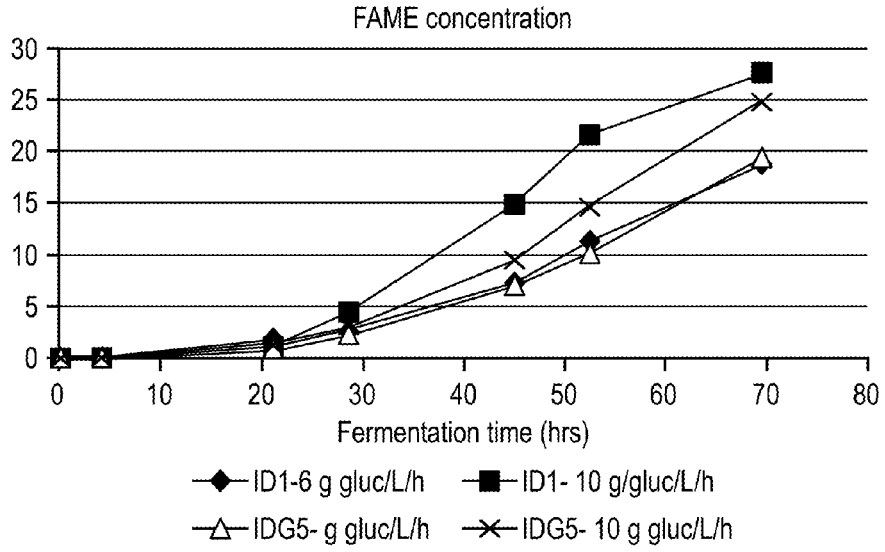
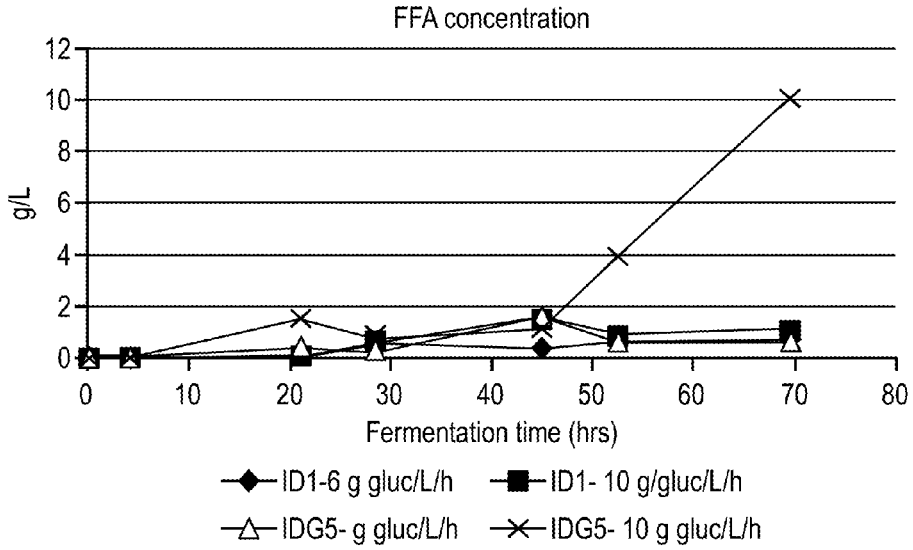

FAME concentration
30
25
20
15
10
5
0
0
10
20
30
40
50
60
70
80
Fermentation time (hrs)
ID1-6 g gluc/L/h
ID1- 10 g/gluc/L/h
IDG5- g gluc/L/h
IDG5- 10 g gluc/L/h

FIG. 64


FFA concentration
12
10
8
6
4
2
0
g/L
0
10
20
30
40
50
60
70
80
Fermentation time (hrs)
ID1-6 g gluc/L/h
ID1- 10 g/gluc/L/h
IDG5- g gluc/L/h
IDG5- 10 g gluc/L/h

METHODS AND COMPOSITIONS RELATED TO THIOESTERASE ENZYMES

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 61/140,600, filed Dec. 23, 2008, the entire content of which is hereby incorporated by reference.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Oct. 19, 2011, is named LS00017U.txt and is 147,429 bytes in size.

FIELD OF THE INVENTION

The present invention relates to novel thioesterase compositions, novel recombinant host cells comprising thioesterases, novel methods of production of fatty acid derivatives, and fatty acid derivatives produced thereby and uses thereof. One particular aspect of the present invention relates to the production of industrial chemicals and fuels.

BACKGROUND OF THE INVENTION

Developments in technology have been accompanied by an increased reliance on fuel and industrial chemicals from petrochemical sources. Such fuel sources are becoming increasingly limited and difficult to acquire. With the burning of fossil fuels taking place at an unprecedented rate, it is likely that the world's demand for fuel and petrochemical derived chemicals will soon outweigh current supplies.

As a result, efforts have been directed toward harnessing sources of renewable energy, such as sunlight, water, wind, and biomass. The use of biomass to produce new sources of fuel and chemicals which are not derived from petroleum sources (e.g., biofuel) has emerged as one alternative option.

Biofuel is a biodegradable, clean-burning combustible fuel which can be comprised of alkanes and/or esters. An exemplary biofuel is biodiesel. Biodiesel can be used in most internal combustion diesel engines in either a pure form, which is referred to as "neat" biodiesel, or as a mixture in any concentration with regular petroleum diesel or other biodiesels.

Biodiesel offers a number of beneficial properties compared to petroleum-based diesel, including reduced emissions (e.g., carbon monoxide, sulphur, aromatic hydrocarbons, soot particles, etc.) during combustion. Biodiesel also maintains a balanced carbon dioxide cycle because it is based on renewable biological materials. Biodiesel is typically completely biodegradable, and has good safety profile due to its relative high flash point and low flammability. Furthermore, biodiesel provides good lubrication properties, thereby reducing wear and tear on engines.

Current methods of making biodiesel involve transesterification of triacylglycerides from vegetable oil feedstocks, such as from rapeseed in Europe, from soybean in North America, and from palm oil in South East Asia. Industrial-scale biodiesel production is thus geographically and seasonally restricted to areas where vegetable oil feedstocks are produced. The transesterification process leads to a mixture of fatty esters which can be used as biodiesel, but also to an undesirable byproduct, glycerin. To be usable as biodiesel, the fatty esters must be further purified from the heterogeneous product. This increases costs and the amount of energy required for fatty ester production and, ultimately, biodiesel production as well. Furthermore, vegetable oil feedstocks are inefficient sources of energy because they require extensive acreage for cultivation. For example, the yield of biodiesel from rapeseed is only 1300 L/hectare because only the seed oil is used for biodiesel production, and not the rest of the rapeseed biomass. Additionally, cultivating some vegetable oil feedstocks, such as rapeseed and soybean, requires frequent crop rotation to prevent nutrient depletion of the land.

PCT Publication No. WO 2007/136762 discloses recombinant microorganisms that are capable of synthesizing products derived from the fatty acid synthetic pathway, including, inter alia, fatty acid esters and fatty alcohols. In particular, certain fatty acid derivatives are described having defined carbon chain length, branching and saturation levels. The '762 publication describes recombinant cells that utilize endogenous overexpression or heterologous expression of thioesterase proteins in the production of fatty acid derivatives.

PCT Publication No. WO 2008/119082 discloses genetically engineered cells and microorganisms that produce products from the fatty acid biosynthetic pathway, including, inter alia, fatty acid esters and fatty alcohols. The '082 publication describes recombinant cells that utilize overexpression of acyl-CoA synthetase enzymes to more efficiently produce fatty acid derivatives.

U.S. Pat. No. 5,955,329 discloses genetically engineered plant acyl-ACP thioesterase proteins having altered substrate specificity. In particular, the '329 patent discloses producing engineered plant acyl-ACP thioesterases, wherein the engineered plant acyl-ACP thioesterases demonstrate altered substrate specificity with respect to the acyl-ACP substrates hydrolyzed by the plant thioesterases as compared to the native acyl-ACP thioesterase.

While the prior art discloses certain useful disclosures regarding the production of certain fatty acid derivatives, a need exists in the field for improved methods and processes for more efficient and economical production of such fatty acid derivatives, and also for technology facilitating the production of compositions that have altered product specifications. As a specific example, a need exists for the production of fatty acid compositions having pre-designed, or "tailored," specifications and properties for particular applications such as fuels, detergents, lubricants, industrial precursor molecule and other valuable applications of fatty acid derivatives.

SUMMARY OF THE INVENTION

It is an object of the present invention to provide useful mutant and naturally-occurring thioesterase enzymes, polynucleotides encoding these enzymes, vectors comprising polynucleotides encoding the useful thioesterase enzymes, recombinant host cells comprising mutated endogenous thioesterase enzymes, recombinant host cells transformed with the vectors, recombinant host cells having polynucleotides encoding useful thioesterase enzymes chromosomally integrated therein, thioesterases produced by the host cells, fatty acid derivative compositions (such as industrial chemicals and biofuels) produced in vitro and/or in vivo, methods for producing fatty acid derivative compositions in vitro and/or in vivo, and methods of using the produced fatty acid derivative compositions.

It is an object of the present invention to provide methods of producing fatty acid derivative compositions through microbial fermentations that have predetermined product

profiles with regard to carbon chain lengths and proportional yields. These compositions are well suited for applications in the fuel and chemical industries because their properties can be tailored to the particular applications for which they are intended. For example, it is possible to tailor a fatty ester product, according to the methods described herein, such that it can be used as an automobile fuel, and/or to design a composition to have, for example, improved fuel characteristics such as cloud point, lubricity, cetane number, kinematic viscosity, acid number, boiling point, oxidative stability, cold filter-plugging point, impurity profile, sulfated ash level, and/or flash point. Similarly, it is possible to produce industrial chemicals in accordance with the methods described herein that can replace current chemicals sourced from petroleum, and that are tailored to particular applications, for example, to produce fatty alcohols that are optimally suited for use as surfactants and/or detergents.

It is an object of the invention to provide for alternative methods of making fatty esters without the presence of (or in the absence of) an ester synthase. This method is energetically more favorable than the heretofore disclosed methods for producing fatty ester compositions through microbial fermentation processes, which required at least both a thioesterase enzyme and an ester synthase enzyme. As such, the novel thioesterases of the invention provide further advantages.

In one embodiment of the invention, mutant thioesterases (or naturally-occurring equivalents thereof) are provided that derive from a precursor thioesterase, wherein each of the mutants (or the naturally-occurring equivalents) has at least one altered property in vitro and/or in vivo, as compared to the properties of the precursor thioesterase. The altered property can be, for example, a biophysical property such as thermal stability (melting point T_m); solvent, solute, and/or oxidative stability; lipophilicity; hydrophilicity; quaternary structure; dipole moment; and/or isoelectric point. The altered property can also be, for example, a biochemical property such as pH optimum, temperature optimum, and/or ionic strength optimum. The altered property can further be, for example, an enzyme catalytic parameter such as product distribution (including, for example, a higher or lower percentage or proportional yield for a particular product vs. other products in the product mixture), specific activity, substrate preference, substrate affinity, substrate inhibition, product affinity, turnover rate or catalytic rate, product inhibition, kinetic mechanism, K_M, k_{cat}, k_{cat}/K_m, and/or V_{Max}. The altered property can additionally be, for example, an increase or a decrease in activity or a changed preference for alcoholysis vs. hydrolysis, acyl-CoA vs. acyl-acyl carrier protein substrates, ester vs. thioester substrates, saturated vs. unsaturated substrates, straight-chain vs. branched substrates; changes in positions of unsaturations, ranges of cetane numbers, or specific carbon chain lengths, branched substrates, position of branching, hydroxy-acyl substrates, keto-acyl substrates; and/or products with a changed range of or specific cetane numbers, octane rating, oxidative stability, lubricity, flash point, viscosity, boiling point, melting point, pour point, cloud point, cold filter plugging point, cold flow characteristics, aromaticity, and/or iodine number. Altered properties can also include, for example, a decrease in activity or an attenuation of ester hydrolysis, such that the hydrolysis of desired product molecules is reduced or eliminated. Altered properties can further include, for example, a decrease in the protein's toxicity to the cell and/or a change in the protein's expression level in the cell, as compared to the precursor protein's toxicity to and/or expression level in the same cell. In an exemplary embodiment, an altered property can include a change in the ability to catalyze the synthesis of fatty acyl derivatives directly or indirectly in vivo or in vitro. In another exemplary embodiment, an altered property is the improvement or increase of in vitro and/or in vivo yield or proportional yield of a particularly desirable fatty acid derivative.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is derived from a precursor thioesterase. In a particular embodiment of the invention, the precursor thioesterase is a naturally-occurring thioesterase, a previously modified thioesterase, or a synthetic thioesterase.

In one embodiment of the invention, the mutant thioesterase (or a naturally-occurring equivalent thereof) is derived from a precursor thioesterase that is a naturally-occurring thioesterase. The naturally-occurring precursor thioesterase can be obtained from, for example, a plant, animal, bacterial, fungal, yeast, or other microbial sources. The mutant thioesterase (or a naturally-occurring equivalent thereof) can be derived from a precursor thioesterase from *Acidovorax, Acinetobacter, Aeromonas, Alcanivorax, Aliivibrio, Alkalilimnicola, Alteromonadales, Alteromonas, Aurantimonas, Azoarcus, Azorhizobium, Azotobacter, Beggiatoa, Beijerinckia, Bordetella, Bradyrhizobium, Burkholderia, Caulobacter, Cellvibrio, Chromobacterium, Citrobacter, Comamonas, Cupriavidus, Dechloromonas, Delftia, Desulfovibrio, Enterobacter, Erwinia, Escherichia, Geobacter, Hahella, Halorhodospira, Herminiimonas, Idiomarina, Janthinobacterium, Klebsiella, Leptospira, Leptothrix, Limnobacter, Magnetospirillum, Marinobacter, Marinomonas, Methylibium, Methylobacillus, Methylobacterium, Methylocella, Methylococcus, Moritella, Nitrobacter, Nitrococcus, Nitrosomonas, Nitrosospira, Oceanospirillum, Oligotropha, Pectobacterium, Photobacterium, Photorhabdus, Polaromonas, Proteus, Providencia, Pseudoalteromonas, Pseudomonas, Psychromonas, Ralstonia, Reinekea, Rhodobacterales, Rhodoferax, Rhodopseudomonas, Rhodospirillum, Saccharophagus, Salmonella, Serratia, Shewanella, Shigella, Stenotrophomonas, Streptococcus, Thauera, Thioalkalivibrio, Thiobacillus, Vibrio, Xanthomonas*, or *Yersinia.*

In a particular embodiment, the precursor thioesterase of the invention can be derived from any one of *Acidovorax avenae* subsp. *citrulli* AAC00-1, *Acidovorax* sp. JS42, *Acinetobacter baumannii* ACICU, *Acinetobacter baumannii* ATCC 17978, *Aeromonas hydrophila* subsp. *Hydrophila* ATCC 7966, *Aeromonas salmonicida* subsp. *salmonicida* A449, *Alcanivorax borkumensis* SK2, *Alcanivorax* sp. DG881, *Aliivibrio salmonicida* LFI1238, *Alkalilimnicola ehrlichei* MLHE-1, alpha *proteobacterium* HTCC2255, *Alteromonadales bacterium* TW-7, *Alteromonas macleodii* deep ecotype, *Aurantimonas* sp. SI85-9A1, *Azoarcus* sp. BH72, *Azorhizobium caulinodans* ORS 571, *Azotobacter vinelandii* AvOP, *Beggiatoa* sp. PS, *Beijerinckia indica* subsp. *indica* ATCC 9039, *Bordetella avium* 197N, *Bordetella bronchiseptica* RB50, *Bordetella parapertussis* 12822, *Bordetella pertussis* Tohama I, *Bordetella petrii* DSM 12804, *Bradyrhizobium* sp. BTAi1, *Bradyrhizobium* sp. ORS278, *Burkholderia ambifaria* AMMD, *Burkholderia ambifaria* IOP40-10, *Burkholderia ambifaria* MC40-6, *Burkholderia ambifaria* MEX-5, *Burkholderia cenocepacia* AU 1054, *Burkholderia cenocepacia* H12424, *Burkholderia cenocepacia* J2315, *Burkholderia cenocepacia* MC0-3, *Burkholderia cenocepacia* PC184, *Burkholderia dolosa* AUO158, *Burkholderia graminis* C4D1M, *Burkholderia mallei* ATCC 23344, *Burkholderia mallei* GB8 *horse* 4, *Burkholderia mallei* NCTC 10229, *Burkholderia multivorans* ATCC 17616, *Burkholderia oklahomensis* C6786, *Burkholderia oklahomensis* E0147, *Burkholderia phymatum* STM815, *Burkhold-*

eria pseudomallei 1106a, *Burkholderia pseudomallei* 1106b, *Burkholderia pseudomallei* 14, *Burkholderia pseudomallei* 1655, *Burkholderia pseudomallei* 1710b, *Burkholderia pseudomallei* 305, *Burkholderia pseudomallei* 406e, *Burkholderia pseudomallei* 668, *Burkholderia pseudomallei* 7894, *Burkholderia pseudomallei* K96243, *Burkholderia pseudomallei* NCTC 13177, *Burkholderia* sp. 383, *Burkholderia thailandensis* Bt4, *Burkholderia thailandensis* E264, *Burkholderia thailandensis* MSMB43, *Burkholderia thailandensis* TXDOH, *Burkholderia ubonensis* Bu, *Burkholderia vietnamiensis G4*, *Caulobacter crescentus* CB15, *Cellvibrio japonicus* Ueda107, *Chromobacterium violaceum* ATCC 12472, *Chromohalobacter salexigens* DSM 3043, *Citrobacter koseri* ATCC BAA-895, *Comamonas testosteroni* KF-1, *Cupriavidus taiwanensis, Dechloromonas aromatica* RCB, *Delftia acidovorans* SPH-1, *Desulfovibrio desulfuricans* subsp. *desulfuricans* str. G20, *Desulfovibrio desulfuricans* subsp. *desulfuricans* str. G20, *Enterobacter cancerogenus* ATCC 35316, *Enterobacter sakazakii* ATCC BAA-894, *Enterobacter* sp. 638, *Erwinia tasmaniensis, Escherichia albertii* TW07627, *Escherichia coli* O157:H7 EDL933, *Escherichia coli* O157:H7 str.EC4024, *Escherichia coli* O157:H7 str. EC4196, *gamma proteobacterium* HTCC5015, *gamma proteobacterium* KT 71, *Geobacter* sp. M21, *Hahella chejuensis* KCTC 2396, *Halorhodospira halophila* SL1, *Herminiimonas arsenicoxydans, Idiomarina baltica* OS145, *Idiomarina loihiensis* L2TR, *Janthinobacterium* sp. *Marseille, Klebsiella pneumoniae* 342, *Klebsiella pneumoniae* subsp. *pneumoniae* MGH 78578, *Klebsiella* sp. ZD414, *Leptospira interrogans serovar Copenhageni* str. *Fiocruz* L1-130, *Leptospira interrogans serovar Lai str.* 56601, *Leptothrix cholodnii* SP-6, *Limnobacter* sp. MED105, *Magnetospirillum magneticum* AMB-1, *marine gamma proteobacterium* HTCC2080, *marine gamma proteobacterium* HTCC2143, *marine gamma proteobacterium* HTCC2207, *marine metagenome, Marinobacter algicola* DG893, *Marinobacter aquaeolei* VT8, *Marinobacter* sp. ELB17, *Marinomonas* sp. MWYL1, *Methylibium petroleiphilum* PM1, *Methylobacillus flagellates* KT, *Methylobacterium chloromethanicum* CM4, *Methylobacterium extorquens* PA1, *Methylobacterium populi* BJ001, *Methylocella silvestris* BL2, *Methylococcus capsulatus* str. *Bath, Moritella* sp. PE36, *Nitrobacter* sp. Nb-311A, *Nitrobacter winogradskyi* Nb-255, *Nitrococcus mobilis* Nb-231, *Nitrosococcus oceani* ATCC 19707, *Nitrosococcus oceani* C-27, *Nitrosomonas europaea* ATCC 19718, *Nitrosomonas eutropha* C91, *Nitrosospira multiformis* ATCC 25196, *Oceanospirillum* sp. MED92, *Oligotropha carboxidovorans* OM5, *Pectobacterium atrosepticum* SCRI1043, *Photobacterium profundum* 3TCK, *Photobacterium profundum* SS9, *Photobacterium* sp. SKA34, *Photorhabdus luminescens, Photorhabdus luminescens* subsp. *laumondii* TTO1, *Polaromonas naphthalenivorans* CJ2, *Polaromonas* sp. JS666, *Polynucleobacter* sp. QLW-P1DMWA-1, *Proteus mirabilis* HI4320, *Providencia stuartii* ATCC 25827, *Pseudoalteromonas atlantica* T6c, *Pseudoalteromonas haloplanktis* TAC125, *Pseudoalteromonas* sp. 643A, *Pseudoalteromonas tunicata* D2, *Pseudomonas aeruginosa* PA7, *Pseudomonas aeruginosa* PACS2, *Pseudomonas aeruginosa* PAO1, *Pseudomonas aeruginosa* UCBPP-PA14, *Pseudomonas entomophila* L48, *Pseudomonas fluorescens* Pf0-1, *Pseudomonas fluorescens* Pf-5, *Pseudomonas mendocina* ymp, *Pseudomonas putida* F1, *Pseudomonas putida* GB-1, *Pseudomonas putida* KT2440, *Pseudomonas putida* W619, *Pseudomonas stutzeri* A1501, *Pseudomonas syringae* pv. *Phaseolicola* 1448A, *Pseudomonas syringae* pv. *syringae* B728a, *Pseudomonas syringae* pv. *tomato* str. DC3000, *Psychromonas ingrahamii* 37, *Ralstonia eutropha* H16, *Ralstonia eutropha* JMP134, *Ralstonia metallidurans* CH34, *Ralstonia pickettii* 12D, *Ralstonia pickettii* 12J, *Ralstonia solanacearum* GMI1000, *Ralstonia solanacearum* IPO1609, *Ralstonia solanacearum* MolK2, *Ralstonia solanacearum* UW551, *Reinekea* sp. MED297, *Rhodobacterales bacterium* Y4I, *Rhodoferax ferrireducens* T118, *Rhodopseudomonas palustris* BisA53, *Rhodopseudomonas palustris* BisB18, *Rhodopseudomonas palustris* BisB5, *Rhodopseudomonas palustris* CGA009, *Rhodopseudomonas palustris* HaA2, *Rhodopseudomonas palustris* TIE-1, *Rhodospirillum centenum* SW, *Saccharophagus degradans* 2-40, *Salmonella enterica* subsp. *arizonae serovar* 62:z4,z23:--, *Salmonella enterica* subsp. *enterica serovar Choleraesuis* str. SC-B67, *Salmonella enterica* subsp. *enterica serovar allinarum* str. 287/91, *Salmonella enterica* subsp. *enterica serovar Hadar* str. RI_05P066, *Salmonella enterica* subsp. *enterica serovar Javiana* str. GA_MM04042433, *Salmonella enterica* subsp. *enterica serovar Saintpaul* str. SARA23, *Salmonella enterica* subsp. *enterica serovar Saintpaul* str. SARA29, *Salmonella enterica* subsp. *enterica serovar Typhi* str. CT18, *Salmonella typhimurium* LT2, *Serratia proteamaculans* 568, *Shewanella amazonensis* SB2B, *Shewanella baltica* OS155, *Shewanella baltica* OS185, *Shewanella baltica* OS195, *Shewanella baltica* OS223, *Shewanella benthica* KT99, *Shewanella denitrificans* OS217, *Shewanella frigidimarina* NCIMB 400, *Shewanella halifaxensis* HAW-EB4, *Shewanella loihica* PV-4, *Shewanella oneidensis* MR-1, *Shewanella pealeana* ATCC 700345, *Shewanella putrefaciens* 200, *Shewanella sediminis* HAW-EB3, *Shewanella* sp. ANA-3, *Shewanella* sp. MR-4, *Shewanella* sp. MR-7, *Shewanella* sp. W3-18-1, *Shewanella woodyi* ATCC 51908, *Shigella boydii* Sb227, *Shigella dysenteriae* Sd197, *Stenotrophomonas maltophilia* K279a, *Stenotrophomonas maltophilia* R551-3, *Streptococcus* sp. (N1), *synthetic construct, Thauera* sp. MZ1T, *Thioalkalivibrio* sp. HL-EbGR7, *Thiobacillus denitrificans* ATCC25259, *Thiomicrospira crunogena* XCL-2, *Vibrio alginolyticus* 12G01, *Vibrio angustum* S14, *Vibrio campbellii* AND4, *Vibrio cholerae* 2740-80, *Vibrio cholerae* MZO-2, *Vibrio cholerae* O1 *biovar eltor* str. N16961, *Vibrio cholerae* V51, *Vibrio fischeri* ES114, *Vibrio fischeri* MJ11, *Vibrio harveyi* ATCC BAA-1116, *Vibrio mimicus, Vibrionales bacterium* SWAT-3, *Vibrio parahaemolyticus* AQ3810, *Vibrio parahaemolyticus* RIMD 2210633, *Vibrio shilonii* AK1, *Vibrio splendidus* 12B01, *Vibrio* sp. MED222, *Vibrio vulnificus* CMCP6, *Vibrio vulnificus* YJ016, *Xanthomonas axonopodis* pv. *citri* str. 306, *Xanthomonas campestris* pv. *campestris* str. ATCC 33913, *Xanthomonas campestris* pv. *campestris* str. B100, *Xanthomonas campestris* pv. *Vesicatoria* str. 85-10, *Xanthomonas oryzae* pv. *oryzae* KACC10331, *Xanthomonas oryzae* pv. *oryzae* PXO99A, *Xanthomonas oryzae* pv. *oryzicola* BLS256, *Yersinia bercovieri* ATCC 43970, *Yersinia enterocolitica* subsp. *enterocolitica* 8081, *Yersinia frederiksenii* ATCC 33641, *Yersinia intermedia* ATCC 29909, *Yersinia mollaretii* ATCC 43969, *Yersinia pestis Angola, Yersinia pestis biovar Orientalis* str. F1991016, *Yersinia pestis* CO92, *Yersinia pestis* KIM or *Yersinia pseudotuberculosis* IP 31758.

In one embodiment of the invention, the precursor thioesterase is a thioesterase that has an analogous sequence to that of 'TesA (e.g., a TesA enzyme sans the signal peptide). In a preferred embodiment, the precursor thioesterase has at least about 20%, for example, at least about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to 'TesA. In yet another example, the precursor thioesterase has at least about 20%, for example, at

least about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to a 'TesA that is obtained from an *E. coli*., such as an *E. coli* K12. In a further example, the precursor thioesterase is a thioesterase that has an analogous sequence to the sequence of SEQ ID NO:31 in FIG. **57**, and preferably at least about 20%, for example, at least about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO:31 in FIG. **57**. The analogous sequence can be from a naturally-occurring protein or can be from a previously modified protein.

In one embodiment of the invention, the precursor thioesterase is a thioesterase that comprises the amino acid strings:

G-D-S-L-X(5)-M (SEQ ID NO:28), wherein:

the "X" refers to any amino acid residue; the number in the parenthetical adjacent thereto, when present, refers to the number of X residues in the stretch of amino acid residues;

the S residue at position 3 is a catalytic residue;

the D residue at position 2 may be substituted with N or T;

the L residue at position 4 may be substituted with C or Q;

the M residue at position 10 may be substituted with C, D, L, N, T, or V; and/or

V-X(2)-G-X-N-D-X-L (SEQ ID NO:29), wherein:

each "X" refers to any amino acid residue; the number in the parentheses adjacent thereto, when present, refers to the number of X residues in the stretch of amino acid residues;

the N residue at position 6 is in the oxyanion hole;

the V residue at position 1 may be substituted with L;

the N residue at position 6 may be substituted with V, L, C, A, G, H, I, T, or W;

the D residue at position 7 may be substituted with E;

the L residue at position 9 may be substituted with I, W, F, T, M, A, E, N, or V; and/or

D-X(2)-H-P-X(7)-I (SEQ ID NO:30), wherein:

each "X" refers to any amino acid residue; each number in the parentheses adjacent thereto, when present, refers to the number of X residues in the respective stretch of amino acid residues;

the D and H residues at positions 1 and 4 respectively are the catalytic residues;

the P residue at position 5 may be substituted with G, A, F, L, S, or V;

the I residue at position 13 may be substituted with L or V.

In one embodiment of the invention, the precursor thioesterase is a thioesterase having immunological cross-reactivity with a 'TesA obtained from an *E. coli*. In a particular embodiment, the precursor thioesterase has immunological cross-reactivity with the 'TesA obtained from an *E. coli* K-12. In a particular embodiment, the precursor thioesterase has immunological cross-reactivity with a thioesterase comprising the amino acid sequence of SEQ ID NO:31 as set forth in FIG. **57**. In a particular embodiment, the precursor thioesterase has cross-reactivity with fragments (or portions) of any of the thioesterases obtained from an *E. coli*, or from an *E. coli* K-12, and/or of any thioesterase that comprises the amino acid sequence of SEQ ID NO:31 as set forth in FIG. **57**. The precursor enzyme having immunological cross-reactivity with 'TesA can be a naturally-occurring protein, a previously modified protein, or a synthetic protein.

In another particular example, the precursor thioesterase is a 'TesA from an *E. coli*, or is a homolog, a paralog or an ortholog of a 'TesA from an *E. coli*, such as a 'TesA from an *E. coli* K12. The thioesterase precursor from which a mutant of the present invention is derived can also be an enzymatically active portion or a fragment of any one of the aforedescribed thioesterases.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided that comprises an amino acid sequence having at least one substitution of an amino acid, as compared to a precursor thioesterase, such that the mutant thioesterase has at least one altered property in relation to the precursor thioesterase. In an exemplary embodiment of the invention, a mutant thioesterase is provided that has an amino acid sequence with a single substitution mutation, and exhibits at least one altered property as compared to the precursor thioesterase from which the mutant is derived. In an exemplary embodiment of the invention, a mutant thioesterase is provided that comprises an amino acid sequence having two or more substitution mutations from the sequence of its precursor thioesterase, and the mutant thioesterase has at least one altered property as compared to the precursor thioesterase.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is a variant of a precursor thioesterase, and which has at least one altered property in vitro or in vivo in relation to such a precursor thioesterase, wherein the precursor thioesterase is a thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57** and accordingly comprises corresponding amino acid residues 2-183 of SEQ ID NO:31, and wherein the precursor thioesterase is modified at one or more amino acid positions selected from positions corresponding to one or more residues 2-183 of SEQ ID NO:31 in FIG. **57**.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57** and accordingly comprises corresponding amino acid residues 2-183 of SEQ ID NO:31, and which has at least one altered property in vitro or in vivo in relation to such precursor thioesterase, wherein the precursor thioesterase is mutated at one or more positions corresponding to one or more amino acid positions of SEQ ID NO:73 (which is residues 2-183 of SEQ ID NO:31 in FIG. **57**) selected from 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, and/or 182.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent) is provided, which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 of FIG. **57** and accordingly comprises corresponding amino acid residues 2-183 of SEQ ID NO:31, and which has at least one altered property in vitro or in vivo in relation to such precursor thioesterase, wherein the precursor thioesterase is mutated with one or more substitutions selected from A1C, A1F, A1L, A1Q, A1R, A1S, A1V, A1Y, D2E, D2H, D2K, D2L, D2M, D2P, D2R, D2W, T3E, T3G, T3K, T3L, T3R, T3W, L4A, L4G, L4M, L4N, L4S, L4V, L4Y, L5C, L5E, L5F, L5G, L5H, L5K, L5N, L5Q,

L5S, L5W, L5Y, 16A, 16L, 16T, 116V, L7A, L7C, L7E, L7K, L7M, L7N, L7S, L7T, L7V, L7W, L7Y, G8A, G8K, G8S, D9N, D9T, S10C, L11A, L11C, L11I, L11M, L11Q, L11V, S12A, S12I, S12L, S12M, S12N, S12T, S12V, S12Y, A13C, A13D, A13G, A13H, A13I, A13L, A13N, A13S, A13T, A13V, A13W, A13Y, G14A, G14C, G14E, G14F, G14I, G14K, G14M, G14N, G14P, G14Q, G14R, G14S, G14T, G14V, Y15A, Y15C, Y15D, Y15E, Y15G, Y15I, Y15L, Y15M, Y15N, Y15Q, Y15R, Y15S, Y15V, R16A, R16D, R16E, R16G, R16H, R16I, R16L, R16M, R16N, R16P, R16Q, R16S, R16T, R16V, R16W, M17A, M17C, M17D, M17E, M17G, M17K, M17L, M17N, M17P, M17Q, M17R, M17S, M17T, M17V, S18E, S18M, S18N, S18T, A19C, A19E, A19L, A19V, S20A, S20C, S20D, S20G, S20L, S20T, S20W, A21G, A21I, A21L, A21P, A21Y, A22C, A22D, A22E, A22F, A22G, A22H, A22I, A22K, A22L, A22M, A22N, A22P, A22R, A22S, A22T, A22Y, W23A, W23H, W23N, W23P, W23Y, P24A, P24C, P24D, P24E, P24F, P24G, P24I, P24M, P24N, P24S, P24T, P24V, P24W, A25D, A25E, A25L, A25N, A25P, A25Q, A25R, A25S, A25V, L26C, L26D, L26E, L26F, L26G, L26H, L26I, L26I, L26K, L26N, L26P, L26Q, L26R, L26S, L26V, L26W, L26Y, L27A, L27C, L27F, L27H, L27M, L27R, L27S, L27T, L27V, L27W, L27Y, N28A, N28G, N28I, N28K, N28M, N28P, N28R, N28W, D29M, D29P, D29V, K30P, W31D, W31E, W31G, W31L, W31N, W31P, W31R, W31S, W31T, Q32V, Q32Y, S33F, S33G, S33I, S33M, S33R, K34A, K34H, K34M, K34R, T35F, T35G, T35K, T35L, T35M, T35Q, T35V, T35Y, S36A, S36F, S36H, S36I, S36L, S36W, V37A, V37F, V37G, V37H, V37L, V37N, V37S, V37Q, V37S, V37W, V37Y, V38D, V38E, V38F, V38G, V38K, V38L, V38P, V38R, V38S, N39A, N39C, N39E, N39F, N39G, N39K, N39M, N39P, N39Q, N39R, N39T, N39V, N39W, N39Y, A40D, A40G, A40H, A40L, A40M, A40P, A40T, A40V, A40Y, S41C, S41P, S41T, I42A, I42C, I42D, I42E, I42G, I42K, I42L, I42M, I42P, I42S, I42T, 142W, I42Y, S43A, S43C, S43D, S43E, S43F, S43G, S43H, S43L, S43M, S43N, S43P, S43R, S43T, S43V, S43W, G44A, G44C, G44E, G44F, G44H, G44K, G44L, G44M, G44N, G44Q, G44R, G44S, G44W, G44Y, D45A, D45C, D45E, D45F, D45G, D45H, D45I, D45K, D45L, D45M, D45P, D45Q, D45S, D45T, D45V, D45W, T46A, T46C, T46D, T46E, T46F, T46G, T46I, T46K, T46L, T46N, T46R, T46S, T46V, T46W, S47A, S47C, S47E, S47F, S47G, S47L, S47M, S47P, S47Q, S47R, S47T, S47V, S47W, S47Y, Q48C, Q48D, Q48E, Q48F, Q48G, Q48I, Q48M, Q48S, Q48T, Q48V, Q48W, Q48Y, Q49A, Q49C, Q49D, Q49E, Q49G, Q49H, Q49I, Q49K, Q49L, Q49M, Q49P, Q49R, Q49S, Q49V, Q49W, Q49Y, G50A, G50C, G50E, G50F, G50I, G50K, G50L, G50M, G50N, G50P, G50Q, G50R, G50S, G50T, G50W, G50Y, L51A, L51C, L51D, L51F, L51H, L51N, L51P, L51S, L51T, L51V, L51W, L51Y, A52C, A52D, A52H, A52I, A52L, A52M, A52P, A52R, A52V, A52W, A52Y, R53A, R53C, R53D, R53E, R53F, R53G, R53I, R53K, R53L, R53N, R53S, R53T, R53V, R53W, R53Y, L54A, L54C, L54E, L54F, L54G, L54M, L54N, L54S, L54T, L54W, L54Y, P55A, P55G, P55Y, A56P, A56R, A56W, A56Y, L57A, L57C, L57F, L57G, L57H, L57I, L57K, L57N, L57P, L57Q, L57R, L57S, L57T, LS57V, L57W, L57Y, L58A, L58D, L58E, L58F, L58G, L58H, L58I, L58M, L58N, L58R, L58S, L58V, L58W, L58Y, K59E, K59R, K59V, Q60E, Q60M, Q60P, H61A, H61D, H61E, H61G, H61P, H61W, Q62G, Q62M, Q62P, Q62W, P63D, P63E, P63G, P63I, P63K, P63L, P63M, P63N, P63Q, P63R, P63S, P63T, P63V, P63W, R64D, R64E, R64F, R64L, R64M, R64P, R64Q, R64W, R64Y, W65A, W65E, W65G, W65K, W65L, W65M, W65N, W65P, W65R, W65V, V66C, V66G, V66I, V66M, V66N, V66Q, V66S, V66W, V66Y, L67A, L67C, L67E, L67G, L67M, L67Q, L67Q, L67S, L67T, L67W, V68A, V68E, V68G, V68L, V68M, V68N, V68P, V68Q, V68S, V68T, E69A, E69C, E69D, E69F, E69G, E69H, E69K, E69L, E69M, E69N, E69P, E69Q, E69S, E69V, E69W, E69Y, L70A, L70C, L70E, L70F, L70G, L70H, L70I, L70K, L70Q, L70S, L70T, L70V, L70W, G71A, G71C, G71S, G72A, G72C, G72M, G72P, G72S, N73A, N73C, N73G, N73H, N73I, N73L, N73P, N73R, N73S, N73T, N73V, N73W, D74A, D74C, D74E, D74F, D74G, D74Q, D74S, D74W, D74Y, G75A, G75C, G75D, G75E, G75F, G75I, G75K, G75L, G75M, G75N, G75P, G75R, G75T, G75V, G75W, G75Y, L76A, L76C, L76D, L76E, L76F, L76G, L76I, L76K, L76M, L76N, L76P, L76Q, L76R, L76T, L76V, L76W, R77A, R77C, R77D, R77E, R77F, R77G, R77H, R77K, R77L, R77N, R77Q, R77S, R77V, R77W, G78A, G78C, G78D, G78E, G78F, G78M, G78N, G78P, G78Q, G78R, G78S, G78T, G78V, G78Y, F79A, F79D, F79E, F79G, F79H, F79K, F79M, F79N, F79P, F79Q, F79S, F79V, F79W, F79Y, Q80A, Q80E, Q80G, Q80L, Q80M, Q80S, Q80W, Q80Y, P81A, P81E, P81K, P81L, P81M, P81N, P81T, P81W, P81Y, Q82A, Q82F, Q82I, Q82M, Q82N, Q82P, Q82R, Q82S, Q82T, Q82V, Q82W, Q82Y, Q83A, Q83C, Q83F, Q83G, Q83K, Q83L, Q83M, Q83N, Q83R, Q83S, Q83T, Q83V, Q83W, Q83Y, T84A, T84D, T84E, T84F, T84G, T84H, T84K, T84L, T84M, T84N, T84Q, T84R, T84S, T84V, T84W, T84Y, E85A, E85C, E85D, E85F, E85G, E85L, E85P, E85Q, E85R, E85S, E85T, E85V, E85W, E85Y, Q86A, Q86G, Q86H, Q86K, Q86P, Q86T, Q86V, Q86W, Q86Y, T87A, T87C, T87D, T87E, T87F, T87G, T87H, T87L, T87M, T87P, T87R, T87S, T87V, T87W, L88A, L88C, L88E, L88F, L88G, L88H, L88Q, L88S, L88W, L88Y, R89A, R89G, R89H, R89L, R89P, R89T, R89V, R89W, Q90E, Q90L, Q90N, Q90P, Q90W, Q90Y, I91E, I91G, I91L, I91M, I91N, 191Q, I91S, I91V, I91Y, L92A, L92C, L92E, L92G, L92H, L92N, L92Q, L92R, L92S, L92T, L92V, L92Y, Q93A, Q93E, Q93F, Q93G, Q93H, Q93I, Q93L, Q93M, Q93N, Q93P, Q93S, Q93V, Q93W, Q93Y, D94C, D94E, D94F, D94G, D94H, D94K, D94L, D94N, D94P, D94Q, D94R, D94S, D94V, V95A, V95C, V95D, V95E, V95F, V95G, V95I, V95L, V95M, V95N, V95P, V95Q, V95T, V95W, V95Y, K96A, K96C, K96L, K96N, K96P, K96Q, K96R, K96V, K96Y, A97C, A97E, A97F, A97K, A97N, A97P, A97R, A97V, A97W, A98E, A98G, A98K, A98L, A98P, A98V, A98W, A98Y, N99A, N99C, N99D, N99G, N99L, N99M, N99P, N99Q, N99R, N99S, N99W, N99Y, A100D, A100E, A100G, A100H, A100I, A100K, A100L, A100M, A100Q, A100R, A100S, A100T, A100V, A100 W, A100Y, E101A, E101D, E101G, E101L, E101M, E101P, E101S, E101T, E101V, P102E, P102F, P102G, P102H, P102I, P102L, P102Q, P102R, P102S, P102V, P102W, P102Y, L103A, L103C, L103E, L103G, L103I, L103K, L103N, L103Q, L103R, L103S, L103T, L103V, L103W, L104A, L104C, L104E, L104G, L104I, L104N, L104P, L104Q, L104S, L104W, L104Y, M105A, M105C, M105E, M105F, M105G, M105I, M105K, M105L, M105P, M105T, M105V, M105W, Q106A, Q106C, Q106D, Q106G, Q106H, Q106K, Q106L, Q106M, Q106R, Q106S, Q106T, Q106V, Q106W, Q106Y, I107A, 1107C, I107E, I107F, I107G, I107K, I107L, I107M, I107Q, I107S, I107T, I107V, I107Y, R108A, R108C, R108D, R108E, R108F, R108G, R108H, R108I, R108L, R108M, R108S, R108V, R108W, R108Y, L109A, L109C, L109D, L109E, L109F, L109G, L109K, L109M, L109P, L109Q, L109R, L109S, L109T, L109V, L109Y, P110A, P110C, P110D, P110E, P110F, P110G, P110H, P110K, P110L, P110M, P110N, P110R, P110S, P110V, P110W, A11C, A111E, A111L, A111M, A111N, A111P, A111Q, A111R, A111S, A11V, A111W, A111Y,

N112A, N112F, N112G, N112I, N112K, N112L, N112P, N112R, N112V, N112W, N112Y, Y113A, Y113C, Y113D, Y113E, Y113G, Y113I, Y1113M, Y113P, Y113Q, Y113S, Y113S, Y113W, G114A, G114F, G114K, G114L, G114M, G114P, G114W, G114Y, R115A, R115C, R115E, R115G, R115I, R115N, R115P, R115Q, R115S, R115V, R115W, R15Y, R116C, R116D, R16E, R116H, R116T, R116V, R116W, Y117A, Y117C, Y117D, Y117E, Y117G, Y117H, Y117I, Y117L, Y117M, Y117N, Y117P, Y117Q, Y117R, Y117S, Y117T, Y117V, Y117W, N118A, N18C, N118E, N118F, N118G, N118H, N118I, N118K, N118L, N118M, N118P, N118Q, N118S, N118T, N118V, N118W, E119C, E119D, E119F, E119G, E119K, E119L, E119M, E119P, E119Q, E119R, E119T, E119W, E119Y, A120D, A120E, A120G, A120I, A120L, A120P, A120T, A120 W, F121A, F121C, F121D, F121E, F121G, F121K, F121L, F121M, F121N, F121P, F121Q, F121R, F121S, F121V, F121W, F121Y, S122A, S122C, S122D, S122E, S122F, S122G, S122I, S122L, S122M, S122P, S122R, S122V, S122W, S122Y, A123C, A123E, A123F, A123H, A123L, A123R, A123T, A123V, A123W, A123Y, I124A, 1124C, I124D, I124E, I124O, I124K, I124L, I124R, I124S, I124T, I124W, I124Y, Y125C, Y125F, Y125G, Y125H, Y125I, Y125L, Y125P, Y125Q, Y125R, Y125S, Y125T, Y125V, Y125W, P126C, P126F, P126H, P126K, P126R, P126T, P126V, P126Y, K127A, K127I, K127P, K127S, L128A, L128C, L128E, L128F, L128G, L128Q, L128R, L128S, L128T, L128V, L128W, A129D, A129F, A129H, A129I, A129K, A129L, A129N, A129W, A129Y, K130E, K130I, K130P, K130V, E131A, E131C, E131D, E131F, E131G, E131I, E131K, E131L, E131N, E131P, E131V, E131W, F132C, F132D, F132E, F132K, F132L, F132N, F132P, F132T, F132V, D133C, D133K, D133R, D133S, D133T, D133V, D133Y, V134C, V134D, V134E, V134I, V134K, V134M, V134N, V134P, V134Q, V134R, V134S, V134W, V134Y, P135A, P135E, P135K, P135Q, L136A, L136C, L136D, L136E, L136F, L136G, L136H, L136K, L136M, L136N, L136P, L136Q, L136R, L136S, L136T, L137A, L137C, L137D, L137E, L137G, L137H, L137K, L137P, L137Q, L137R, L137S, L137Y, P138E, P138F, P138G, P138N, P138R, P138T, P138V, F139A, F139C, F139D, F139E, F139G, F139H, F139L, F139M, F139N, F139S, F139T, F139V, F139W, F140A, F140C, F140G, F140I, F140L, F140M, F140N, F140P, F140S, F40T, F140V, F140 W, M141A, M141C, M141D, M141E, M141F, M141G, M141K, M141L, M141P, M141Q, M141R, M141T, M141V, M141W, M141Y, E142A, E142C, E142G, E142I, E142L, E142M, E142N, E142P, E142Q, E142R, E142S, E142T, E142V, E142W, E142Y, E143A, E143D, E143F, E143G, E143I, E143M, E143P, E143W, V144A, V144D, V144E, V144G, V144H, V144N, V144P, V144Q, V144R, V144S, V144W, V144Y, Y145A, Y145C, Y145D, Y145E, Y145G, Y145I, Y145L, Y145M, Y145N, Y145Q, Y145R, Y145S, Y145T, Y145W, L146A, L146C, L146D, L146E, L146G, L146H, L146P, L146S, L146W, K147G, K147P, K147R, K147W, P148D, P148E, P148W, Q149L, W150C, W150D, W150E, W150G, W150L, W150P, W150Q, W150R, W150T, M150V, M151A, M151C, M151D, M151E, M151F, M151G, M151I, M115L, M151Q, M151R, M151S, M151T, M151V, M151W, Q152A, Q152D, Q152E, Q152F, Q152H, Q152I, Q152K, Q152L, Q152N, Q152P, Q152R, Q152S, Q152T, Q152V, Q152Y, D153A, D153E, D153F, D153I, D153K, D153M, D153P, D153Q, D153V, D153W, D154A, D154C, D154E, D154F, D154G, D154H, D154I, D154K, D154L, D154M, D154N, D154P, D154R, D154S, D154T, D154V, D154W, G155A, G155F, G155H, G155I, G155P, G155V, G155W, G155Y, I156A, I156C, I156E, I156F, I156G, I156K, I156L, 11156M, I156Q, I156R, I156S, I156T, I156V, I156Y, H157C, H157E, P158A, P158F, P158G, P158H, P158I, P158L, P158Q, P158S, P158T, P158V, P158W, N159C, N159E, N159G, N159I, N159K, N159L, N159M, N159P, N159Q, N159R, N159T, N159V, N159W, R160A, R160C, R160D, R160E, R160G, R160H, R160I, R160K, R160N, R160Q, R160S, R160W, D161E, D161G, D161I, D161K, D161L, D161M, D161N, D161Q, D161R, D161S, D161V, D161W, A162G, A162I, A162K, A162L, A162N, A162R, A162T, A162V, A162Y, Q163A, Q163C, Q163D, Q163E, Q163F, Q163G, Q163I, Q163L, Q163M, Q163S, Q163T, Q163V, Q163W, Q163Y, P164A, P164C, P164D, P164K, P164L, P164M, P164N, P164R, P164T, P164V, P164W, F165D, F165E, F165G, F165H, F165I, F165K, F165L, F165M, F165R, F165S, F165T, F165V, F165W, F165Y, I166A, I166C, I166F, I166L, I166M, I166S, I166V, I166Y, A167C, A167D, A167E, A167F, A167G, A167K, A167L, A167M, A167N, A167Q, A167R, A167T, A167V, A167W, A167Y, D168A, D168G, D168H, D168L, D168M, D168P, D168R, D168T, D168V, D168W, W169A, W169D, W169E, W169G, W169K, W169M, W169Q, W169R, W169S, W169T, W169V, M170A, M170E, M170F, M170G, M170H, M170L, M170N, M170Q, M170S, M170T, M170V, M170 W, M170Y, A171E, A171F, A171I, A171S, A171V, A171W, K172A, K172M, K172P, Q173D, Q173I, Q173N, Q173P, Q173W, Q173Y, L174A, L174F, L174G, L174Q, L174S, L174T, L174W, L174W, L174Y, Q175F, Q175I, Q175L, Q175M, Q175Y, P176D, P176H, P176K, P176L, P176N, P176Q, P176R, P176V, P176W, P176Y, L177D, L177F, L177G, L177M, L177S, L177T, V178A, V178F, V178G, V178K, V178L, V178R, V178S, V178T, V178W, N179G, N179H, N179R, N179T, N179V, N179W, N179Y, H180A, H180E, H180G, H180L, H180P, H180R, H180S, H80V, H180 W, D181A, D181C, D181E, D181G, D181H, D181I, D181L, D181P, D181Q, D181R, D181S, D181T, D181W, S182A, S182C, S182D, S182E, S182G, S182I, S182K, S182L, S182N, S182P, S182Q, S182R, S182T, and/or S180V, wherein the numbers in the substitution mutation designations refer to amino acid positions of SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO:31).

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which has an increased substrate specificity for, and/or activity (e.g., catalytic rate) with respect to C_{10} substrates (i.e., substrates, the carbon chains of which are 10 carbons in length), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to one or more of residues selected from 5-30, 35-60, 65-98, 102-139, and/or 140-180 of SEQ ID NO: 73. The increased substrate specificity for, and/or activity with respect to C_{10} substrates can be measured in vitro and/or in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which has an increased substrate specificity for, and/or activity (e.g., catalytic rate) with respect to C_{10} substrates, and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to one or more residues of SEQ ID NO: 73 selected from 1, 3, 4, 7, 9, 12, 13, 14, 16, 17, 20, 22, 24, 25, 28, 32, 38, 39, 40, 42, 43, 46, 47, 48, 49, 50, 51, 52, 54, 56, 59, 60, 64, 68, 72, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 89, 90, 91, 92, 93, 94, 95, 96, 98, 99, 100, 101, 102, 103, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127,

128, 130, 132, 133, 134, 138, 139, 140, 141, 142, 144, 145, 146, 147, 148, 150, 151, 152, 156, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 175, 176, 177, 178, 179, 180, 181, and/or 182. The increased substrate specificity for, and/or activity with respect to C_{10} substrates can be measured in vitro and/or in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent) is provided, which has an increased substrate specificity for, and/or activity (e.g., catalytic rate) with respect to C_{10} substrates, and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated with one or more substitutions selected from A1L, A1S, T3K, L4A, L7M, L7V, D9N, S12A, A13D, G14A, G14E, G14P, G14Q, G14R, G14S, G14V, R16G, R16L, R16M, R16N, R16P, R16Q, R16T, M17C, M17L, M17T, M17V, S20A, S20C, S20D, S20G, S20L, S20T, S20W, A22C, A22D, A22E, A22G, A22H, A22I, A22K, A22N, P24A, P24C, P24D, P24F, P24I, P24S, P24T, P24V, P24W, A25E, A25L, A25N, A25Q, A25V, N28A, N28R, Q32V, Q32Y, V38E, V38K, V38R, N39A, N39T, A40D, A40H, I42A, I42E, I42L, I42S, I42T, 142W, I42Y, S43A, S43C, S43D, S43E, S43L, S43N, S43P, T46E, T46F, T46I, T46L, T46V, S47A, S47C, S47F, S47G, S47L, S47M, S47T, S47V, Q48D, Q48E, Q48G, Q48S, Q48T, Q48V, Q48W, Q49A, Q49C, Q49D, Q49G, Q49H, Q49L, Q49M, Q49S, G50A, G50Q, L51A, L51F, L51H, L51Y, A52D, A52M, L54T, A56P, K59R, Q60M, R64D, R64E, R64Q, V68L, G72A, G72C, G72P, G72S, G75A, G75C, G75D, G75E, G75F, G75I, G75K, G75L, G75M, G75N, G75P, G75T, G75V, G75W, G75Y, L76A, L76D, L76G, L76I, L76K, L76M, L76N, L76P, L76Q, L76R, L76W, R77G, R77L, R77Q, G78A, G78C, G78E, G78F, G78M, G78N, G78Q, G78R, G78S, G78T, G78V, G78Y, F79A, F79D, F79E, F79G, F79H, F79N, F79Q, F79W, F79Y, Q80E, P81N, P81T, P81Y, Q82R, Q82S, Q82T, Q83A, Q83C, Q83F, Q83G, Q83K, Q83L, Q83M, Q83N, Q83R, Q83S, Q83T, Q83V, Q83W, Q83Y, T84A, T84F, T84L, T84M, T84N, T84Q, T84V, T84Y, E85A, E85C, E85L, E85Q, E85R, E85S, E85T, E85W, E85Y, Q86A, Q86G, Q86K, Q86T, T87D, T87P, R89A, R89G, Q90E, Q90Y, I91V, L92V, Q93A, Q93E, Q93G, Q93H, Q93I, Q93L, Q93S, Q93W, Q93Y, D94E, D94F, D94G, D94H, D94K, D94N, D94Q, D94R, D94S, D94V, V95L, V95T, K96V, K96Y, A98W, N99G, N99L, N99P, N99Q, N99R, N99Y, A100G, A100V, E101A, E101D, E101G, E101L, E101M, E101S, E101T, E101V, P102S, L103G, M105C, M105I, M105V, Q106A, Q106D, Q106H, Q106W, I107Y, R108A, R108D, R108E, R108F, R108G, R108H, R108I, R108L, R108M, R108S, R108W, R108Y, L109A, L109D, L109E, L109F, L109G, L109K, L109P, L109R, L109S, L109Y, P110C, P110D, P110E, P110F, P110G, P110H, P110K, P110L, P110M, P110N, P110R, P110S, P110V, P110W, A111C, A111E, A111L, A111M, A111P, A111Q, A111R, A111V, A111W, A111Y, N112A, N112F, N112G, N112K, N112R, N112W, Y113A, Y113C, Y113G, Y113I, Y113M, G114K, G114L, G114P, R115A, R115C, R115E, R115G, R115N, R115S, R115W, R115Y, R116D, R116E, R116W, Y117A, Y117C, Y117E, Y117I, Y117L, Y117N, Y117Q, Y117R, Y117S, Y117T, Y117V, N118C, N118G, N118, N118K, N118S, N118T, N118V, N118W, E119C, E119F, E119G, E119K, E119M, E119R, E119W, E119Y, A120D, A120E, A120G, A120 W, F121A, F121D, F121E, F121M, F121P, F121Q, F121R, F121S, F121Y, S122D, S122E, S122F, S122I, S122L, S122M, S122V, S122W, S122Y, A123H, A123L, A123V, I124T, Y125C, Y125F, Y125G, Y125P, Y125S, Y125V, Y125W, P126R, P126T, P126V, P126Y, K127S, L128C, L128T, L128V, K130E, K130I, K130V, F132D, F132E, F132N, F132T, D133K, D133R, D133S, D133T, D133V, D133Y, V134I, V134M, V134S, P138E, P138N, P138R, P138T, P138V, F139A, F139D, F139G, F139H, F139M, F139S, F139W, F140C, F140G, F140M, F140N, F140P, F140S, M141A, M141C, M141D, M141E, M141F, M141G, M141K, M141L, M141P, M141Q, M141R, M141T, M141V, M141W, M141Y, E142A, E142C, E142P, E142Q, E142W, E142Y, V144D, V144E, V144G, V144H, V144N, V144P, V144Q, V144R, V144S, V144W, V144Y, Y145A, Y145C, Y145D, Y145E, Y145G, Y145I, Y145L, Y145M, Y145N, Y145Q, Y145T, Y145W, L146A, L146C, L146D, L146E, L146G, L146H, L146S, L146W, K147G, K147P, K147W, P148D, P148E, W150C, W150D, W150E, W150G, W150L, W150Q, W150T, M151A, M151C, M151E, M151F, M151G, M151I, M151Q, M151S, M151T, M151V, M151W, Q152D, Q152F, Q152I, Q152L, Q152T, I156L, P158A, P158F, P158G, P158H, P158I, P158L, P158Q, P158T, P158V, N159C, N159E, N159G, N159I, N159K, N159L, N159M, N159R, N159T, N159V, R160A, R160C, R160D, R160E, R160G, R160H, R160N, R160Q, R160S, R160W, D161E, D161G, D161I, D161K, D161L, D161M, D161Q, D161R, D161W, A162I, A162L, A162T, A162V, A162Y, Q163G, Q163L, Q163M, Q163S, P164A, P164C, P164D, P164M, P164N, P164R, P164V, P164W, F165D, F165E, F165G, F165H, F165I, F165K, F165L, F165M, F165R, F165S, F165T, F165V, F165Y, I166F, I166L, I166M, I166V, A167C, A167M, A167R, A167T, D168G, D168P, D168R, W169E, W169K, W169Q, M170F, M170H, M170L, M170T, M170V, M170Y, A171E, A171F, A171V, A171W, K172A, K172M, Q173N, Q175I, P176H, P176K, P176N, P176W, L177M, L177T, V178T, V178W, N179G, N179H, N179R, N179T, N179V, N179Y, H180E, H180G, H180R, H180V, H180 W, D181A, D181H, D181I, D181L, D181P, D181R, D181W, S182A, S182G, S182K, S182L, S182P, and/or S182R, wherein the numbers in the substitution mutation designations refer to amino acid positions of SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO:31). The increased substrate specificity for, and/or activity with respect to C_{10} substrates can be measured in vitro and/or in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which has an increased substrate specificity for, and/or activity (e.g., catalytic rate) with respect to C_{12} substrates (i.e., substrates, the carbon chains of which are 12 carbons in length), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to residues 10-25, 35-85, 90-103, 110-143, 146-180 of SEQ ID NO: 73. The increased substrate specificity for, and/or activity with respect to C_{12} substrates can be measured in vitro and/or in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent) is provided, which has an increased substrate specificity for, and/or activity (e.g., catalytic rate) with respect to C_{12} substrates, and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding one or more residues of SEQ ID NO: 73 selected from 1, 2, 3, 4, 5, 6, 7, 9, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 24, 25, 26, 27, 28, 29, 30, 31, 35, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 57, 58, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 111, 112, 113, 114, 115, 116, 117, 119, 120, 122, 123,

124, 125, 126, 127, 128, 129, 130, 131, 133, 134, 136, 137, 140, 141, 142, 145, 149, 152, 153, 155, 156, 158, 159, 160, 161, 162, 163, 164, 166, 167, 168, 169, 170, 172, 173, 174, 175, 176, 177, 179, 180, 181, and/or 182. The increased substrate specificity for, and/or activity with respect to C_{12} substrates can be measured in vitro and/or in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which has an increased substrate specificity for, and/or activity (e.g., catalytic rate) with respect to C_{12} substrates, and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated with one or more substitutions selected from A1Q, A1S, A1V, D2E, D2K, D2P, D2W, T3R, T3W, L4A, L4Y, L5F, L5G, L5S, L5Y, 16T, 16V, L7A, L7C, L7M, L7N, L7S, L7T, L7V, L7Y, D9N, L11M, S12A, S12I, S12V, A13C, A13G, A13H, A13I, A13L, A13N, A13T, A13W, G14F, G14I, G14K, G14M, G14V, Y15A, Y15C, Y15D, Y15E, Y15G, Y15I, Y15L, Y15M, Y15N, Y15Q, Y15R, Y15S, Y15V, R16D, R16E, R16G, R16H, R16I, R16L, R16N, R16P, R16S, R16T, R16V, R16W, M17A, M17C, M17G, M17K, M17N, M17P, M17Q, M17R, M17S, M17T, S18M, S18N, A19L, S20A, S20C, S20D, S20G, S20L, S20T, S20W, A21I, A21L, A21P, A21Y, A22F, A22L, A22M, A22N, A22R, A22Y, P24G, P24V, A25D, A25E, A25L, A25N, A25Q, A25R, A25V, L26D, L26E, L26F, L26G, L26H, L261,126K, L26N, L26R, L26S, L26W, L26Y, L27A, L27C, L27F, L27M, L27W, L27Y, N28R, N28W, D29P, K30P, W31E, W31N, T35L, T35Y, V37F, V37S, V37W, V38D, V38F, V38G, V38P, N39A, N39C, N39E, N39G, N39Q, N39W, A40D, A40L, A40M, A40P, A40V, A40Y, S41C, S41T, I42A, I42C, I42D, I42E, I42G, I42K, I42L, I42M, I42P, I42S, I42T, I42W, I42Y, S43A, S43D, S43E, S43F, S43G, S43H, S43L, S43M, S43N, S43R, S43T, S43V, G44C, G44E, G44H, G44K, G44L, G44N, G44Q, G44R, G44S, D45A, D45C, D45E, D45F, D45H, D45I, D45K, D45L, D45M, D45P, D45Q, D45S, D45T, D45V, D45W, T46A, T46C, T46D, T46G, T46K, T46N, T46R, T46S, S47P, S47Q, Q48E, Q48V, Q48W, Q48Y, Q49A, Q49C, Q49D, Q49E, Q49G, Q49H, Q49I, Q49K, Q49L, Q49M, Q49P, Q49R, Q49S, Q49V, Q49W, Q49Y, G50A, G50C, G50F, G50I, G50K, G50L, G50M, G50N, G50P, G50Q, G50R, G50S, G50T, G50Y, L51A, L51D, L51N, L5 IT, L51V, L51W, A52C, A52M, A52P, A52W, R53A, R53C, R53D, R53E, R53F, R53G, R53I, R53K, R53L, R53N, R53S, R53T, R53V, R53W, R53Y, L54A, L54C, L54E, L54F, L54G, L54M, L54N, L54S, L54W, L54Y, P55Y, L57A, L57C, L57F, L57K, L57P, L57Q, L57R, L57Y, L58A, L58D, L58E, L58G, L58H, L58N, L58R, L58S, L58W, L58Y, Q60P, H61D, H61G, H61P, Q62P, Q62W, P63I, P63L, P63N, P63S, P63T, P63V, P63W, R64F, R64P, R64W, R64Y, W65A, W65E, W65G, W65K, W65M, W65N, W65V, V66M, V66S, L67A, L67T, V68A, V68L, V68M, V68S, V68T, E69A, E69C, E69D, E69G, E69H, E69K, E69L, E69M, E69N, E69P, E69V, E69Y, L70A, L70C, L70E, L70F, L70H, L70I, L70K, L70Q, L70S, L70T, L70V, G71A, G72A, N73G, N73H, N73L, N73R, N73S, N73T, D74E, D74G, L76I, L76M, L76W, R77C, R77D, R77E, R77G, R77K, R77L, R77Q, R77S, R77V, R77W, G78D, F79P, Q80G, Q80M, Q80S, Q80Y, P81A, P81E, P81K, P81L, P81M, P81W, P81Y, Q82F, Q82V, Q82W, Q82Y, Q83A, T84E, T84R, T84W, Q86A, Q86T, T87E, T87G, T87L, L88C, R89L, R89P, Q90N, Q90P, Q90W, I91G, I91M, I91S, I91V, I91Y, L92A, L92C, L92G, L92H, L92N, L92S, L92T, L92V, L92Y, Q93A, Q93G, Q93H, Q93I, Q93P, Q93Y, D94P, V95F, V95G, V95L, V95N, V95Q, V95T, V95W, K96A, K96L, K96P, K96Y, A97K, A97P, A98L, A98P, A98V, A98W, A98Y, N99C, N99D, N99G, N99L, N99M, N99P, N99Q, N99R, N99W, N99Y, A100D, A100E, A100G, A100H, A100I, A100K, A100L, A100Q, A100R, A100V, A100 W, A100Y, E101G, E101L, E101M, E101P, E101S, E101T, E101V, P102E, P102F, P102H, P102L, P102Q, P102R, P102S, P102W, P102Y, L103E, L103K, L103N, L103Q, L103R, L104C, L104P, L104S, L104W, M105C, M105E, M105G, M105V, Q106A, Q106C, Q106G, Q106K, Q106R, Q106S, Q106T, I107C, I107E, I107K, I107L, I107M, I107S, I107V, R108F, R108W, L109M, A111C, A111Q, A111W, N112A, N112G, N112W, Y113A, Y113D, Y113G, Y113, G114K, G114L, G114M, G114Y, R115A, R115C, R115E, R115G, R115N, R115S, R115Y, R116H, R116W, Y117C, Y117H, Y117I, Y117L, Y117M, Y117N, Y117S, Y117T, Y117V, E119C, E119F, E119K, E119M, E119R, E119W, E119Y, A120D, A120G, A120I, A120T, A120W, S122F, S122I, S122L, S122M, S122V, S122W, S122Y, A123C, A123F, A123H, A123L, A123R, A123T, A123V, A123W, A123Y, I124G, I124H, I124K, I124L, I124R, I124S, I124Y, Y125F, Y125R, P126C, P126F, P126H, P126Y, K127I, K127P, L128A, L128S, L128T, A129H, A129I, A129K, A129N, A129W, A129Y, K130P, E131A, E131C, E131F, E131G, E131K, E131L, E131N, E131V, E131W, D133K, V134D, V134E, V134K, V134N, V134Q, V134R, V134W, V134Y, L136A, L136D, L136E, L136F, L136G, L136H, L136K, L136N, L136P, L136Q, L136R, L136S, L136T, L137E, L137G, L137H, L137P, L137Q, L137S, L137Y, F140M, M141A, M141C, M141L, M141P, E142C, Y145E, Q149L, Q152A, Q152D, Q152E, Q152H, Q152K, Q152R, Q152Y, D153K, G155F, G155W, G155Y, I156C, I156F, I156M, I156V, P158A, P158G, N159G, N159Q, N159T, N159V, R160A, R160D, R160E, R160G, R160H, R160N, R160Q, R160S, R160W, D161I, D161K, D161L, D161M, D161N, D161Q, D161W, A162G, Q163A, Q163C, Q163G, Q163L, Q163M, Q163S, Q163T, P164C, P164M, I166L, I166V, A167C, A167E, A167F, A167G, A167K, A167L, A167N, A167Q, A167R, A167T, A167V, A167Y, D168G, D168, D168L, D168R, D168V, D168W, W169A, W169D, W169E, W169G, W169K, W169Q, W169S, M170F, M170G, M170N, M170Q, M170S, M170V, M170 W, K172M, K172P, Q173N, L174A, L174F, L174G, L174T, L174W, Q175I, P176H, P176K, P176L, P176N, P176W, L177D, L177G, N179H, N179R, N179Y, H180A, H180G, D181H, D181I, D181L, D181R, D181W, S182K, S182L, S182P, and/or S182R, wherein the numbers in the substitution mutation designations refer to amino acid positions of SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO:31). The increased substrate specificity for, and/or activity with respect to C_{12} substrates can be measured in vitro and/or in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which has an increased substrate specificity for, and/or activity (e.g., catalytic rate) with respect to C_{14} substrates (i.e., substrates, the carbon chains of which are 14 carbons in length), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to residues 5-20, 35-58, 65-80, 83-90, 110-130, 140-145, 155-160, 165-180 of SEQ ID NO: 73. The increased substrate specificity for, and/or activity with respect to C_{14} substrates can be measured in vitro and/or in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which has an increased substrate specificity for, and/or activity (e.g., catalytic rate) with respect to C_{14} substrates, and which is a variant of a precursor thioesterase that comprises

an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding one or more residues of SEQ ID NO: 73 selected from 1, 4, 5, 7, 8, 9, 11, 12, 13, 14, 15, 16, 17, 20, 21, 22, 23, 25, 26, 28, 29, 33, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 56, 57, 58, 66, 68, 69, 70, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 89, 91, 92, 93, 95, 96, 97, 98, 99, 100, 101, 102, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 131, 133, 134, 136, 137, 138, 139, 140, 141, 142, 143, 147, 148, 151, 152, 153, 155, 156, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 173, 174, 175, 176, 178, 179, 180, 181, and/or 182. The increased substrate specificity for, and/or activity with respect to C_{14} substrates can be measured in vitro and/or in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which has an increased substrate specificity for, and/or activity (e.g., catalytic rate) with respect to C_{14} substrates, and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated with one or more substitutions selected from A1S, L4S, L4Y, L5H, L5Y, L7C, L7M, L7N, L7S, L7T, L7Y, G8S, D9N, D9T, L11C, L11I, L11M, L11Q, L11V, S12I, S12L, S12M, S12T, S12V, A13H, A13I, A13L, A13T, A13V, G14F, G14I, G14R, G14T, G14V, Y15A, Y15C, Y15D, Y15E, Y15G, Y15I, Y15L, Y15M, Y15N, Y15Q, Y15R, Y15S, Y15V, R16G, R16N, R16P, R16W, M17C, M17D, M17G, M17K, M17N, M17P, M17R, M17S, M17T, S20A, S20D, S20G, S20L, S20T, S20W, A21G, A22L, A22N, A22Y, W23Y, A25E, A25N, A25Q, A25V, L26C, L26F, L26H, L26Q, L26V, L26Y, N28K, N28P, D29V, S33F, S36H, V37H, V37Q, V38F, N39F, N39M, N39Q, N39V, N39W, N39Y, A40G, A40P, A40T, A40V, S41P, S41T, I42A, I42D, I42E, I42G, I42L, I42M, I42P, I42S, I42T, I42W, I42Y, S43A, S43D, S43E, S43F, S43G, S43H, S43L, S43M, S43N, S43T, S43V, S43W, G44A, G44C, G44E, G44F, G44H, G44K, G44L, G44M, G44N, G44Q, G44R, G44S, G44W, G44Y, D45A, D45C, D45E, D45F, D45G, D45H, D45M, D45P, D45Q, D45S, D45T, D45V, D45W, T46A, T46C, T46D, T46G, T46K, T46N, T46S, T46W, S47E, S47P, S47Q, S47W, S47Y, Q48C, Q48F, Q48I, Q48M, Q48V, Q48W, Q48Y, Q49A, Q49C, Q49D, Q49E, Q49G, Q49H, Q49I, Q49K, Q49L, Q49M, Q49P, Q49R, Q49S, Q49V, Q49W, Q49Y, G50A, G50C, G50E, G50F, G50I, G50K, G50L, G50M, G50N, G50P, G50Q, G50R, G50S, G50T, G50W, G50Y, L51A, L515C, L1D, L51S, L51V, A52H, A52I, A52L, A52M, A52P, A52R, A52V, A52W, A52Y, R53A, R53C, R53D, R53E, R53F, R53G, R53I, R53K, R53L, R53N, R53S, R53T, R53V, R53W, R53Y, L54W, L54Y, A56R, A56W, A56Y, L57F, L58F, L58I, L58Y, V66I, V68L, E69A, E69C, E69D, E69F, E69G, E69H, E69K, E69L, E69M, E69N, E69Q, E69S, E69V, E69Y, L70A, L70C, L70E, L70F, L70H, L70Q, L70S, L70T, L70V, L70W, G72A, G72C, G72P, G72S, N73A, N73C, N73G, N73H, N73I, N73L, N73P, N73R, N73S, N73T, N73V, N73W, D74E, D74G, G75A, G75C, G75D, G75E, G75F, G75I, G75K, G75L, G75M, G75N, G75P, G75T, G75W, G75Y, L76A, L76C, L76D, L76E, L76F, L76G, L76I, L76K, L76M, L76N, L76P, L76Q, L76R, L76T, L76V, L76W, R77A, R77C, R77D, R77E, R77F, R77G, R77H, R77K, R77L, R77N, R77Q, R77S, R77V, R77W, G78P, F79M, F79P, F79V, Q80A, Q80G, Q80L, Q80M, Q80S, Q80W, Q80Y, P81A, P81E, P81K, P81L, P81M, P81W, P81Y, Q82F, Q82I, Q82N, Q82P, Q82V, Q82W, Q82Y, Q83A, T84S, E85D, Q86A, Q86T, Q86V, Q86W, T87A, T87C, T87E, T87F, T87G, T87H, T87L, T87M, T87S, T87V, T87W, R89H, R89T, R89V, R89W, I91L, I91V, I91Y, L92V, Q93A, Q93G, Q93H, Q93I, Q93P, Q93Y, V95L, V95M, V95T, V95W, K96A, K96L, K96P, K96Y, A97W, A98K, A98L, A98W, N99G, N99L, N99P, N99Q, N99R, N99Y, A100G, A100H, A00I, A100K, A100L, A100M, A100R, A100T, A100V, A100Y, E101G, E101L, E101M, E101S, E101T, E101V, P102S, M105A, M105C, M105E, M105G, M105I, M105L, M105V, Q106A, Q106C, Q106D, Q106G, Q106H, Q106K, Q106L, Q106M, Q106R, Q106S, Q106T, Q106V, Q106W, Q106Y, I107C, I107E, I107G, 1107L, I107M, I107Q, I107V, R108A, R108C, R108D, R108F, R108I, R108L, R108S, R108V, R108W, R108Y, L109C, L109M, L109Q, L109T, L109V, L109Y, P110A, P110E, P110H, P110N, P110R, P110V, A111C, A111L, A111Q, A111R, A111V, A111W, N112A, N112F, N112G, N112I, N112L, N112P, N112V, N112W, N112Y, Y113A, Y113D, Y113G, Y113I, Y113M, Y113W, G114F, G114K, G114L, G114M, G114W, G114Y, R115A, R115C, R115E, R115G, R115I, R115N, R115P, R115Q, R115S, R115V, R115W, R15Y, R16C, R116H, R116T, R116V, R116W, Y117C, Y117H, Y117I, Y117L, Y117M, Y117N, Y117S, Y117W, N118A, N118C, N118E, N118G, N118H, N118I, N118L, N118M, N118P, N118Q, N118T, N118V, N118W, E119C, E119D, E119F, E119K, E119M, E119P, E119R, E119T, E119W, E119Y, A120D, A120G, A120I, A120L, A120T, A120W, F121A, F121C, F121D, F121E, F121K, F121L, F121M, F121P, F121Q, F121R, F121S, F121V, F121Y, S122A, S122C, S122D, S122E, S122F, S122G, S122I, S122L, S122M, S122P, S122V, S122W, S122Y, A123C, A123E, A123F, A123H, A123L, A123T, A123V, A123W, A123Y, I124A, 11124C, 11124G, I124L, I124Y, Y125C, Y125F, Y125G, Y125I, Y125L, Y125P, Y125Q, Y125R, Y125S, Y125T, Y125V, P126C, P126H, P126Y, E131I, E131L, D133K, D133Y, V134S, L136C, L136M, L136Q, L136S, L137P, P138E, P138R, P138T, F139M, F140M, M141A, M141C, M141L, M141P, E142A, E142C, E142L, E142M, E142N, E142P, E142Q, E142S, E142Y, E143I, E143P, K147R, P148W, M151I, M151Q, M151V, Q152A, Q152K, Q152S, D153I, D153K, D153M, D153W, G155F, G155H, G155W, G155Y, 11156C, I156F, I156M, I156Q, I156R, I156S, I156V, P158A, P158G, P158S, N159G, N159T, R160A, R160G, R160H, R160N, R160W, D161G, D161I, D161K, D161L, D161M, D161N, D161Q, D161R, D161S, D161V, D161W, A162G, Q163G, Q163L, Q163M, Q163S, P164A, P164C, P164K, P164L, P164M, P164N, P164R, P164T, P164W, F165G, F165H, F165S, F165W, F165Y, I166L, 166V, A167T, D168A, D168G, D168H, D168P, D168R, D168T, W169A, W169E, W169K, W169M, W169Q, W169R, W169S, W169T, W169V, M170A, M170F, M170V, A171I, Q173N, Q173W, Q173Y, L174Q, L174W, Q175I, Q175Y, P176H, P176K, P176L, P176R, P176W, P176Y, V178A, V178T, V178W, N179H, N179R, N179T, N179V, N179Y, H180G, H180R, H180S, H180 W, D181A, D181H, D181I, D181L, D181Q, D181R, D181S, D181W, S182A, S182E, S182G, S182I, S182K, S182L, S182P, S182Q, S182R, and/or S182T, wherein the numbers in the substitution mutation designations refer to amino acid positions of SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO:31). The increased substrate specificity for, and/or activity with respect to C_{14} substrates can be measured in vitro and/or in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which has a preference for ester substrates (e.g., acyl-PNP) over thioester substrates (e.g., acyl-CoA), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the

precursor thioesterase is mutated at one or more amino acid positions corresponding to residues selected from 95, 96, 97, 98, 99, 100, 101, 102, 104, 105, 106, 107, 108, 109, and/or 110 of SEQ ID NO: 73. The preference for ester substrates over thioester substrates can be measured in vitro and/or in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which has a preference for ester substrates (e.g., acyl-PNP) over thioester substrates (e.g., acyl-CoA), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated with one or more substitutions selected from V95L, V95M, V95T, K96A, K96L, K96W, K96Y, A97F, A97K, A97S, A97T, A97W, A98E, A98F, A98K, A98L, A98Q, A98W, N99Y, A100K, A100V, E101L, P102S, L104C, M105F, Q106A, Q106C, Q106T, Q106Y, I107A, I107C, I107G, I107L, I107M, I107Q, I107V, R108A, R108C, R108D, R108F, R108I, R108L, R108S, R108V, R108W, R108Y, L109M, L109V, P110A, P110F, P110H, P110N, P110V, and/or P110 W, wherein the numbers in the substitution mutation designations refer to amino acid positions of SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO:31). The preference for ester substrates over thioester substrates can be measured in vitro and/or in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which has a preference for thioester substrates (e.g., acyl-CoA) over ester substrates (e.g., acyl-PNP), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to residues selected from 95, 96, 97, 101, 102, 103, 104, 105, 107, 109, and/or 110 of SEQ ID NO: 73. The preference for thioester substrates over ester substrates can be measured in vitro and/or in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which has a preference for thioester substrates (e.g., acyl-CoA) over ester substrates (e.g., acyl-PNP), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated with one or more substitutions selected from V95E, V95I, V95W, V95Y, K96P, A97E, A97M, E101P, P102D, P102K, P102Y, L103E, L103K, L103N, L104A, L104D, L104E, L104N, L104Q, L104W, L104Y, M105W, I107E, I107K, I107P, L109A, L109C, L109D, L109E, L109G, L109K, L109N, L109P, L109Q, L109S, L109T, L109Y, and/or P110R, wherein the numbers in the substitution mutation designations refer to amino acid positions of SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO:31). The preference for thioester substrates over ester substrates can be measured in vitro and/or in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of producing an increased proportional or percentage yield of fatty esters over other non-fatty ester products (e.g., free fatty acids and/or fatty acid derivatives other than fatty esters), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to residues of SEQ ID NO:73 selected from 1-14, 22-29, 33-58, 65-100, 103-109, 114-117, 119-121, 127-136, 139-144, 150-151, 155-170, and/or 173-174. The increased proportional or percentage yield of fatty esters over other products (e.g., fatty acid derivatives other than fatty esters) can be observed or determined in vitro and/or in vivo. Preferably, the increased proportional or percentage yield of fatty esters over other products is determined in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of producing an increased proportional or percentage yield of fatty esters over other products (e.g., free fatty acids and/or fatty acid derivatives other than fatty esters), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to residues of SEQ ID NO:73 selected from 1, 2, 4, 5, 6, 7, 8, 12, 13, 14, 22, 23, 24, 25, 26, 28, 29, 33, 34, 35, 36, 37, 38, 39, 40, 41, 44, 45, 46, 47, 49, 50, 53, 58, 65, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 79, 81, 84, 86, 87, 88, 89, 90, 91, 92, 93, 95, 96, 99, 100, 103, 104, 105, 106, 107, 108, 109, 114, 115, 117, 119, 120, 121, 127, 128, 129, 131, 132, 134, 135, 136, 139, 141, 142, 143, 144, 150, 151, 155, 156, 158, 159, 160, 161, 162, 163, 164, 165, 166, 169, 170, 173, and/or 174. The increased proportional or percentage yield of fatty esters over other products (e.g., fatty acid derivatives other than fatty esters) can be observed or determined in vitro and/or in vivo. Preferably, the increased proportional or percentage yield of fatty esters over other products (e.g., fatty acid derivatives other than fatty esters) is determined in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of producing an increased proportional or percentage yield of fatty esters over other products (e.g., free fatty acids and/or fatty acid derivatives other than fatty esters), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated with one or more substitutions selected from A1R, D2H, D2R, L4G, L4M, L5Q, 16A, 16L, L7E, G8A, S12N, A13I, A13L, A13S, A13T, A13W, A13Y, G14K, G14R, G14S, G14T, A22D, A22E, A22H, A22Y, W23Y, P24C, P24G, P24T, A25P, L26C, L26D, L26E, L26G, L26N, N28A, N28M, D29V, S33G, S33M, K34A, K34H, K34M, T35G, T35M, S36A, V37A, V37G, V37H, V37S, V38D, V38G, V38P, N39E, N39Q, N39R, A40M, A40P, S41T, G44F, G44Y, D45P, D45Q, T46W, S47F, Q49I, G50A, G50K, G50M, G50S, R53S, L58D, L58M, L58R, W65L, L67G, V68G, V68M, V68N, E69P, E69Q, L70A, L70E, L70H, G71C, G72A, N73C, N73G, N73L, N73R, N73T, N73V, D74C, D74S, D74W, G75A, G75K, G75L, G75M, L76A, L76F, L76G, L76I, L76M, L76N, L76T, L76W, R77G, F79A, F79M, F79P, P81E, P81W, T84F, T84H, T84Y, Q86P, Q86W, T87M, T87S, T87W, L88C, L88F, L88G, L88H, L88Y, R89G, Q90P, Q90W, I91M, I91S, L92C, L92G, Q93F, Q93P, V95A, V95D, V95E, V95L, V95M, K96P, N99L, N99M, N99S, A100D, A100K, A100L, A100M, A100V, A100Y, L103A, L104A, L104C, L104P, L104Q, L104W, M105A, Q106A, Q106C, Q106T, Q106W, 11107C, I107M, R108E, L109F, L109M, G114F, R115W, Y117P, E119D, E119P, A120P, F121A, F121C, F121W, K127P, L128F, A129L, A129Y, E131A, F132P, V134P, P135A, L136A, F139M, M141A, M141P, E142A, E143P, V144A, W150D, W150E, M151S, G155V, I156K, I156M, P158A, P158G, P158Q, P158S, N159E, N159I, R160H, R160I, R160K, D161G, A162T, A162Y, Q163A, Q163C, Q163E, Q163G, Q163I, Q163M, Q163S, Q163T, Q163V, P164C, F165D, F165S, I166A, I166L, W169M, M170E, M170G, M170N, M170S, Q173P, and/or L174A, wherein the numbers in the substitution mutation designations refer to amino acid positions of SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO:31). The increased

proportional or percentage yield of fatty esters over other products (e.g., fatty acid derivatives other than fatty esters) can be observed or determined in vitro and/or in vivo. Preferably, the increased proportional or percentage yield of fatty esters over other products (e.g., fatty acid derivatives other than fatty esters) is determined in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of producing a decreased proportional or percentage yield of fatty esters over other products (e.g., free fatty acids and/or fatty acid derivatives other than fatty esters) when fatty ester production is undesirable, and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to residues of SEQ ID NO: 73 selected from 3, 5, 15-18, 27-42, 46, 57-68, 77-78, 95-106, 121-123, 152-154, 167, and/or 175-182. The decreased proportional or percentage yield of fatty esters over other products (e.g., fatty acid derivatives other than fatty esters) can be observed or determined in vitro and/or in vivo. Preferably, the decreased proportional or percentage yield of fatty esters over other products (e.g., fatty acid derivatives other than fatty esters) is determined in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of producing a decreased proportional or percentage yield of fatty esters over other products (e.g., free fatty acids and/or fatty acid derivatives other than fatty esters) when fatty ester production is undesirable, and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to residues of SEQ ID NO: 73 selected from 3, 5, 15, 16, 18, 27, 28, 33, 34, 35, 36, 37, 38, 40, 42, 46, 57, 59, 60, 62, 65, 68, 77, 78, 95, 96, 97, 98, 99, 100, 102, 103, 105, 106, 121, 123, 152, 153, 154, 167, 175, 176, 178, 179, 180, 181, and/or 182. The decreased proportional or percentage yield of fatty esters over other products (e.g., fatty acid derivatives other than fatty esters) can be observed or determined in vitro and/or in vivo. Preferably, the decreased proportional or percentage yield of fatty esters over other products (e.g., fatty acid derivatives other than fatty esters) is determined in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of producing a decreased proportional or percentage yield of fatty esters over other products (e.g., free fatty acids and/or fatty acid derivatives other than fatty esters) when production of fatty esters is undesirable, and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated with one or more substitutions selected from T3E, T3G, T3K, T3L, L5C, L5G, Y15A, Y15L, Y15Q, Y15R, Y15V, R16D, R16E, R16G, R16I, R16V, S18E, L27V, N28G, N28I, S33I, S33R, K34R, T35F, T35K, T35L, T35Q, T35V, S36F, S36I, S36L, S36W, V37L, V38E, V38F, V38K, V38L, A40D, A40G, I42T, T46L, L57A, L57F, L57G, L57H, L57K, L57N, L57P, L57R, L57S, L57T, L57V, L57W, L57Y, K59V, Q60E, Q60P, Q62G, W65V, V68L, R77L, G78M, V95F, V95N, K96C, K96L, K96N, K96Q, K96R, K96Y, A97E, A97F, A97R, A97W, A98E, N99A, N99D, A100S, P102I, L103Q, L103W, M105L, Q106G, Q106H, Q106K, Q106S, Q106V, F121P, A123E, Q152D, Q152E, Q152F, Q152H, Q152I, Q152K, Q152L, Q152S, Q152T, Q152Y, D153P, D153V, D154E, A167V, Q175L, P176D, V178K, N179H, N179W, H180E, H180L, H180P, H180R, D181C, D181E, S182K, S182L, S182N, S182R, S182T, and/or S182V, wherein the numbers in the substitution mutation designations refer to amino acid positions of SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO:31). The decreased proportional or percentage yield of fatty esters over other products (e.g., fatty acid derivatives other than fatty esters) can be observed or determined in vitro and/or in vivo. Preferably, the decreased proportional or percentage yield of fatty esters over other products (e.g., fatty acid derivatives other than fatty esters) is determined in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of increased and/or improved production of one or more fatty acid derivatives, and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to residues of SEQ ID NO: 73 selected from 2, 4, 11-22, 25-31, 37-45, 49-58, 63-80, 84-130, 136-146, and/or 150-174. An exemplary fatty acid derivative that is produced accordingly is a free fatty acid. The increased and/or improved production of fatty acid derivatives can be measured in vitro and/or in vivo. Preferably, the increased and/or improved production of fatty acid derivatives is measured in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of increased and/or improved production of one or more fatty acid derivatives, and which is a variant of a precursor thioesterase that comprises an analogous sequence of SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to residues of SEQ ID NO: 73 selected from 2, 4, 11, 12, 13, 14, 15, 16, 17, 19, 21, 22, 25, 26, 27, 28, 29, 30, 31, 37, 39, 41, 42, 43, 44, 45, 49, 50, 51, 53, 54, 58, 63, 65, 66, 67, 68, 69, 70, 71, 73, 74, 75, 76, 77, 78, 79, 80, 84, 87, 88, 90, 91, 92, 93, 94, 95, 96, 97, 98, 100, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 115, 117, 118, 119, 120, 121, 122, 124, 127, 128, 129, 130, 136, 137, 138, 139, 140, 141, 143, 144, 145, 146, 150, 151, 152, 154, 155, 156, 158, 162, 163, 166, 167, 169, 170, 173, and/or 174. An exemplary fatty acid derivative that is produced accordingly is a free fatty acid. The increased and/or improved production of a fatty acid derivative can be measured in vitro and/or in vivo. Preferably, the increased and/or improved production of a fatty acid derivative is measured in vivo.

In one embodiment of the invention, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of increased and/or improved production of one or more fatty acid derivatives, and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated with one or more substitutions selected from: D2L, D2P, D2R, L5G, L11I, S12N, S12T, A13N, G14C, G14P, G14S, G14T, G14V, Y15C, Y15I, Y15V, R16T, M17D, M17E, M17N, M17R, M17S, M17V, A19C, A21G, A22L, A22R, A22T, A25P, L26D, L26G, L26W, L27C, L27F, L27W, L27Y, N28I, N28P, D29P, K30P, W31D, W31G, W31N, W31P, W31R, W31S, W31T, V37Y, N39P, S41C, I42D, I42G, S43E, G44K, G44R, G44W, D45G, Q49E, G50A, G50K, G50M, G50Q, L51D, L51T, R53A, R53G, R53L, R53N, R53S, R53V, L54E, L54F, L54G, L54N, L54S, L54W, L58R, P63G, P63M, P63N, P63T, P63W, W65E, W65G, V66G, V66S, L67T, V68S, E69F, E69V, L70C, L70F, L70Q, L70S, L70T, L70V, G71A, N73G, N73L, D74A, D74C, G75A, G75C, G75F, G75R, G75W, L76I, R77A, R77C, R77D, R77F, R77G, R77H, R77K, R77L,

R77N, R77Q, R77S, R77W, G78D, G78E, F79K, Q84G, T84H, T84N, T84Q, T87A, T87F, T87H, T87W, L88A, L88C, L88H, Q90N, Q90W, I91G, I91L, I91M, I91S, L92G, L92N, L92Q, L92S, L92T, L92Y, Q93P, D94P, V95F, V95N, V95Q, K96P, A97C, A97P, A98P, A98V, A100D, A100E, A100Q, A100Y, P102L, P102Q, P102R, L103E, L103K, L104A, L104Q, L104W, L104Y, M105C, M105E, M105F, M105L, Q106D, Q106G, Q106L, Q106V, Q106W, Q106Y, I107A, I107C, I107E, I107G, I107K, I107L, I107Q, I107S, I107T, R108G, L109F, L109V, L109Y, P110A, P110E, P110F, P110G, P110H, P110N, P110S, P110V, A111Y, N112F, N112P, Y113D, Y113E, Y113P, R115W, Y117A, Y117D, Y117E, Y117G, Y117P, Y117Q, N118F, E119P, A120P, F121C, F121L, F121M, F121N, F121Q, F121R, F121V, F121W, F121Y, S122D, S122F, S122L, S122P, S122W, S122Y, I124A, I124G, I124H, I124K, I124R, K127P, L128S, A129I, A129W, A129Y, K130P, L136A, L136D, L136E, L136G, L136K, L136N, L136P, L136Q, L136S, L136T, L137A, L137C, L137H, L137K, L137Q, L137S, L137Y, P138F, F139L, F139M, F140C, F140I, F140L, F140M, F140V, M141T, E143P, V144H, Y145I, L146G, L146P, W150G, W150I, W150V, M151F, M151L, M151R, M151S, M151T, M151W, Q152N, Q152V, Q152Y, D154C, D154E, G155I, I156C, I156K, I156T, I156V, P158G, P158T, A162T, Q163A, Q163C, Q163E, Q163I, Q163S, Q163T, Q163V, I166C, A167E, A167F, A167L, A167N, A167R, A167V, A167Y, W169K, M170N, M170S, Q173D, L174A, L174T, and/or L174W, wherein the numbers in the substitution mutation designations refer to amino acid positions of SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO:31). An exemplary fatty acid derivative produced accordingly is a free fatty acid. The increased and/or improved production of a fatty acid derivative can be measured in vitro and/or in vivo. Preferably, the increased and/or improved production of a fatty acid derivative is measured in vivo.

In one embodiment, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of producing an increased proportional or percentage yield of short-chain (e.g., C_8, C_9, C_{10}, C_{11}, C_{12}, C_{13}, C_{14}) fatty acid derivatives (e.g., short-chain fatty acids, short-chain fatty esters, short-chain fatty alcohols, etc.) vs. other products (e.g., non-short-chain fatty acid derivatives, including, for example, long-chain (e.g., C_{15}, C_{16}, C_{17}, C_{18}, C_{19}, C_{20}) fatty acids, long-chain fatty esters, long-chain fatty alcohols, etc.), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to one or more residues of SEQ ID NO: 73 selected from 13, 16-17, 25-38, 55-67, 78-98, 105-119, 122, 126, 132-145, 153, and/or 161-182. An exemplary short-chain fatty acid derivative is a C_{12} fatty acid derivative. An alternative short-chain fatty acid derivative is a C_{14} fatty acid derivative. In certain circumstances, the increased proportional or percentage yield of short-chain fatty acid derivative can be correlated to a decreased proportional yield of long-chain fatty acid derivatives. The increased proportional or percentage yield of short-chain fatty acid derivatives and/or the corresponding decreased proportional or percentage yield of long-chain fatty acid derivatives can be measured in vitro or in vivo. Preferably, the increased proportional yield of short-chain fatty acid derivatives or the corresponding decreased proportional or percentage yield of long-chain fatty acid derivatives is measured in vivo.

In one embodiment, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of producing an increased proportional or percentage yield of short-chain (e.g., C_8, C_9, C_{10}, C_{11}, C_{12}, C_{13}, C_{14}) fatty acid derivatives (e.g., short-chain fatty acids, short-chain fatty esters, short-chain fatty alcohols, etc.) vs. other products (e.g., non-short-chain fatty acid derivatives, including, for example, long-chain fatty acids, long-chain fatty esters, long-chain fatty alcohols, etc.), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to one or more residues of SEQ ID NO: 73 selected from 13, 16, 17, 25, 29, 31, 35, 36, 38, 55, 57, 58, 59, 61, 62, 63, 64, 65, 66, 67, 78, 79, 82, 83, 84, 85, 86, 87, 89, 90, 93, 94, 95, 96, 97, 98, 105, 106, 108, 111, 113, 114, 117, 119, 122, 126, 132, 135, 136, 139, 142, 144, 145, 153, 161, 162, 165, 168, 173, 175, 176, 178, 179, 180, 181, and/or 182. An exemplary short-chain fatty acid derivative is a C_{12} fatty acid derivative. An alternative short-chain fatty acid derivative is a C_{14} fatty acid derivative. In certain circumstances, the increased proportional or percentage yield of short-chain fatty acid derivatives can be correlated to a decreased proportional yield of long-chain fatty acid derivatives. The increased proportional or percentage yield of short-chain fatty acid derivatives and/or the corresponding decreased proportional or percentage yield of long-chain fatty acid derivatives can be measured in vitro or in vivo. Preferably, the increased proportional yield of short-chain fatty acid derivatives or the corresponding decreased proportional yield of long-chain fatty acid derivatives is measured in vivo.

In one embodiment, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of producing an increased proportional or percentage yield of short-chain (e.g., C_8, C_9, C_{10}, C_{11}, C_{12}, C_{13}, C_{14}) fatty acid derivatives (e.g., short-chain fatty acids, short-chain fatty esters, short-chain fatty alcohols, etc.) vs. other products (e.g., non-short-chain fatty acid derivatives including, for example, long-chain fatty acids, long-chain fatty esters, long-chain fatty alcohols, etc.), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated with one or more substitution selected from: A13V, R16A, M17T, A25S, D29M, W31L, T35Y, S36W, V38S, P55A, P55G, L57I, L58M, L58V, K59E, H61W, Q62M, P63V, R64M, W65L, V66C, L67C, L67M, G78F, G78M, G78R, G78T, G78V, F79K, F79Y, Q82A, Q82M, Q82R, Q83G, Q83K, T84M, T84V, E85A, E85C, E85G, E85Q, E85S, E85T, E85V, E85W, E85Y, Q86H, Q86Y, T87R, R89V, Q90L, Q93M, Q93N, Q93V, D94C, D94L, V95G, K96C, A97N, A97V, A98G, A98Y, M105I, Q106K, Q106R, R108W, A111E, A111N, A11S, A111W, A111Y, Y113A, Y113S, Y113V, G114K, G114Y, Y117R, E119M, E119Q, E119R, S122F, S122I, S122M, S122R, P126K, F132C, F132D, F132K, F132L, F132N, F132V, P135A, P135E, P135K, P135Q, L136H, F139L, E142W, V144Y, Y145A, Y145C, Y145D, Y145E, Y145G, Y145I, Y145L, Y145M, Y145N, Y145R, Y145S, Y145T, D153K, D153Q, D161K, A162I, F165K, D168W, Q173I, Q175M, P176Q, P176R, P176V, V178F, V178G, V178L, V178R, V178S, V178T, N179H, H180E, H180P, H180R, H180S, H180V, H180 W, D181R, D181T, S182C, S182D, S182G, and/or S182R, wherein the numbers in the substitution mutation designations refer to amino acid positions of SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO:31). An exemplary short-chain fatty acid derivative is a C_{12} fatty acid derivative. An alternative short-chain fatty acid derivative is a C_{14} fatty acid derivative. In certain circumstances, the increased proportional or percentage yield of short-chain fatty acid derivatives can be correlated to a decreased proportional yield of long-chain fatty acid derivatives. The increased proportional or percent-

age yield of short-chain fatty acid derivatives and/or the corresponding decreased proportional yield of long-chain fatty acid derivatives can be measured in vitro or in vivo. Preferably, the increased proportional yield of short-chain fatty acid derivatives or the corresponding decreased proportional yield of long-chain fatty acid derivatives is measured in vivo.

In one embodiment, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of producing a decreased proportional or percentage yield of short-chain (e.g., C_8, C_9, C_{10}, C_{11}, C_{12}, C_{13}, C_{14}) fatty acid derivatives (e.g., short-chain fatty acids, short-chain fatty esters, short-chain fatty alcohols, etc.) vs. other products (e.g., non-short-chain fatty acid derivatives including, for example, long-chain (e.g., C_{15}, C_{16}, C_{17}, C_{18}, C_{19}, C_{20}) fatty acids, long-chain fatty esters, long-chain fatty alcohols, etc.), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to one or more residues of SEQ ID NO: 73 selected from 1-31, 36-81, 84-159, 162-177, and/or 181. An exemplary short-chain fatty acid derivative is a C_{12} fatty acid derivative. An alternative short-chain fatty acid derivative is a C_{14} fatty acid derivative. In certain circumstances, the decreased proportional or percentage yield of short-chain fatty acid derivatives can be correlated to an increased proportional yield of long-chain fatty acid derivatives. The decreased proportional or percentage yield of short-chain fatty acid derivatives and/or the corresponding increased proportional yield of long-chain fatty acid derivatives can be measured in vitro or in vivo. Preferably, the decreased proportional yield of short-chain fatty acid derivatives or the corresponding increased proportional yield of short-chain fatty acid derivatives is measured in vivo.

In one embodiment, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of producing a decreased proportional or percentage yield of short-chain (e.g., C_8, C_9, C_{10}, C_{11}, C_{12}, C_{13}, C_{14}) fatty acid derivatives (e.g., short-chain fatty acids, short-chain fatty esters, short-chain fatty alcohols, etc.) vs. other products (e.g., non-short-chain fatty acid derivatives including, for example, long-chain fatty acids, long-chain fatty esters, long-chain fatty alcohols, etc.), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated at one or more amino acid positions corresponding to one or more residues of SEQ ID NO: 73 selected from 1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 12, 13, 14, 15, 16, 17, 18, 19, 21, 22, 23, 24, 26, 27, 30, 31, 36, 37, 38, 42, 44, 45, 46, 47, 48, 50, 51, 52, 53, 54, 55, 57, 61, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 81, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 99, 100, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 117, 118, 119, 120, 121, 122, 124, 125, 127, 128, 129, 130, 131, 132, 133, 134, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 162, 163, 165, 166, 167, 168, 170, 171, 173, 174, 175, 176, 177, and/or 181. An exemplary short-chain fatty acid derivative is a C_{12} fatty acid derivative. An alternative short-chain fatty acid derivative is a C_{14} fatty acid derivative. In certain circumstances, the decreased proportional or percentage yield of short-chain fatty acid derivatives can be correlated to an increased proportional yield of long-chain fatty acid derivatives. The decreased proportional or percentage yield of short-chain fatty acid derivatives and/or the corresponding increased proportional yield of long-chain fatty acid derivatives can be measured in vitro or in vivo. Preferably, the decreased proportional yield of short-chain fatty acid derivatives or the corresponding increased proportional yield of short-chain fatty acid derivatives is measured in vivo.

In one embodiment, a mutant thioesterase (or a naturally-occurring equivalent thereof) is provided, which is capable of producing a decreased proportional or percentage yield of short-chain (e.g., C_8, C_9, C_{10}, C_{11}, C_{12}, C_{13}, C_{14}) fatty acid derivatives (e.g., short-chain fatty acids, short-chain fatty esters, short-chain fatty alcohols, etc.) vs. other products (e.g., non-short-chain fatty acid derivatives including, for example, long-chain fatty acids, long-chain fatty esters, long-chain fatty alcohols, etc.), and which is a variant of a precursor thioesterase that comprises an analogous sequence to SEQ ID NO:31 in FIG. **57**, wherein the precursor thioesterase is mutated with one or more substitution selected from: A1C, A1F, A L, A1Y, D2L, D2M, D2P, D2W, T3R, L4A, L4M, L4N, L4S, L4V, L4Y, L5E, L5F, L5G, L5K, L5N, L5S, L5W, 16T, L7A, L7E, L7K, L7M, L7W, G8K, D9N, D9T, L11A, L11C, L11I, L11M, L11Q, L11V, S12I, S12L, S12M, S12N, S12T, S12V, S12Y, A13C, G14C, G14E, G14I, G14M, G14N, G14P, G14S, G14T, G14V, Y15C, Y15E, Y15G, Y15I, Y15N, Y15V, R16T, M17D, M17E, M17G, M17L, M17N, M17P, M17R, M17S, M17V, S18M, S18N, S18T, A19E, A19L, A19V, A21P, A22D, A22E, A22F, A22H, A22I, A22K, A22L, A22P, A22R, A22S, A22T, A22Y, W23A, W23H, W23N, W23P, P24A, P24C, P24D, P24E, P24F, P24G, P24I, P24M, P24N, P24S, P24T, P24V, P24W, L26P, L27A, L27C, L27F, L27H, L27R, L27S, L27T, L27W, L27Y, K30P, W31D, W31P, W31R, S36F, S36L, V37G, V37H, V37N, V37Q, V37W, V37Y, V38P, N39E, N39G, N39K, N39M, N39P, N39Q, N39Y, I42D, I42G, I42P, G44A, G44E, G44K, G44M, G44N, G44R, G44S, G44W, G44Y, D45G, D45M, T46D, S47E, S47P, S47Q, S47R, S47Y, Q48Y, G50C, G50E, G50F, G50I, G50K, G50L, G50M, G50N, G50P, G50Q, G50R, G50S, G50T, G50W, G50Y, L51D, L51P, L51T, A52P, R53A, R53C, R53D, R53E, R53F, R53G, R53I, R53K, R53L, R53N, R53S, R53T, R53V, R53W, R53Y, L54C, L54E, L54G, L54N, L54Y, P55Y, L57P, H61A, H61D, H61E, P63D, P63E, P63G, P63K, P63M, P63N, P63Q, P63R, R64L, W65G, W65P, W65R, V66N, V66Q, V66S, V66W, V66Y, L67E, L67G, L67Q, L67R, L67S, L67W, V68E, V68G, V68N, V68P, V68Q, E69A, E69C, E69D, E69F, E69G, E69H, E69K, E69L, E69M, E69N, E69P, E69Q, E69S, E69V, E69W, E69Y, L70A, L70C, L70E, L70F, L70G, L70H, L70K, L70Q, L70S, L70T, L70W, G71C, G71S, G72A, G72M, G72P, N73A, N73G, N73H, N73I, N73L, N73P, N73R, N73S, N73T, N73W, D74A, D74C, D74F, D74G, D74Q, D74S, D74W, D74Y, G75A, G75C, G75D, G75E, G75F, G75I, G75K, G75L, G75M, G75N, G75P, G75R, G75T, G75V, G75W, G75Y, L76A, L76C, L76D, L76E, L76F, L76G, L76I, L76K, L76M, L76N, L76P, L76Q, L76R, L76T, L76V, L76W, R77A, R77C, R77D, R77E, R77F, R77G, R77H, R77N, R77S, R77V, R77W, G78A, G78C, G78D, G78E, G78N, G78P, G78Q, G78Y, F79P, F79Q, F79S, F79V, P81E, P81W, T84D, T84E, T84G, T84H, T84K, T84L, T84N, T84Q, T84R, T84W, T84Y, E85F, E85P, Q86A, T87F, L88A, L88E, L88G, L88H, L88Q, L88S, L88W, L88Y, R89P, Q90P, Q90W, I91E, I91L, I91M, I91N, I91Q, I91S, I91Y, L92C, L92E, L92G, L92H, L92N, L92Q, L92R, L92S, L92Y, Q93P, D94P, D94V, V95A, V95C, V95D, V95E, V95F, V95I, V95P, V95Q, V95W, V95Y, K96P, A97C, A97P, N99D, A100Q, A100Y, P102E, P102G, P102H, P102L, P102R, P102V, P102W, L103C, L103E, L103I, L103K, L103N, L103R, L103S, L103T, L103V, L104A, L104C, L104E, L104G, L104I, L104N, L104P, L104Q, L104S, L104W, L104Y, M105A, M105C, M105E, M105F, M105G, M105K, M105L, M105P, M105T, M105W, Q106D, Q106G, Q106H, Q106L, Q106W, I107A, I107E, 11107F, I107G, I107K,

I1107L, I107Q, I107S, I107T, I107Y, R108A, R108C, R108D, R108E, R108F, R108G, R108H, R108I, R108L, R108M, R108S, R108V, R108Y, L109C, L109F, L109G, L109K, L109Q, L109R, L109T, L109V, L109Y, P110A, P110C, P110D, P110E, P110F, P110G, P110H, P110K, P110L, P110M, P110N, P110R, P110S, P110V, P110W, A111C, A111L, A11P, A111Q, A111R, A111V, N112I, N112L, N112P, N112Y, Y113D, Y113E, Y113Q, G114A, R115W, Y117D, Y117G, Y117P, N118F, E119C, E119L, A120P, F121A, F121C, F121D, F121E, F121G, F121K, F121L, F121N, F121P, F121Q, F121R, F121S, F121V, F121W, F121Y, S122D, S122E, S122L, S122P, 11124D, I124E, I124G, I124H, I124K, I124R, I124W, I124Y, Y125C, Y125G, Y125H, Y125I, Y125L, Y125P, Y125Q, Y125R, Y125S, Y125T, Y125V, K127A, L128E, L128F, L128G, L128K, L128Q, L128R, L128S, L128W, A129D, A129F, A129L, A129W, A129Y, K130P, K130V, E131A, E131C, E131D, E131P, E131V, F132P, D133C, V134C, V134D, V134N, V134P, V134W, L136A, L136D, L136E, L136G, L136N, L136P, L136T, L137D, L137E, L137G, L137H, L137K, L137P, L137Q, L137R, L137S, P138G, P138N, P138V, F139A, F139C, F139D, F139E, F139G, F139H, F139M, F139N, F139S, F139T, F139V, F139W, F140A, F140C, F140G, F140I, F140L, F140M, F140N, F140P, F140S, F140T, F140V, F140 W, M141C, M141D, M141E, M141F, M141G, M141K, M141L, M141P, M141Q, M141R, M141T, M141W, M141Y, E142A, E142C, E142G, E142I, E142L, E142M, E142P, E142Q, E142R, E142T, E142V, E143A, E143D, E143F, E143G, E143I, E143M, E143P, E143W, V144A, V144D, V144E, V144G, V144H, V144N, V144P, V144Q, V144R, V144S, Y145Q, Y145W, L146C, L146P, W150P, W150R, M151A, M151C, M151D, M151E, M151F, M151G, M151I, M151L, M151Q, M151R, M151S, M151T, M151V, M151W, Q152P, D153A, D153E, D153F, D154A, D154C, D154E, D154F, D154G, D154H, D154I, D154K, D154L, D154M, D154N, D154P, D154R, D154S, D154T, D154V, D154W, G155A, G155P, G155V, 11156A, I156C, 11156E, I156F, I156G, I156K, I156M, I156Q, I156R, I156S, 156T, I156Y, H157C, H157E, P158F, P158H, P158I, P158L, P158Q, P158V, P158W, N159P, N159W, A162K, A162L, A162N, A162R, A162Y, Q163A, Q163D, Q163E, Q163F, Q163I, Q163V, Q163W, Q163Y, F165L, I166A, I166F, I166M, I166S, I166Y, A167C, A167D, A167E, A167F, A167L, A167N, A167R, A167V, A167W, A167Y, D168M, D168R, M170E, M170F, M170G, M170N, M170S, M170T, A171S, Q173D, Q173P, L174A, L174G, L174S, L174T, L174W, L174Y, Q175F, P176L, P176Y, L177F, L177M, L177S, D181C, D181E, and/or D181G, wherein the numbers in the substitution mutation designations refer to amino acid positions of SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO:31). An exemplary short-chain fatty acid derivative is a C_{12} fatty acid derivative. An alternative short-chain fatty acid derivative is a C_{14} fatty acid derivative. In certain circumstances, the decreased proportional or percentage yield of short-chain fatty acid derivatives can be correlated to an increased proportional yield of long-chain fatty acid derivatives. The decreased proportional or percentage yield of short-chain fatty acid derivatives and/or the corresponding increased proportional yield of long-chain fatty acid derivatives can be measured in vitro or in vivo. Preferably, the decreased proportional yield of short-chain fatty acid derivatives or the corresponding increased proportional yield of short-chain fatty acid derivatives is measured in vivo.

In one embodiment of the invention, a polynucleotide (or a gene) encoding a mutant thioesterase (or a naturally-occurring equivalent thereof) of the invention is provided. In another embodiment of the invention, a vector is provided comprising the polynucleotide (or the gene) according to the invention.

In one embodiment of the invention, the precursor thioesterase is encoded by a gene that is selectively hybridizable to the polynucleotide sequence of 'tesA, or an ortholog, paralog or homolog thereof. FIG. **55** lists GenBank Accession Numbers of protein homologs of 'TesA having at least 40% amino acid sequence identity to 'TesA. The precursor thioesterase can be encoded by a polynucleotide that is selectively hybridizable under conditions of intermediate stringency, under high stringency, or under maximum stringency.

In one embodiment of the invention, a polynucleotide encoding a precursor thioesterase is provided wherein the precursor thioesterase comprises the amino acid sequence of 'TesA, an ortholog thereof, a paralog thereof, or a homolog thereof. For example, the precursor thioesterase comprises the amino acid sequence of a 'TesA obtained from an *E. coli*, such as an *E. coli* K12. In a particular embodiment, a polynucleotide encoding the precursor thioesterase is provided wherein the precursor thioesterase comprises the amino acid sequence, a variant, or a fragment of SEQ ID NO:31 of FIG. **57**. In a particular embodiment, the gene encoding the precursor thioesterase comprises the polynucleotide sequence of SEQ ID NO:32 in FIG. **58**, or a fragment thereof.

In one embodiment of the invention, a polynucleotide encoding a precursor thioesterase is provided wherein the precursor thioesterase comprises a protein having at least about 20%, for example, at least about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the sequence SEQ ID NO:31 of FIG. **57**. In one embodiment, a polynucleotide encoding a precursor thioesterase is provided wherein the precursor thioesterase comprises a protein having at least about 20%, for example, at least about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the sequence of an *E. coli* K12 'TesA. In one embodiment of the invention, a polynucleotide is provided, which comprises a sequence having at least about 20%, for example, at least about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO:32 in FIG. **58**.

In one embodiment of the invention, a vector is provided that comprises a gene (or a polynucleotide) encoding a mutant thioesterase or a naturally-occurring equivalent thereof. Vectors according to the invention can be transformed into suitable host cells to produce recombinant host cells.

In one embodiment of the invention, a probe is provided that comprises a polynucleotide of about 4 to about 150 nucleotides long, which is substantially identical to a corresponding fragment of SEQ ID NO:32 in FIG. **58**, wherein the probe is useful for detecting and/or identifying polynucleotide sequences encoding enzymes that have thioesterase activity. A probe according to the invention can be used to detect and isolate potential precursor thioesterases from sources not known to produce such precursor thioesterases or for which the amino acid or nucleic sequence is unknown.

In certain embodiments of the invention, a recombinant host cell is provided comprising a polynucleotide encoding a mutant thioesterase or a naturally-occurring equivalent thereof. In one embodiment, known genomic alteration or modification techniques can be employed to alter or modify the endogenous thioesterases of the host cell, effectuating one

or more of the aforementioned mutations, such that at least one of the mutant endogenous thioesterases has at least one altered property. In another embodiment, the recombinant host cell is engineered to include a plasmid comprising a polynucleotide encoding a mutant thioesterase or a naturally-occurring equivalent thereof. In yet another embodiment, the recombinant host cell expresses the thioesterase after the polynucleotide encoding the thioesterase is integrated into the chromosome of the host cell.

In one embodiment of the invention, the recombinant host cell of the invention can be selected from any cell capable of expressing a recombinant gene construct, and can be selected from a microbial, plant or animal cell. In a particular embodiment, the host cell is bacterial, cyanobacterial, fungal, yeast, algal, human or mammalian in origin. In a particular embodiment, the host cell is selected from any of Gram positive bacterial species such as *Actinomycetes; Bacillaceae*, including *Bacillus alkalophilus, Bacillus subtilis, Bacillus licheniformis, Bacillus lentos, Bacillus brevis, Bacillus stearothennophilus, Bacillus alkalophilus, Bacillus amyloliquefaciens, Bacillus coagulans, Bacillus circulans, Bacillus lautus, Bacillus megaterium, B. thuringiensis; Brevibacteria* sp., including *Brevibacterium flavum, Brevibacterium lactofermentum, Brevibacterium ammoniagenes, Brevibacterium butanicum, Brevibacterium divaricatum, Brevibacterium healii, Brevibacterium ketoglutamicum, Brevibacterium ketosoreductum, Brevibacterium lactofermentum, Brevibacterium linens, Brevibacterium paraffinolyticum; Corynebacterium* spp. such as *C. glutamicum* and *C. melassecola, Corynebacterium herculis, Corynebacterium lilium, Corynebactertium acetoacidophilum, Corynebacterium acetoglutamicum, Corynebacterium acetophilum, Corynebacterium ammoniagenes, Corynebacterium fujiokense, Corynebacterium nitrilophilus*; or lactic acid bacterial species including *Lactococcus* spp. such as *Lactococcus lactis; Lactobacillus* spp. including *Lactobacillus reuteri; Leuconostoc* spp.; *Pediococcus* spp.; *Serratia* spp. such as *Serratia marcescens; Streptomyces* species, such as *Streptomyces lividans, Streptomyces murinus, S. coelicolor* and *Streptococcus* spp. Alternatively, strains of a Gram negative bacterial species belonging to *Enterobacteriaceae* including *E. coli, Cellulomonas* spp.; or to *Pseudomonadaceae* including *Pseudomonas aeruginosa, Pseudomonas alcaligenes, Pseudomonas fluorescens, Pseudomonas putida, Pseudomonas syringae* and *Burkholderia cepacia, Salmonella* sp., *Stenotrophomonas* spp., and *Stenotrophomonas maltophilia*. Oleaginous microorganisms such as *Rhodococcus* spp, *Rhodococcus opacus, Ralstonia* spp., and *Acetinobacter* spp. are useful as well. Furthermore, yeasts and filamentous fungal strains can be useful host cells, including *Absidia* spp.; *Acremonium* spp.; *Agaricus* spp.; *Anaeromyces* spp.; *Aspergillus* spp., including *A. aculeates, A. awamori, A. flavus, A. foetidus, A. fumaricus, A. fumigatus, A. nidulans, A. niger, A. oryzae, A. terreus; A. tubingensis* and *A. versicolor; Aeurobasidium* spp.; *Cephalosporum* spp.; *Chaetomium* spp.; *Coprinus* spp.; *Dactyllum* spp.; *Fusarium* spp., including *F. conglomerans, F. decemcellulare, F. javanicum, F. lini, F. oxysporum* and *F. solani; Gliocladium* spp.; *Kluyveromyces* sp.; *Hansenula* sp.; *Humicola* spp., including *H. insolens* and *H. lanuginosa; Hypocrea* spp.; *Mucor* spp.; *Neurospora* spp., including *N. crassa* and *N. sitophila; Neocallimastix* spp.; *Orpinomyces* spp.; *Penicillium* spp.; *Phanerochaete* spp.; *Phlebia* spp.; *Pichia* sp.; *Piromyces* spp.; *Rhizopus* spp.; *Rhizomucor* species such as *Rhizomucor miehei; Schizophyllum* spp.; *Schizosaccharomyces* such as, for example, *S. pombe* species; *chytalidium* sp., *Sulpholobus* sp., *Thermoplasma* sp., *Thermomyces* sp.; *Trametes* spp.; *Trichoderma* spp., including *T. reesei, T. reesei* (*longibrachiatum*) and *T. viride; Yarrowinia* sp.; and *Zygorhynchus* spp and in particular include oleaginous yeast just *Phafia* spp., *Rhorosporidium toruloides* Y4, *Rhodotorula Glutinis* and *Candida* 107.

In one embodiment of the invention, a recombinant host cell is provided, which expresses or overexpresses a gene encoding the mutant thioesterase (or a naturally-occurring equivalent thereof), and which also expresses (or overexpresses) one or more genes encoding one or more enzymes that utilize, as a substrates, reaction products of the mutant thioesterase (e.g., fatty acids, fatty acyl-CoAs, fatty acyl-phosphate esters, fatty aldehydes, fatty esters, or fatty alcohols) or reaction products of one or more other enzymes that are parts of a metabolic pathway, including reaction products of the mutant thioesterase (e.g., fatty acids) as precursors and/or substrates.

In one embodiment of the invention, a recombinant host cell is provided, which expresses or overexpresses a gene encoding a mutant thioesterase (or a naturally-occurring equivalent thereof) and which also expresses (or overexpresses) one or more genes encoding one or more enzymes that react with a substrate that is necessary as a precursor to a reaction in a fatty acid biosynthetic pathway. In a particular embodiment, the recombinant host cell includes a gene that encodes thioesterase and a gene that encodes an enzyme that reacts with a substrate that is necessary as a precursor to a reaction in a fatty acid synthetic pathway, which comprises the overexpression or modification of a gene selected from pdh, panK, aceEF, fabH, fabD, fabG, acpP, and/or fabF.

In one embodiment of the invention, the recombinant host cell comprises a gene (or a polynucleotide) that encodes a mutant thioesterase (or a naturally-occurring equivalent thereof) and also comprises the attenuation or deletion of a gene that reduces carbon flowthrough, or a gene that competes for substrates, cofactors, or energy requirements within a fatty acid biosynthetic pathway. In a particular embodiment, the attenuated gene comprises at least one of fadE, gpsA, ldhA, pflB, adhE, pta, poxB, ackA, ackB, plsB, and/or sfa.

In one embodiment of the invention, a recombinant host cell comprises a gene (or a polynucleotide) encoding a mutant thioesterase (or a naturally-occurring equivalent thereof) and a heterologously-introduced exogenous gene encoding at least one fatty acid derivative enzyme. In certain embodiments, the exogenous gene or polynucleotide encodes, for example, an acyl-CoA synthase, an ester synthase, an alcohol acyltransferase, an alcohol dehydrogenase, an acyl-CoA reductase, a fatty-alcohol-forming acyl-CoA reductase, a carboxylic acid reductase, a decarboxylase, an aldehyde reductase, a fatty alcohol acetyl transferase, an acyl condensing enzyme, an aminotransferase, or a decarbonylase.

In one embodiment of the invention, the recombinant host cell comprises a gene encoding a mutant thioesterase (or a naturally-occurring equivalent thereof) and at least two heterologously-introduced exogenous genes encoding fatty acid derivative enzymes. In certain embodiments, the exogenous genes or polynucleotides encode, for example, an acyl-CoA synthase, an ester synthase, an alcohol acyltransferase, an alcohol dehydrogenase, an acyl-CoA reductase, a fatty-alcohol-forming acyl-CoA reductase, a carboxylic acid reductase, a decarboxylase, an aldehyde reductase, a fatty alcohol acetyl transferase, an acyl condensing enzyme, an aminotransferase, or a decarbonylase.

In a preferred embodiment of the invention, a gene encoding the mutant thioesterase (or a naturally-occurring equivalent thereof) and/or a fatty acid derivative enzyme, for example, an acyl-CoA synthase, an ester synthase, an alcohol acyltransferase, an alcohol dehydrogenase, an acyl-CoA

reductase, a fatty-alcohol forming acyl-CoA reductase, a carboxylic acid reductase, a decarboxylase, an aldehyde reductase, a fatty alcohol acetyl transferase, an acyl condensing enzyme, an alcohol acetyltransferase, an aminotransferase, an additional thioesterase or a decarbonylase that is overexpressed.

In one embodiment of the invention, genes encoding mutant thioesterases (or naturally-occurring equivalents thereof), fatty acid derivative enzymes and/or other recombinantly expressed genes in a recombinant host cell are modified to optimize at least one codon for expression in the recombinant host cell.

In one embodiment of the invention, the recombinant host cell comprises at least one gene encoding a mutant thioesterase (or a naturally-occurring equivalent thereof) and a gene encoding an acyl-CoA synthase. The acyl-CoA synthase can be any of fadD, fadK, BH3103, yhfL, Pfl-4354, EAV15023, fadD1, fadD2, RPC_4074, fadDD35, fadDD22, faa3p, or the gene encoding the protein ZP_01644857. Other examples of acyl-CoA synthase genes include fadDD35 from *M. tuberculosis* HR7Rv [NP_217021], yhfL from *B. subtilis* [NP_388908], fadD1 from *P. aeruginosa* PAO1 [NP_251989], the gene encoding the protein ZP_01644857 from *Stenotrophomonas maltophilia* R551-3, or faa3p from *Saccharomyces cerevisiae [NP_*012257].

In one embodiment of the invention, a recombinant host cell is provided comprising at least one gene or polynucleotide encoding a mutant thioesterase (or a naturally-occurring equivalent thereof) and a gene or polynucleotide encoding an ester synthase, such as an ester synthase gene obtained from *Acinetobacter* spp., *Alcanivorax borkumensis, Arabidopsis thaliana, Saccharomyces cerevisiae, Homo sapiens, Simmondsia chinensis, Mortierella alpina, Cryptococcus curvatus, Alcanivorax jadensis, Alcanivorax borkumensis, Acinetobacter* sp. HO1-N, or *Rhodococcus opacus*. Examples of ester synthase genes include wax/dgat, encoding a bifunctional ester synthase/acyl-CoA: diacylglycerol acyltransferase from *Simmondsia chinensis, Acinetobacter* sp. strain ADP1, *Alcanivorax borkumensis, Pseudomonas aeruginosa, Fundibacter jadensis, Arabidopsis thaliana*, or *Alkaligenes eutrophus*. In a preferred embodiment, the gene encoding the ester synthase is overexpressed.

In one embodiment of the invention, the recombinant host cell comprises at least one gene encoding a fatty aldehyde biosynthetic enzyme. A fatty aldehyde biosynthetic gene can be, for example, a carboxylic acid reductase gene (e.g., a car gene), having a polynucleotide sequence and/or polypeptide motif listed in FIGS. **32** and **33**, or a variant thereof. In some instances, the fatty aldehyde biosynthetic gene encodes one or more of the amino acid motifs depicted in FIG. **33**.

In one embodiment of the invention, the recombinant host cell comprises at least one fatty alcohol production gene. Fatty alcohol production genes include, for example, acrl. Fatty alcohol production genes are described in, for example, PCT Publication Nos. 2008/119082 and 2007/136762, the disclosures of which are herein incorporated by reference.

In one embodiment of the invention, the recombinant host cell comprises a gene encoding a mutant thioesterase (or a naturally-occurring equivalent thereof) and a gene encoding at least one olefin producing gene. The gene may be a terminal olefin producing gene or an internal olefin producing gene. As examples of terminal olefin producing genes, those described in PCT Publication No. 2009/085278, including orf880, are appropriate. As examples of internal olefin producing genes, those described in PCT Publication No. 2008/147781 A2 are appropriate. The disclosures of PCT Publication Nos. 2009/085278 and 2008/147781 A2 are herein incorporated by reference.

In one embodiment of the invention, a recombinant host cell is provided comprising at least one gene or polynucleotide encoding a mutant thioesterase (or a naturally-occurring equivalent thereof), and at least one of (a) a gene or polynucleotide encoding a fatty acid derivative enzyme and (b) a gene or polynucleotide encoding an acyl-CoA dehydrogenase enzyme that is attenuated. Preferably that gene encoding a fatty acid derivative enzyme that is attenuated or deleted is endogenous to the host cell, encoding, for example, an acyl-CoA synthase, an ester synthase, an alcohol acyltransferase, an alcohol dehydrogenase, an acyl-CoA reductase, a carboxylic acid reductase, a decarbonylase, a fatty alcohol acetyl transferase, a fatty acid decarboxylase, or a fatty-alcohol-forming acyl-CoA reductase. In one embodiment, the attenuated gene encodes an acyl-CoA synthase or an ester synthase.

In one embodiment of the invention, a recombinant host cell is provided that expresses, or preferably overexpresses, a thioesterase enzyme under conditions that result in the direct synthesis of fatty esters from acyl-ACP or acyl-CoA, such as fatty acid methyl esters (FAME) and fatty acid ethyl esters (FAEE), by such thioesterase. In this embodiment, the thioesterase directly converts acyl-ACP or acyl-CoA to fatty ester without necessarily expressing an enzyme that is a fatty acyl CoA synthase or an ester synthase to produce fatty esters. Nonetheless, while expression or overexpression of a fatty acyl-CoA synthase or ester synthase is unnecessary, such enzymes may be desirable to increase product yields. In this embodiment, the thioesterase enzyme can be any of an endogenous thioesterase, a heterologously-expressed thioesterase, a mutant thioesterase, or a naturally-occurring equivalent thereof.

In one embodiment of the invention, the recombinant host cell has an endogenous gene encoding an acyl-CoA dehydrogenase enzyme that is deleted or attenuated.

In one embodiment of the invention, a method is provided wherein the recombinant host cell according to the invention is cultured under conditions that permit expression or overexpression of one or more thioesterase enzymes, which can be selected from endogenous thioesterases, heterologously-expressed thioesterases, mutant thioesterases (or naturally-occurring equivalents thereof), or a combination of these thioesterases. In a particular embodiment, the thioesterase enzyme that is expressed or overexpressed can be recovered, and more preferably substantially purified, after the host cell is harvested and/or lysed.

In one embodiment of the invention, a method is provided wherein the recombinant host cell according to the invention is cultivated under conditions that permit production of fatty acid derivatives. In a preferred embodiment, the fatty acid derivative can be recovered, and more preferably the fatty acid derivative is substantially purified. In a particularly preferred embodiment, the fatty acid derivative composition is substantially purified from other components produced during cultivation by centrifugation.

In one aspect of the invention, a method is provided for producing a fatty acid derivative, comprising cultivating a recombinant host cell of the invention under conditions suitable to ensure expression or overexpression of a mutant thioesterase (or a naturally-occurring equivalent thereof), and recovering the fatty acid derivative that is produced.

In one embodiment, a method is provided for extracellularly producing a fatty acid derivative in vitro, comprising cultivating a recombinant host cell under conditions suitable for expression or overexpression of a thioesterase enzyme

(including, for example, an endogenous thioesterase, a heterologously-expressed thioesterase, a mutant thioesterase, or a naturally-occurring equivalent thereof), harvesting the cells, and lysing the cells, such that the thioesterase enzyme that is produced can be recovered and used to produce fatty acid derivatives in vitro. In an exemplary embodiment, the thioesterase enzyme is substantially purified. In another exemplary embodiment, the thioesterase enzyme is not purified from the cell lysate. The purified thioesterase enzyme or the cell lysate comprising such an enzyme can then be subject to suitable thioesterase substrates under conditions that allow the production of fatty acid derivatives extracellularly. Techniques for introducing substrates to enzymes are well known in the art. A non-limiting example is adding the substrate(s) in a solution form to the enzyme solution or the cell lysate, and allowing the mixture to incubate. Another non-limiting example involves incubating the substrate(s) and enzyme solution or cell lysate by either attaching the substrate(s) or the enzyme to a solid medium (e.g., beads, resins, plates, etc.) and pass the enzyme solution/lysate or the substrate(s), respectively through the solid medium in a speed that allows for sufficient contact between the substrate(s) and the enzyme.

In another embodiment of the invention, a method is provided for producing a fatty acid derivative, which comprises cultivating a recombinant host cell under conditions suitable to ensure expression of a thioesterase enzyme (including, for example, an endogenous thioesterase, a heterologously-expressed thioesterase, a mutant thioesterase, or a naturally-occurring equivalent thereof), and recovering the fatty acid derivative that is secreted or released extracellularly. Accordingly, the fatty acid derivative product is recovered from, for example, the supernatant of a fermentation broth wherein the host cell is cultured.

In one embodiment of the invention, a method is provided for obtaining a fatty acid derivative composition extracellularly by cultivating a recombinant host cell that has been transformed with a polynucleotide encoding a thioesterase enzyme (including, for example, an endogenous thioesterase, a heterologous thioesterase, a mutant thioesterase, or a naturally-occurring equivalent thereof), cultivating under conditions that permit production of a fatty acid derivative, a major or minor portion of which is secreted or released extracellularly, and recovering the fatty acid derivative that is produced. In an exemplary embodiment, the fatty acid derivative is produced within the cell, but a portion of it is released by the host cell. Accordingly, the method further comprises harvesting the cells, lysing the cells, and recovering the fatty acid derivative.

In one embodiment of the invention, a method of producing fatty acid derivatives is provided wherein a recombinant host cell that expresses, or preferably overexpresses, a thioesterase enzyme under conditions that result in the synthesis of fatty esters from acyl-ACP or acyl-CoA by such thioesterase is cultured under conditions that permit such direct production of fatty esters.

In one embodiment of the invention, a method of producing fatty acid derivatives is provided comprising: modifying one or more endogenous thioesterases of the host cell using suitable genomic alteration techniques such that the endogenous thioesterases comprise one or more mutations and have one or more altered properties, as compared to the endogenous thioesterase precursors; and cultivating the host cell under conditions suitable for said host cell to express or overexpress such mutant thioesterases; and recovering the fatty acid derivatives. In an exemplary embodiment, the fatty acid derivative that is produced can be secreted or released extracellularly, such that it can be recovered from, for example, the supernatant of the fermentation broth wherein the host cell is cultured.

In one embodiment of the invention, a method of producing fatty acid derivatives is provided comprising: transforming the host cell with a polynucleotide sequence encoding a mutant thioesterase (or a naturally-occurring equivalent thereof), such that the production of fatty acid derivatives in the host cell is altered relative to a cell that has not been transformed with the mutant thioesterase gene (or a naturally-occurring equivalent thereof).

In one embodiment of the invention, a method of producing fatty acid derivatives is provided comprising: providing a polynucleotide sequence comprising a gene encoding a mutant thioesterase (or a naturally-occurring equivalent thereof); transforming a suitable host cell under conditions wherein said polynucleotide sequence is incorporated into said chromosome of said cell and said gene is expressible within said host cell; cultivating the transformed host cell under conditions suitable for said host cell to express said gene and produce a mutant thioesterase protein (or a naturally-occurring equivalent thereof); and recovering the fatty acid derivatives.

In any of the embodiments above, derivatives of a certain carbon chain length can be recovered at a greater proportional yield, in comparison with the production of such fatty acid derivatives of the same carbon chain length in the same host cell in the absence of the mutant thioesterase (or a naturally-occurring equivalent thereof). In a particular embodiment, the fatty acid derivatives that are recovered at an increased or decreased yield comprise a primary chain length of C_6, C_7, C_8, C_9, C_{10}, C_{11}, C_{12}, C_{13}, C_{14}, C_{15}, C_{16}, C_{17}, C_{18}, C_{19}, C_{20}, C_{21}, C_{22}, C_{23}, C_{24}, C_{25}, C_{26}, C_{28}, C_{29}, C_{30}, C_{31}, C_{32}, C_{33}, C_{34}, C_{35}, C_{36}, C_{37}, C_{38} or C_{39} fatty acyl chain. The fatty acid derivatives that are recovered at an increased or decreased yield in the composition can be selected from all types of fatty acid derivatives, including, for example, hydrocarbons, fatty acids, fatty esters, fatty aldehydes, fatty alcohols terminal olefins, internal olefins, alkanes, diols, fatty amines, dicarboxylic acids, or ketones, or combinations thereof.

Alternatively, in any of the embodiments above, a particular fatty acid derivative can be produced at an increased or decreased proportional or percentage yield relative to the other fatty acid derivatives, when compared to the proportional or percentage yield of that particular fatty acid derivative in the same host cell in the absence of the mutant thioesterase (or a naturally-occurring equivalent thereof). In a particular embodiment, the fatty acid derivative that is produced at an increased proportional or percentage yield is a fatty ester. In another embodiment, the fatty acid derivative that is produced at a decreased proportional or percentage yield is a fatty ester.

Alternatively, in any of the embodiments above, fatty acid derivatives can be produced at an increased yield, or at an increased proportional yield of short-chain (e.g., C_8, C_9, C_{10}, C_{11}, C_{12}, C_{13}, or C_{14}) products. Conversely, in any of the embodiments above, fatty acid derivatives can be produced at a decreased yield, or at a decreased proportional yield of short-chain (e.g., C_8, C_9, C_{10}, C_{11}, C_{12}, C_{13}, or C_{14}) products.

In one embodiment of the invention, a method of producing fatty acid derivatives is provided wherein the yield of fatty acid derivatives produced by the method of the invention is at least about 0.001 g of fatty acid derivative product/g of carbon source, for example, at least about 0.01 g of fatty acid derivative product/g of carbon source, about 0.1 g of fatty acid derivative product/g of carbon source, about 0.2 g of fatty acid derivative product/g of carbon source, about 0.3 g of fatty acid

derivative product/g of carbon source, about 0.4 g of fatty acid derivative product/g of carbon source, or about 0.45 g of fatty acid derivative product/g of carbon source.

In one embodiment of the invention, a method of producing fatty acid derivatives is provided wherein the method results in a titer of at least about 0.5 g/L, for example, at least about 1 g/L, 2 g/L, 5 g/L, 10 g/L, 20 g/L, 30 g/L, 40 g/L, 50 g/L, 75 g/L, 100 g/L, 150 g/L or 200 g/L.

In one embodiment of the invention, a method of producing fatty acid derivatives is provided wherein the productivity of the method is such that at least about 0.1 g/L·h, for example, at least about 0.5 g/L·h, 1 g/L·h, 2 g/L·h, 3 g/L·h, 4 g/L·h, 5 g/L·h, 6 g/L·h, 7 g/L·h or 8 g/L·h is produced.

In one embodiment of the invention, fatty acid derivative compositions are provided that are produced by the host cells of the invention. Such compositions can comprise hydrocarbons, esters, alcohols, ketones, aldehydes, fatty acids, dicarboxylic acids, internal olefins, terminal olefins, and/or combinations thereof. Such compositions are useful in applications in the chemical industry, for example in the production of surfactants and detergents, or as a biofuel and a substitute for petroleum, heating oil, kerosene, diesel, jet fuel or gasoline.

In one embodiment of the invention, fatty acid derivative compositions are provided comprising less than or equal to about 50 ppm arsenic, about 30 ppm, about 25 ppm, or between about 10 and about 50 ppm arsenic; less than or equal to about 200 ppm calcium, about 150 ppm calcium, about 119 ppm calcium or between about 50 and about 200 ppm calcium; less than or equal to about 200 ppm chlorine, about 150 ppm chlorine, about 119 ppm chlorine or between about 50 and about 200 ppm chlorine; less than or equal to about 50 ppm copper, about 30 ppm copper, about 23 ppm copper, or between about 10 and about 50 ppm copper; less than or equal to about 300 ppm iron, about 200 ppm iron, about 136 ppm iron, or between about 50 and about 250 ppm iron; less than or equal to about 50 ppm lead, about 30 ppm lead, about 25 ppm lead, or between about 10 and about 50 ppm lead; less than or equal to about 50 ppm manganese, about 30 ppm manganese, about 23 ppm manganese, or between about 10 and about 50 ppm manganese; less than or equal to about 50 ppm magnesium, about 30 ppm magnesium, about 23 ppm magnesium, or between about 10 and about 50 ppm magnesium; less than or equal to about 0.5 ppm mercury, about 0.1 ppm mercury, about 0.06 ppm mercury or between about 0.01 and about 0.2 ppm mercury; less than or equal to about 50 ppm molybdenum, about 30 ppm molybdenum, about 23 ppm molybdenum or between about 10 and about 50 ppm molybdenum; less than or equal to about 2% nitrogen; about 1% nitrogen, about 0.5% nitrogen, or between about 0.1-1% nitrogen; less than or equal to about 200 ppm potassium, about 150 ppm potassium, about 103 ppm potassium, or between about 50 and about 200 ppm potassium; less than or equal to about 300 ppm sodium, 200 ppm sodium, about 140 ppm sodium, or between about 50 and about 300 ppm sodium; less than or equal to about 1 ppm sulfur, less than or equal to about 1% sulfur, about 0.14% sulfur, or between about 0.05 and about 0.3% sulfur; less than or equal to about 50 ppm zinc, about 30 ppm zinc, about 23 ppm zinc, or between about 10 and about 50 ppm zinc; or less than or equal to about 700 ppm phosphorus, about 500 ppm phosphorus, about 350 ppm phosphorus, or between about 100 and about 700 ppm phosphorus.

In one embodiment of the invention, fatty acid derivatives having fractions of modern carbon of about 1.003 to about 1.5 are provided.

In one embodiment of the invention, a fatty acid derivative composition is provided wherein the composition includes constituents comprising an acyl group that has a double bond at position 7 in the carbon chain (between carbon number 7 on the carbon chain and carbon number 8 on the carbon chain) from its reduced end.

In a particular embodiment, the fatty acid derivative composition comprises C_5-C_{25} (i.e., a carbon chain length of 5 to 25 carbons) fatty esters, C_5-C_{25} fatty acids, C_5-C_{25} fatty aldehydes, C_5-C_{25} fatty alcohols; or C_{10}-C_{20} (i.e., a carbon chain length of 10 to 20 carbons) fatty esters, C_{10}-C_{20} fatty acids, C_{10}-C_{20} fatty aldehydes, C_{10}-C_{20} fatty alcohols; or C_{12}-C_{18} (i.e., a carbon chain length of 12 to 18 carbons) fatty esters, C_{12}-C_{18} fatty acids, C_{12}-C_{18} fatty aldehydes, C_{12}-C_{18} fatty alcohols.

In a particular embodiment, the fatty acid derivatives of the invention comprise straight chain fatty acid derivatives, branched chain fatty acid derivatives, and/or cyclic moieties. In a particular embodiment, the fatty acid derivatives are unsaturated (e.g., monounsaturated) or saturated.

In one embodiment of the invention, the fatty acid derivative composition comprises a fatty ester that is produced from an alcohol and an acyl-CoA, wherein the alcohol is at least about 1, for example, at least about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 10, about 12, about 14, about 16, or about 18 carbons in length, and the acyl-CoA is at least about 2, for example, at least about 4, about 6, about 8, about 10, about 12, about 14, about 16, about 18, about 20, about 22, about 24, or about 26 carbons in length. In some embodiments, the alcohol and acyl-CoA from which the fatty ester are produced vary by about 2, about 4, about 6, about 8, about 10, about 12, or about 14 carbon atoms.

In another embodiment, the fatty acid derivative composition comprises a fatty ester that is produced from an alcohol and an acyl-ACP, wherein the alcohol is at least about 1, for example, at least about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 10, about 12, about 14, about 16, or about 18 carbons in length, and the acyl-ACP is at least about 2, for example, about 4, about 6, about 8, about 10, about 12, about 14, about 16, about 18, about 20, about 22, about 24, or about 26 carbons in length. In some embodiments, the alcohol and acyl-ACP from which the fatty ester are produced vary by about 2, about 4, about 6, about 8, about 10, about 12 or about 14 carbon atoms.

In one embodiment of the invention, the fatty acid derivative composition comprises a mixture of derivatives including free fatty acids. In one embodiment, the percentage of free fatty acids by weight is at least about 0.5%, for example, at least about 1%, about 2%, about 3%, about 4%, about 5%, about 6%, about 7%, about 8%, about 9%, about 10%, about 15%, about 20%, or about 25%. In a certain embodiment, the percentage of fatty esters produced by weight is at least about 50%, for example, at least about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, or about 90%. In a further embodiment, the ratio of fatty acid derivatives other than free fatty acids to free fatty acids is greater than about 90:1, for example, greater than about 80:1, about 50:1, about 20:1, about 10:1, about 9:1, about 8:1, about 7:1, about 5:1, about 2:1 or about 1:1, by weight.

In one embodiment, the fatty acid derivative composition comprises a mixture of derivatives including free fatty acids. In one embodiment, the percentage of free fatty acids by weight is at least about 50%, for example, at least about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, or about 90%. In a certain embodiment, the percentage of fatty ester produced by weight is at least about at least about 0.5%, for example, at least about 1%, about 2%,

about 3%, about 4%, about 5%, about 6%, about 7%, about 8%, about 9%, about 10%, about 15%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, or about 50%. In a further embodiment, the ratio of the fatty acid derivative produced other than free fatty acids to free fatty acids is less than about 60:1, for example, less than about 50:1, about 40:1, about 30:1, about 20:1, about 10:1, about 1:1, about 1:2; about 1:3, about 1:5, or about 1:10, by weight.

In one embodiment of the invention, the fatty acid derivative composition includes one or more fatty esters selected from: ethyl decanoate, ethyl dodecanoate, ethyl tridecanoate, ethyl tetradecanoate, ethyl pentadecanoate, ethyl cis-9-hexadecenoate, ethyl hexadecanoate, ethyl heptadecanoate, ethyl cis-11-octadecenoate, ethyl octadecanoate, methyl decanoate, methyl dodecanoate, methyl tridecanoate, methyl tetradecanoate, methyl pentadecanoate, methyl cis-9-hexadecenoate, methyl hexadecanoate, methyl heptadecanoate, methyl cis-11-octadecenoate, methyl octadecanoate, or a combination thereof.

In one embodiment of the invention, the fatty acid derivative composition includes one or more free fatty acids selected from: octanoic acid, decanoic acid, dodecanoic acid, tetradecanoic acid, pentadecanoic acid, cis-9-hexadecenoic acid, hexadecanoic acid, cis-11-octadecenoic acid, or combinations thereof.

Compositions comprising the fatty acid derivatives of the invention can be used as fuels. For example, the fatty acid derivatives can be used as, or as a component of, a biodiesel, a fatty alcohol, a fatty ester, a triacylglyceride, a gasoline, a diesel, or a jet fuel. A gasoline or a biodiesel composition can be used in an internal combustion engine. A jet fuel can be used in a jet engine. Accordingly, fuel compositions comprising the fatty acid derivatives prepared according to the present disclosures are provided herein.

Compositions comprising fatty acid derivatives of the invention can be used as fuel additives. For example, they can be added to a petroleum-based diesel or biodiesel to improve its renewable fuel content, lubricity, kinematic viscosity, acid number, boiling point, oxidative stability, cold filter-plugging point, impurity profiles, sulfated ash level, cetane number, cloud point, or pour point. Accordingly, fuel additive compositions comprising fatty acid derivatives produced according to the present disclosures are also provided.

Compositions comprising fatty acid derivatives of the invention can also be used as biocrude compositions, which can serve as feedstocks for making other petroleum-derivative compounds. For example, long chain hydrocarbons, internal or terminal olefins, alkanes, fatty aldehydes and fatty esters made according to the current invention can be further processed to produce fuels, fuel additives, fuel blends, and/or chemical products. Accordingly, biocrude compositions comprising fatty acid derivatives prepared according to the present disclosures are provided.

Compositions comprising fatty acid derivatives of the invention can be used as feedstocks in manufacturing detergents and surfactants, nutritional supplements, polymers, paraffin replacements, lubricants, solvents, personal care products, rubber processing additives, corrosion inhibitors, emulsifiers, plastics, textiles, cosmetics, paper products, coatings, metalworking fluids, dielectrics, oiling agents, and/or emollients. Accordingly, feedstock compositions comprising fatty acid derivatives prepared according to the present disclosures are also provided.

DESCRIPTION OF THE FIGURES

FIG. **1** is a table identifying various genes that can be over-expressed or attenuated to increase fatty acid derivative production. The table also identifies various genes that can be modulated to alter the structure of the fatty acid derivative product. Certain of the genes that are used to alter the structure of the fatty acid derivative will also increase the production of fatty acid derivatives.

FIG. **2** is a diagram illustrating the beta-oxidation pathway, including steps catalyzed by the following enzymes (1) acyl-CoA synthase (EC 6.2.1.-). (2) acyl-CoA dehydrogenase (EC 1.3.99.3), (3) enoyl-CoA hydratase (EC 4.2.1.17); (4) 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3), and (5) 3-ketoacyl-CoA thiolase (EC 2.3.1.16). This final reaction of the β-oxidation cycle, releases acetyl-CoA and an acyl-CoA fatty acid two carbons shorter, ready to go through β-oxidation reactions again.

FIG. **3** is a diagram illustrating the FAS biosynthetic pathway.

FIG. **4** is a diagram illustrating biosynthetic pathways that produce fatty esters depending upon the substrates provided.

FIG. **5** is a diagram illustrating biosynthetic pathways that produce fatty alcohols.

FIG. **6** is a graph depicting fatty alcohol production by the strain co-transformed with pCDFDuet-1-fadD-acr1 and plasmids containing various thioesterase genes. Saturated C_{10}, C_{12}, C_{14}, C_{16} and C_{18} fatty alcohol were identified.

FIG. **7** is a graph depicting fatty alcohol production by the strain described in Example 3, co-transformed with pCDFDuet-1-fadD-acr1 and plasmids containing various thioesterase genes. The strains were grown aerobically at 25° C. or 37° C. in an M9 mineral medium containing 0.4% glucose in shake flasks. Fatty alcohols were detected in the cell pellets as well as in the supernatants, indicating a substantial extracellular production of such alcohols. Cultivation at 25° C. resulted in the release of about 25% of the product from the cells, whereas cultivation at 37° C. resulted in the release of about 50% of the product from the cell.

FIG. **8**A-D are plots depicting GC-MS spectra of octyl octanoate (C_8C_8) produced by a production host expressing alcohol acetyl transferase (AATs, EC 2.3.1.84) and production hosts expressing ester synthase (EC 2.3.1.20, 2.3.1.75). FIG. **8**A is a GC-MS spectrum showing ethyl acetate extract of strain C41(DE3, ΔfadE/pHZ1.43)/pRSET B+pAS004.114B) wherein the pHZ1.43 plasmid expressed ADP1 ester synthase (EC 2.3.1.20, 2.3.1.75). FIG. **8**B is a GC-MS spectrum showing ethyl acetate extract of strain C41 (DE3, ΔfadE/pHZ1.43)/pRSET B+pAS004.114B) wherein the pHZ1.43 plasmid expressed SAAT. FIG. **8**C is a GC-MS spectrum showing acetyl acetate extract of strain C41(DE3, ΔfadE/pHZ1.43)/pRSET B+pAS004.114B) wherein the pHZ1.43 plasmid did not contain ADP1 (an ester synthase) or SAAT. FIG. **8**D is a GC-MS spectrum showing the mass spectrum and fragmentation pattern of C_8C_8 produced by C41(DE3, ΔfadE/pHZ1.43)/pRSET B+pAS004.114B wherein the pHZ1.43 plasmid expressed SAAT).

FIG. **9** is a graph depicting the distribution of ethyl esters made (in accordance with Example 9) when the ester synthase from *A. baylyi* ADP1 (WSadp1) was co-expressed with a thioesterase from *Cuphea hookeriana* in a production host.

FIG. **10** is a graph depicting the production of ethyl esters by various ester synthases at 25° C. The ethyl esters were produced by recombinant *E. coli* strains carrying various ester synthase genes. The recombinant strains were (1) C41 (DE3, ΔfadEΔfabR)/pETDuet-1-'TesA+pCDFDuet-1-fadD with 1 pHZ1.43; (2) pHZ1.97_377; (3) pHZ1.97_atfA2; (4) pHZ1.97_376; (5) pHZ1.97_atfA1; and (6) no plasmids (control).

FIG. **11** is a graph depicting the acyl composition of fatty acid ethyl esters (FAEE) produced from various *E. coli*

strains. The recombinant strains are (1) C41 (DE3, ΔfadEΔfabR)/pETDuet-1-'TesA+pCDFDuet-1-fadD with 1 pHZ1.43; (2) pHZ1.97_377; (3) pHZ1.97_atfA2; (4) pHZ1.97_376; (5) pHZ1.97_atfA1; and (6) no plasmids (control).

FIG. **12** is a graph depicting the production of ethyl esters by various ester synthases at 37° C. The ethyl esters were produced by recombinant *E. coli* strains carrying various ester synthase genes. The recombinant strains were (1) C41 (DE3, ΔfadEΔfabR)/pETDuet-1-'TesA+pCDFDuet-1-fadD with 1 pHZ1.43; (2) pHZ1.97_377; (3) pHZ1.97_atfA2; (4) pHZ1.97_376; (5) pHZ1.97_atfA1; and (6) no plasmids (control).

FIG. **13** is a graph depicting concentrations of free fatty acids (FFA) and fatty acid ethyl esters (FAEE) produced from three individual colonies from the transformants, C41 (DE3, ΔfadEΔfabR)/pETDuet-1-'TesA+pCDFDuet-1-fadD+ pHZ1.97_atfA2. The FFA was converted to fatty acid ethyl ester (FAEE) and quantified by GC/MS.

FIG. **14** is a diagram depicting the control regions for FabA (SEQ ID NO:33) and FabB (SEQ ID NO:34). The FadR and FabR consensus binding sites are shown in bold. Vertical arrows indicate the positions where mutations can be made to alter fabA expression. The proposed base for each position is also indicated by the brackets. The two regions that constitute the −35 and −10 regions of the typical *E. coli* promoter are indicated by the brackets. The proposed mutations that make the promoter closer to the consensus promoter sequence are also shown.

FIGS. **15**A-B are chromatograms depicting GC/MS analysis. FIG. **15**A is a chromatogram depicting the components of an ethyl acetate extract of the culture of *E. coli* LS9001 strain transformed with plasmids pCDFDuet-1-fadD-WSadp1, pETDuet-1-'TesA. FIG. **15**B is a chromatogram depicting the ethyl hexadecanoate and the ethyl oleate, which were used as references.

FIG. **16** is a map of the pOP-80 plasmid.

FIG. **17** is the full DNA sequence of the pOP-80 plasmid (SEQ ID NO:1)

FIG. **18** is the DNA sequence (SEQ ID NO:2) for the *E. coli* codon-optimized fadD35 gene (GenBank Accession No. NP_217021).

FIG. **19** is the DNA sequence (SEQ ID NO:3) for the *E. coli* codon-optimized fadD1 gene (GenBank Accession No. NP_251989).

FIG. **20** (FIG. **20**) is the BsyhfLBspHIF primer (SEQ ID NO:4) based on the DNA sequence deposited at NCBI with GenBank Accession No. NC_000964.

FIG. **21** is the BsyhfLEcoR primer (SEQ ID NO:5) based on the DNA sequence deposited at NCBI with GenBank Accession No. NC_000964.

FIG. **22** is the DNA sequence (SEQ ID NO:6) for the yhfL gene from *Bacillus subtilis.*

FIG. **23** is the Scfaa3pPciF primer (SEQ ID NO:7) based on the DNA sequence deposited at NCBI with GenBank Accession No. NC_001141.

FIG. **24** is the Scfaa3pPciI primer (SEQ ID NO:8) based on the DNA sequence deposited at NCBI with GenBank Accession No. NC_001141.

FIG. **25** is the DNA sequence (SEQ ID NO:9) for the faa3 gene from *Saccharomyces cerevisiae* (GenBank Accession No. NP_012257).

FIG. **26** is the Smprk59BspF primer (SEQ ID NO:10) based on the DNA sequence deposited at NCBI with GenBank Accession No. NZ_AAVZ01000044.

FIG. **27** is the Smprk59HindR primer (SEQ ID NO:11) based on the DNA sequence deposited at NCBI with GenBank Accession No. NZ_AAVZ01000044.

FIG. **28** is the PrkBsp primer (SEQ ID NO:12).

FIG. **29** is the DNA sequence encoding the protein ZP_01644857 from *Stenotrophomonas maltophilia* R551-3 (SEQ ID NO:13).

FIG. **30** is the protein sequence of ZP_01644857 from *Stenotrophomonas maltophilia* ATCC 17679 (SEQ ID NO:14).

FIG. **31** is a schematic of a new pathway for fatty aldehyde production.

FIG. **32** is a listing of the nucleotide sequence (SEQ ID NO:15) and the corresponding amino acid sequence (SEQ ID NO:16) of *Nocardia* sp. NRRL 5646 car gene.

FIG. **33** is a listing of amino acid sequence motifs for CAR homologs.

FIGS. **34**A-B are GC/MS traces of olefins produced by *Jeotgalicoccus* sp. ATCC 8456 cells and *Jeotgalicoccus halotolerans* DSMZ 17274 cells, respectively.

FIGS. **35**A-B are GC/MS traces of olefins produced by *Jeotgalicoccus pinnipedalis* DSMZ 17030 cells and *Jeotgalicoccus psychrophiles* DSMZ 19085 cells, respectively.

FIGS. **36**A-B are mass spectrometry fragmentation patterns of two α-olefins produced by *Jeotgalicoccus* ATCC 8456 cells. Compound A was identified as 1-nonadecene and compound B as 18-methyl-1-nonadecene.

FIG. **37** is a schematic of a phylogenetic analysis of 16s rRNA of *Jeotgalicoccus* ATCC 8456.

FIGS. **38**A-B are GC/MS traces of α-olefins produced by *Jeotgalicoccus* sp. ATCC 8456 cells upon feeding with eicosanoic acid (FIG. **38**A) or stearic acid (FIG. **38**B).

FIG. **39** is a GC/MS trace of α-olefins (1-heptadecene) produced by cell free lysates of *Jeotgalicoccus* sp. ATCC 8456 cells, as compared to a trace of cell-free lysate without the C_{18} fatty acid substrate, and a trace of the C_{18} fatty acid substrate itself.

FIG. **40** is a digital representation of an SDS-PAGE gel of final purified α-olefins-producing protein fraction from *Jeotgalicoccus* sp. ATCC 8456 cells.

FIGS. **41**A-B are orf880 nucleotide (SEQ ID NO:25) and amino acid (SEQ ID NO:26) sequences, respectively. FIG. **41**C is the partial 16s rRNA sequence (SEQ ID NO:27) of *Jeotgalicoccus* sp. ATCC8456.

FIG. **42** is a GC/MS trace of α-olefins produced by *E. coli* upon expression of *Jeotgalicoccus* sp. 8456_orf880 and feeding of stearic acid.

FIG. **43** is a schematic of a bootstrap phylogenetic analysis of 8456_orf880 homologs using ClustalW.

FIG. **44** describes amino acid motifs for identifying precursor thioesterases useful in the present invention.

FIGS. **45**A-B (FIGS. **45**A-B) include a table listing the results of assays identifying mutant thioesterases with altered properties. In particular, FIG. **45**A includes lists of mutants with Z scores of at least 3 for activity (i.e., catalytic rate) with respect to the named substrate or specificity for the named substrate; and FIG. **45**B is a table of mutants having improved and/or increased yield/production of fatty acid derivatives with Z scores of at least 3. The amino acid position numbering is according to SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO: 31).

FIGS. **46**A-E (FIGS. **46**A-E) include tables listing the results of assays identifying mutant thioesterases with altered proportional yield of fatty esters vs. other products (e.g., fatty acid derivatives other than fatty esters). In particular, FIG. **46**A is a table showing mutants having Z scores of at least 3 with respect to the proportional or percentage yield of fatty

esters vs. free fatty acids. FIG. **46**B is a table showing mutants having Z scores of less than −3 with respect to the proportional or percentage yield of fatty esters vs. free fatty acids. FIG. **46**C is a table showing mutants having Z scores of at least 3 with respect to the in vivo yield of fatty acid derivatives. FIG. **46**D is a table showing mutants having Z scores of at least 3 with respect to the proportional yield of short-chain (e.g., C_8, C_9, C_{10}, C_{11}, C_{12}, C_{13}, and/or C_{14}) fatty acid derivatives vs. other fatty acid derivatives (e.g., fatty acid derivatives other than short-chain fatty acid derivatives including, for example, long-chain (e.g., C_{15}, C_{16}, C_{17}, C_{18}, C_{19}, and/or C_{20}) fatty acid derivatives). FIG. **46**E is a table showing mutants having Z scores of less than −3 with respect to the proportional yield of short-chain (e.g., C_8, C_9, C_{1-10}, C_{11}, C_{12}, C_{13}, and/or C_{14}) fatty acid derivatives vs. other fatty acid derivatives (e.g., fatty acid derivatives other than short-chain fatty acid derivatives including, for example, long-chain (e.g., C_{15}, C_{16}, C_{17}, C_{18}, C_{19}, and/or C_{20}) fatty acid derivatives). The amino acid position numbering is according to SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO: 31).

FIG. **47** (FIG. **47**) is a sequence alignment of homologs of 'TesA using the amino acid residues of an *E. coli* 'TesA (i.e., TesA without the signal peptide, SEQ ID NO: 73) as a reference sequence for numbering purposes.

FIG. **48** is a graph depicting the FAME titers and composition for the MG1655 (ΔfadE) pTrc-'TesA JadD strain.

FIG. **49** is a graph depicting the FAME titers and composition for the MG1655 (ΔfadE) and C41(ΔfadE) strains expressing fadD and 'tesA on plasmids during a 25-hour fermentation run.

FIG. **50** is a graph depicting the FAME titers and composition for the MG1655 (ΔfadE) pTrc-'TesA JadD strain.

FIG. **51** is a graph depicting the FAME titers and composition for the MG1655 (ΔfadE) and C41 (ΔfadE) strains expressing fadD and 'tesA on plasmids during a 25-hour fermentation run.

FIG. **52** is a graph depicting the FFA titers and composition for the MG1655 (ΔfadE) and C41 (ΔfadE) strains expressing fadD and 'tesA on plasmids during a 25-hour fermentation run.

FIG. **53** is a graph depicting the FAME titers for the MG1655 (ΔfadE) strains expressing *E. coli* 'tesA, *P. luminescens* 'tesA, *V. harveyi* 'tesA and *P. profundum* tesB on plasmids, during a 24-hour fermentation run. Titers are represented in mg/L and mg/L/OD.

FIG. **54** is a graph of FFA titers for MG1655 (ΔfadE) strains expressing *E. coli* 'tesA, *P. luminescens* 'tesA, *V. harveyi* 'tesA and *P. profundum* tesB on plasmids, during a 24-hour fermentation run. Titers are represented in mg/L (bars) and mg/L/OD (triangles).

FIG. **55** lists GenBank Accession numbers of 'TesA homologs.

FIGS. **56**A-F are graphs depicting substrate specificity (Z score) vs. amino acid residue positions corresponding to 'TesA sequence of SEQ ID NO:31 with symbols to represent levels of conservation in the cons70 alignment for C_{10} specificity (FIG. **56**A), C_{12} specificity (FIG. **56**B) and C_{14} specificity (FIG. **56**C).

FIG. **57** shows the amino acid sequence of an *E. coli* 'TesA (SEQ ID NO:31).

FIG. **58** shows a nucleotide sequence encoding an *E. coli* 'TesA (SEQ ID NO:32).

FIG. **59** is a graph of free fatty acid (FFA) and fatty acyl methyl ester (FAME) titers in cultures of *E. coli* MG1655 ΔfadE cells transformed with pACYC containing the 'tesA homologs from *E. coli* (EcolA), *Pectobacterium atrosepticum* (PatrA), *Pseudomonas putida* (PputA), *Vibrio harveyi* (VharA), *Photorhabdus luminescens* (PlumA), or with pACYC containing no insert (Neg).

FIG. **60** is a graph of FFA and FAME titers in cultures of *E. coli* MG1655 ΔfadE cells overexpressing fadD and 'tesA from *E. coli* (*E coli*), *Pectobacterium atrosepticum* (Patr), *Photorhabdus luminescens* (Plum), *Photobacterium profundum* (Ppro), *Vibrio harveyi* (VhA), *Pseudomonas putida* (Pput), or no 'tesA (Neg). (Data marked with an asterisk (*) are from a separate experiment.)

FIG. **61** is a graph of FFA and FAME titers in cultures of *E. coli* MG1655 ΔfadE expressing wildtype *E. coli* 'tesA (WT), the S10C mutant (S10C), or no 'tesA (Neg).

FIG. **62** is a graph of FAME production against time of a fermentation run with recombinant host cells that express thioesterase in the absence of exogenous ester synthase.

FIG. **63** is a graph of FFA production against time of a fermentation run with recombinant host cells that express thioesterase in the absence of exogenous ester synthase.

DETAILED DESCRIPTION OF THE INVENTION

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein, including GenBank database sequences, are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description, and from the claims.

DEFINITIONS

Throughout the specification, a reference may be made using an abbreviation of a gene name or a polypeptide name, but it is understood that such an abbreviated gene or polypeptide name represents the genus of genes or polypeptides, respectively. Such gene names include all genes encoding the same polypeptide and homologous polypeptides having the same physiological function. Polypeptide names include all polypeptides that have the same activity (e.g., that catalyze the same fundamental chemical reaction).

Unless otherwise indicated, the accession numbers referenced herein are derived from the NCBI database (National Center for Biotechnology Information) maintained by the National Institute of Health, U.S.A. Unless otherwise indicated, the accession numbers are as provided in the database as of March 2008.

EC numbers are established by the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (NC-IUBMB) (available at http://www.chem.qmul/ac/uk/iubmb/enzyme/). The EC numbers referenced herein are derived from the KEGG Ligand database, maintained by the Kyoto Encyclopedia of Genes and Genomics, sponsored in part by the University of Tokyo. Unless otherwise indicated, the EC numbers are as provided in the database as of March 2008.

The articles "a" and "an" are used herein to refer to one or more than one (i.e., to at least one) of the grammatical object

of the article. By way of example, "an element" means one element or more than one element.

The term "about" is used herein to mean a value ±20% of a given numerical value. Thus, "about 60%" refers to a value of 60±(20% of 60) (i.e., between 48 and 70).

As used herein, the term "alcohol dehydrogenase" (EC 1.1.1.*) is a polypeptide capable of catalyzing the conversion of a fatty aldehydes to an alcohol (e.g., a fatty alcohol). Additionally, one of ordinary skill in the art will appreciate that some alcohol dehydrogenases will catalyze other reactions as well. For example, some alcohol dehydrogenases will accept other substrates in addition to fatty aldehydes. Such non-specific alcohol dehydrogenases are, therefore, also included in this definition. Polynucleotide sequences encoding alcohol dehydrogenases are known in the art, and such dehydrogenases are publicly available.

The term "altered property" refers to a modification in one or more properties of a mutant polynucleotide or mutant protein with reference to a precursor polynucleotide or precursor protein. Properties that can be advantageously altered with respect to proteins made according to the present invention include oxidative stability, substrate specificity, substrate selectivity, catalytic activity, thermal stability, pH stability, pH activity profile, resistance to proteolytic degradation, K_m, k_{cat}, k_{cat}/k_m ratio, protein folding, inducing an immune response, ability to bind to a ligand, ability to bind to a receptor, ability to be secreted, ability to translocate in an active manner into a membrane, ability to be displayed on the surface of a cell, ability to oligomerize, ability to signal, ability to stimulate cell proliferation, ability to inhibit cell proliferation, ability to induce apoptosis, ability to be modified by phosphorylation or glycosylation, ability to treat disease. In one embodiment of the invention, mutant thioesterases are provided that derive from a precursor thioesterase, wherein the mutant has at least one altered property either in vitro or in vivo, as compared to the properties of the precursor thioesterase. In one embodiment, the altered property can be a biophysical property such as thermal stability (melting point T_m), solvent stability, solute stability, oxidative stability, lipophilicity, hydrophilicity, quaternary structure, dipole moment, or isoelectric point. In one embodiment, the altered property can be a biochemical property such as pH optimum, temperature optimum, ionic strength optimum, and/or an enzyme catalytic parameter (such as, for example, product distribution, product proportional or percentage yield, specific activity, substrate preference, substrate affinity, substrate inhibition, product affinity, turnover rate, product inhibition, kinetic mechanism, K_M, k_{cat}, k_{cat}/K_m, and/or V_{Max}). In one embodiment, the altered property is a changed preference for particular substrates, as reflected in, for example, a changed preference for alcoholysis or hydrolysis, acyl-CoA or acyl-acyl carrier protein substrates, ester or thioester substrates, saturated or unsaturated substrates, position of unsaturations, broad or narrow specificity (e.g., the ability to catalyze a range of substrates or only substrates of a specific carbon chain length). In one embodiment, the altered property can be an increased preference or activity for branched substrates, substrates having a specific position of branching, hydroxy-acyl substrates, keto-acyl substrates, substrates that result in a product having desirable fuel attributes (i.e., cetane number, octane rating, oxidative stability, lubricity, flash point, viscosity, boiling point, melting point, pour point, cloud point, cold filter plugging point, cold flow characteristics, aromaticity, and/or iodine number). Altered properties also include a decrease in activity or attenuation of ester hydrolysis, such as hydrolysis of desired product molecules, or a decrease in the toxicity of the protein to the cell and/or a change in the expression level of the protein in the cell. In a particular embodiment, the at least one altered property is, for example, a change in the ability of the thioesterase to catalyze the synthesis of fatty acyl esters directly or indirectly, in vivo or in vitro, such as by transesterification.

As used herein, an "analogous sequence" is one wherein the function of the gene is essentially the same as a reference gene such as, for example, a 'tesA gene from *E. coli*. Additionally, analogous genes include at least about 20%, for example, at least about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of a reference gene or polynucleotide such as, for example, the polynucleotide or polypeptide sequence of a 'tesA gene or a 'TesA thioesterase, respectively. In additional embodiments more than one of the above properties applies to the sequence. Analogous sequences are determined by known methods of sequence alignment.

The term "alignment" refers to a method of comparing two or more polynucleotides or polypeptide sequences for the purpose of determining their relationship to each other. Alignments are typically performed by computer programs that apply various algorithms, however it is also possible to perform an alignment by hand. Alignment programs typically iterate through potential alignments of sequences and score the alignments using substitution tables, employing a variety of strategies to reach a potential optimal alignment score. Commonly-used alignment algorithms include, but are not limited to, CLUSTALW, (see, Thompson J. D., Higgins D. G., Gibson T. J., CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice, Nucleic Acids Research 22: 4673-4680, 1994); CLUSTALV, (see, Larkin M. A., et al., CLUSTALW2, ClustalW and ClustalX version 2, Bioinformatics 23(21): 2947-2948, 2007); Jotun-Hein, Muscle et al., MUSCLE: a multiple sequence alignment method with reduced time and space complexity, BMC Bioinformatics 5: 113, 2004); Mafft, Kalign, ProbCons, and T-Coffee (see Notredame et al., T-Coffee: A novel method for multiple sequence alignments, Journal of Molecular Biology 302: 205-217, 2000). Exemplary programs that implement one or more of the above algorithms include, but are not limited to MegAlign from DNAStar (DNAStar, Inc. 3801 Regent St. Madison, Wis. 53705), MUSCLE, T-Coffee, CLUSTALX, CLUSTALV, JalView, Phylip, and Discovery Studio from Accelrys (Accelrys, Inc., 10188 Telesis Ct, Suite 100, San Diego, Calif. 92121). In a non-limiting example, MegAlign is used to implement the CLUSTALW alignment algorithm with the following parameters: Gap Penalty 10, Gap Length Penalty 0.20, Delay Divergent Seqs (30%) DNA Transition Weight 0.50, Protein Weight matrix Gonnet Series, DNA Weight Matrix IUB.

The term "antibodies" refers to immunoglobulins. Antibodies include but are not limited to immunoglobulins obtained directly from any species from which it is desirable to produce antibodies. In addition, the present invention encompasses modified antibodies. The term also refers to antibody fragments that retain the ability to bind to the same epitope to which the intact antibody also binds, and include polyclonal antibodies, monoclonal antibodies, chimeric antibodies, anti-idiotype (anti-ID) antibodies. Antibody fragments include, but are not limited to the complementarity-determining regions (CDRs), single-chain fragment variable regions (scFv), heavy chain variable region (VH), light chain variable region (VL). Polyclonal and monoclonal antibodies

are also encompassed by the present invention. Preferably, the antibodies are monoclonal antibodies.

The term "attenuate" means to weaken, reduce or diminish. In one example, the sensitivity of a particular enzyme to feedback inhibition or inhibition caused by a composition that is not a product or a reactant (non-pathway specific feedback) is reduced such that the enzyme activity is not impacted by the presence of a compound. In a particular example, the expression of fabH gene is temperature sensitive and its sequence can be altered to decrease the sensitivity to temperature fluctuations. Also, expression of the fabH gene can be attenuated when branched amino acids are desired. In another example, an enzyme that has been modified to be less active can be referred to as attenuated. A functional modification of the sequence encoding an enzyme can be used to attenuate expression of an enzyme. Sequence modifications may include, for example, a mutation, deletion, or insertion of one or more nucleotides in a gene sequence or a sequence controlling the transcription or translation of a gene sequence, which modification results in a reduction or inhibition of production of the gene product, or renders the gene product non-functional. For example, functional deletion of fabR in *E. coli* reduces the repression of the fatty acid biosynthetic pathway and allows *E. coli* to produce more unsaturated fatty acids (UFAs). In some instances a functional deletion is described as a knock-out mutation. Other methods are available for attenuating expression of an enzyme. For example, attenuation can be accomplished by modifying the sequence encoding the gene as described above; placing the gene under the control of a less active promoter, expressing interfering RNAs, ribozymes, or antisense sequences that target the gene of interest; by changing the physical or chemical environment, such as temperature, pH, or solute concentration, such that the optimal activity of the gene or gene product is not realized; or through any other techniques known in the art.

The term "biocrude" refers to a biofuel that can be used as a substitute of petroleum-based fuels. In addition, biocrude, like petroleum crude, can be converted into other fuels, for example gasoline, diesel, jet fuel, or heating oil. Moreover, biocrude, like petroleum crude, can be converted into other industrially useful chemicals for use in, for example, pharmaceuticals, cosmetics, consumer goods, industrial processes, etc. A biocrude composition can comprise, for example, hydrocarbons, hydrocarbon products, fatty acid esters, and/or aliphatic ketones, or a combination thereof. In a preferred embodiment, a biocrude composition is comprised of hydrocarbons, for example, aliphatic (e.g., alkanes, alkenes, alkynes) or aromatic hydrocarbons.

The term "biodiesel" refers to a particular kind of biofuel that can be used in diesel engines. Biodiesel can be a substitute for traditional diesel, which is typically derived from petroleum. Biodiesel can be used in internal combustion diesel engines in either a pure form, which is referred to as "neat" biodiesel, or as a mixture in any concentration with a petroleum-based diesel. A biodiesel composition can also comprise various suitable additives. Biodiesel can be comprised of hydrocarbons or esters. In one embodiment, biodiesel is comprised of fatty esters, such as fatty acid methyl esters (FAME) or fatty acid ethyl esters (FAEE). In a preferred embodiment, these FAME and FAEE are comprised of fatty acyl moieties having a carbon chain length of about 8-20, 10-18, or 12-16. Fatty esters used as biodiesel may contain carbon chains that are straight, branched, saturated, or unsaturated.

The term "biofuel" refers to any fuel derived from biomass. Biomass is a biological material that can be converted into a biofuel. One exemplary source of biomass is plant matter. For example, corn, sugar cane, and switchgrass can be used as biomass. Another non-limiting example of biomass is animal matter, for example cow manure. Biomass also includes waste products from industry, agriculture, forestry, and households. Examples of such waste products include, without limitation, fermentation waste, straw, lumber, sewage, garbage and food leftovers and glycerol. Biomass also includes sources of carbon, such as carbohydrates (e.g., sugars). Biofuels can be substituted for petroleum based fuels. For example, biofuels are inclusive of transportation fuels (e.g., gasoline, diesel, jet fuel, etc.), heating fuels, and electricity-generating fuels. A biofuel is a renewable energy source. Non-limiting examples of biofuels include biodiesel, hydrocarbons (e.g., alkanes, alkenes, alkynes, or aromatic hydrocarbons), and alcohols derived from biomass.

The term "carbon chain length" is defined herein as the number of carbon atoms in a carbon chain of a thioesterase substrate or a fatty acid derivative. The carbon chain length of a particular molecule is marked as C_x, wherein the subscript "x" refers to the number of carbons in the carbon chain. As used herein, the term "long-chain" refers to those molecules that have a carbon chain of about 15 to about 20 carbons long (e.g., C_{15}, C_{16}, C_{17}, C_{18}, C_{19}, or C_{20}). The term "short-chain" refers to those molecules that have a carbon chain of about 8 to about 14 carbons long (e.g., C_8, C_9, C_{10}, C_{11}, or C_{12}).

The term "carbon source" means a substrate or compound suitable to be used as a source of carbon for prokaryotic or simple eukaryotic cell growth. Carbon sources can be in various forms, including, but not limited to polymers, carbohydrates, acids, alcohols, aldehydes, ketones, amino acids, peptides, gases (e.g., CO and CO_2), and the like. These include, for example, various monosaccharides such as glucose, fructose, mannose and galactose; oligosaccharides such as fructo-oligosaccharide and galacto-oligosaccharide; polysaccharides such as xylose, and arabinose; disaccharides such as sucrose, maltose and turanose; cellulosic material such as methyl cellulose and sodium carboxymethyl cellulose; saturated or unsaturated fatty acid esters such as succinate, lactate and acetate; alcohols such as ethanol, etc., or mixtures thereof. The carbon source can additionally be a product of photosynthesis, including, but not limited to glucose. Glycerol can be an effective carbon source as well. Suitable carbon sources can be generated from any number of natural and renewable sources, including particularly biomass from agricultural, municipal and industrial waste, so long as the material can be used as a component of a fermentation to provide a carbon source. Biomass sources include corn stover, sugarcane, switchgrass, animal matter, or waste materials.

The term "chromosomal integration" means the process whereby an incoming sequence is introduced into the chromosome of a host cell. The homologous regions of the transforming DNA align with homologous regions of the chromosome. Then, the sequence between the homology boxes can be replaced by the incoming sequence in a double crossover (i.e., homologous recombination). In some embodiments of the present invention, homologous sections of an inactivating chromosomal segment of a DNA construct align with the flanking homologous regions of the indigenous chromosomal region of the microbial chromosome. Subsequently, the indigenous chromosomal region is deleted by the DNA construct in a double crossover.

The term "cloud point" refers to the temperature of a liquid at which the dissolved solids are no longer completely soluble, precipitating as a second phase and giving the fluid a cloudy appearance. This term is relevant to a number of applications with somewhat or completely different conse-

quences. In the petroleum industry, cloud point refers to the temperature below which wax or other heavy hydrocarbons crystalize in a crude oil, refined oil or fuel to form a cloudy appearance. The presence of solidified wax influences the flowing behavior of the fluid, raising the tendency to clog fuel filters/injectors and other machine parts, causing accumulation of wax on cold surfaces (e.g., on pipeline surfaces or heat exchanger surfaces), and changing even the emulsion characteristics with water. Cloud point is an indication of the tendency of the oil to plug filters or small orifices at cold operating temperatures. The cloud point of a nonionic surfactant or glycol solution is the temperature at which the mixture starts to separate into two or more phases, thus becoming cloudy. This behavior is characteristic of non-ionic surfactants containing polyoxyethylene chains, which can exhibit reverse solubility versus temperature behavior in water, and therefore can "cloud out" at some point as the temperature is raised. Glycols demonstrating this behavior are known as "cloud-point glycols" and are used as shale inhibitors. The cloud point is typically also affected by salinity, being generally lower in more saline fluids.

The term "cloud point lowering additive" refers to an additive that can be added to a composition to decrease or lower the cloud point of the composition, as described above.

The term "conditions that permit product production" refers to any fermentation conditions that allow a production host to produce a desired product, such as acyl-CoA or fatty acid derivatives including, for example, fatty acids, hydrocarbons, fatty alcohols, waxes, or fatty esters. Fermentation conditions usually comprise many parameters. Exemplary conditions include, but are not limited to, temperature ranges, levels of aeration, pH ranges, and media composition (e.g., solvents and solutes). Each of these conditions, individually and in combination, allows the production host to grow. Exemplary media include broths or gels. Generally, a suitable medium includes a carbon source, such as glucose, fructose, cellulose, or the like, which can be metabolized by the microorganism directly. In addition, enzymes can be used in the medium to facilitate the mobilization (e.g., the depolymerization of starch or cellulose to fermentable sugars) and subsequent metabolism of the carbon source. To determine if the culture conditions are suitable for product production, the production host can be cultured for about 4, 8, 12, 24, 36, 48, or 72 hours. During culturing or after culturing, samples can be obtained and analyzed to determine if the culture conditions permit product production. For example, the production hosts in the sample or the medium in which the production hosts were grown can be tested for the presence of the desired product. When testing for the presence of a product, assays, such as, but not limited to, TLC, HPLC, GC/FID, GC/MS, LC/MS, MS, as well as those provided in the examples herein, can be used.

The term "consensus sequence" or "canonical sequence" refers to an archetypical amino acid sequence against which all variants of a particular protein or sequence of interest are compared. Either term also refers to a sequence that sets forth the nucleotides that are most often present in a polynucleotide sequence of interest. For each position of a protein, the consensus sequence gives the amino acid that is most abundant in that position in the sequence alignment.

As used herein, the term "consensus mutation" refers to a difference in the sequence of a starting gene and a consensus sequence. Consensus mutations are identified by comparing the sequences of the starting gene and the consensus sequence resulting from a sequence alignment. In some embodiments, consensus mutations are introduced into the starting gene such that it becomes more similar to the consensus sequence. Consensus mutations also include amino acid changes that change an amino acid in a starting gene to an amino acid that is more frequently found in a multiple sequence alignment (MSA) at that position relative to the frequency of that amino acid in the starting gene. Thus, the term "consensus mutation" refers to any amino acid change that replaces an amino acid of the starting gene with an amino acid that is more abundant in the MSA than the native amino acid.

The term "conservative substitutions" or "conserved substitutions" refers to, for example, a substitution wherein one or more of the following amino acid substitutions are made: replacement of an aliphatic amino acid, such as alanine, valine, leucine, and isoleucine, with another aliphatic amino acid; replacement of a serine with a threonine; replacement of a threonine with a serine; replacement of an acidic residue, such as aspartic acid and glutamic acid, with another acidic residue; replacement of a residue bearing an amide group, such as asparagine and glutamine, with another residue bearing an amide group; exchange of a basic residue, such as histidine, lysine and arginine, with another basic residue; and replacement of an aromatic residue, such as tryptophan, phenylalanine and tyrosine, with another aromatic residue; or replacement of small amino acids, such as glycine, alanine, serine, threonine and methionine, with another small amino acid. Amino acid substitutions which do not generally alter the specific activity are known in the art and are described, for example, by H. Neurath and R. L. Hill, in The Proteins, Academic Press, New York, 1979. Useful conservative modifications include Alanine to Cysteine, Glycine, or Serine; Arginine to Isoleucine, Lysine, Methionine, or Ornithin; Asparagine to Aspartic acid, Glutamine, Glutamic acid, or Histidine; Aspartic acid to Asparagine, Glutamine, or Glutamic acid; Cysteine to Methionine, Serine, or Threonine; Glutamine to Asparagine, Aspartic acid, or Glutamic acid; Glutamic acid to Asparagine, Aspartic acid, or Glatmine; Glycine to Aspartic acid, Alanine, or Proline; Histidine to Asparagine, or Glutamine; Isoleucine to Leucine, Methionine, or Valine; Leucine to Isoleucine, Methionine, or Valine; Lysine to Arginine, Glutamine, Glutamic acid, Isoleucine, Methionine, or Ornithin; Methionine to Cysteine, Isoleucine, Leucine, or Valine; Phenylalanine to Histidine, L-Dopa, Leucine, Methionine, Threonine, Tryptophan, Tyrosine, 3-phenylproline, 4-phenylproline, or 5-phenylproline; Proline to L-1-thioazolidine-4-carboxylic acid or D- or L-1-oxazolidine-4-carboxylic acid; Serine to Cysteine, Methionine, or Threonine; Threonine to Methionine, Serine, or Valine; Tryptophan to Tyrosine; Tyrosine to L-Dopa, Histidine, or Phenylalanine; and Valine to Isoleucine, Leucine, or Methionine.

The term "corresponds to" refers to an amino acid residue in a first protein sequence being positionally equivalent to an amino acid residue in a second reference protein sequence by virtue of the fact that the residue in the first protein sequence lines up with the residue in the reference sequence using bioinformatic techniques, for example, using the methods described herein for preparing a sequence alignment. The corresponding residue in the first protein sequence is then assigned the residue number in the second reference protein sequence. The first protein sequence can be analogous to the second protein sequence or non-analogous to the second protein sequence, although it is preferred that the two protein sequences are analogous sequences. For example, when the amino acid sequence of an *E. coli* 'TesA, SEQ ID NO:31 in FIG. **57**, is used as a reference sequence, each of the amino acid residues in another aligned protein of interest or an analogous protein can be assigned a residue number corresponding to the residue numbers 2-183 of SEQ ID NO:31. For example, in FIG. **47**, the aligned amino acid sequences are

referenced or corresponded to the sequence of an *E. coli* 'TesA identified herein as SEQ ID NO: 73 (which is residues 2-183 of SEQ ID NO: 31). Accordingly, a given position in another thioesterase of interest, either a precursor or a mutant thioesterase, can be assigned a corresponding position in the 'TesA sequence, using known bioinformatic techniques such as those described herein.

The term "deletion," when used in the context of an amino acid sequence, means a deletion in or a removal of a residue from the amino acid sequence of a precursor protein, resulting in a mutant protein having one less amino acid residue as compared to the precursor protein. The term can also be used in the context of a nucleotide sequence, which means a deletion in or removal of a residue from the polynucleotide sequence of a precursor polynucleotide.

The term "derived from" and "obtained from" refer to, in the context of a precursor thioesterase, a thioesterase produced or producible by a strain of the organism in question, and also a thioesterase encoded by a polynucleotide sequence isolated from such strain and produced in a host organism containing such a polynucleotide sequence. Additionally, the terms refer to a thioesterase that is encoded by a polynucleotide sequence of synthetic and/or cDNA origin and that has the identifying characteristics of the thioesterase in question. To exemplify, "thioesterases derived from Enterobacteriacaea" refers to those enzymes having thioesterase activity that are naturally produced by Enterobacteriacaea, as well as to thioesterases like those produced by Enterobacteriacaea sources but that, through the use of genetic engineering techniques, are produced by non-Enterobacteriocaea organisms transformed with a polynucleotide encoding said thioesterase.

The term "DNA construct" and "transforming DNA" are used interchangeably herein to refer to a DNA used to introduce sequences into a host cell or organism. Typically a DNA construct is generated in vitro by PCR or other suitable technique(s) known to those in the art. In certain embodiments, the DNA construct comprises a sequence of interest (e.g., an incoming sequence). In some embodiments, the sequence is operably linked to additional elements such as control elements (e.g., promoters, etc.). A DNA construct can further comprise a selectable marker. It can also comprise an incoming sequence flanked by homology boxes. In a further embodiment, the DNA construct comprises other non-homologous sequences, added to the ends (e.g., stuffer sequences or flanks). In some embodiments, the ends of the incoming sequence are closed such that the DNA construct forms a closed circle. The transforming sequences may be wildtype, mutant or modified. In some embodiments, the DNA construct comprises sequences homologous to the host cell chromosome. In other embodiments, the DNA construct comprises non-homologous sequences. Once the DNA construct is assembled in vitro it may be used to: 1) insert heterologous sequences into a desired target sequence of a host cell; 2) mutagenize a region of the host cell chromosome (i.e., replace an endogenous sequence with a heterologous sequence); 3) delete target genes; and/or (4) introduce a replicating plasmid into the host.

A polynucleotide is said to "encode" an RNA or a polypeptide if, in its native state or when manipulated by methods known to those of skill in the art, it can be transcribed and/or translated to produce the RNA, the polypeptide, or a fragment thereof. The antisense strand of such a polynucleotide is also said to encode the RNA or polypeptide sequences. As is known in the art, a DNA can be transcribed by an RNA polymerase to produce an RNA, and an RNA can be reverse transcribed by reverse transcriptase to produce a DNA. Thus a DNA can encode an RNA, and vice versa.

The phrase "equivalent," in this context, refers to thioesterase enzymes that are encoded by a polynucleotide capable of hybridizing to the polynucleotide having the sequence of SEQ ID NO: 32, under conditions of medium to maximum stringency. For example, being equivalent means that an equivalent mature thioesterase comprises at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and/or at least 99% sequence identity to the amino acid sequence of SEQ ID NO:31 in FIG. **57**.

An "ester synthase" is a peptide capable of catalyzing a biochemical reaction to producing esters. For example, an ester synthase is a peptide that is capable of participating in converting a thioester to a fatty ester. In certain embodiments, an ester synthase converts a thioester, acyl-CoA, to a fatty ester. In an alternate embodiment, an ester synthase uses a thioester and an alcohol as substrates to produce a fatty ester. Ester synthases are capable of using short and long chain acyl-CoAs as substrates. In addition, ester synthases are capable of using short and long chain alcohols as substrates. Non-limiting examples of ester synthases include wax synthases, wax-ester synthases, acyl-CoA: alcohol transacylases, acyltransferases, fatty acyl-coenzyme A:fatty alcohol acyltransferases, fatty acyl-ACP transacylase, and alcohol acetyltransferase. An ester synthase that converts an acyl-CoA thioester to a wax is called a wax synthase. Exemplary ester synthases include those classified under the enzyme classification number EC 2.3.1.75. The term "ester synthase" does not comprise enzymes that also have thioesterase activity. The ones that have both ester synthase activity and thioesterase activity are categorized as thioesterases herein.

The term "expressed genes" refers to genes that are transcribed into messenger RNA (mRNA) and then translated into protein, as well as genes that are transcribed into types of RNA, such as transfer RNA (tRNA), ribosomal RNA (rRNA), and regulatory RNA, which are not translated into protein.

The terms "expression cassette" or "expression vector" refers to a polynucleotide construct generated recombinantly or synthetically, with a series of specified elements that permit transcription of a particular polynucleotide in a target cell. A recombinant expression cassette can be incorporated into a plasmid, chromosome, mitochondrial DNA, plasmid DNA, virus, or polynucleotide fragment. Typically, the recombinant expression cassette portion of an expression vector includes, among other sequences, a polynucleotide sequence to be transcribed and a promoter. In particular embodiments, expression vectors have the ability to incorporate and express heterologous polynucleotide fragments in a host cell. Many prokaryotic and eukaryotic expression vectors are commercially available. Selection of appropriate expression vectors is within the knowledge of those of skill in the art. The term "expression cassette" is also used interchangeably herein with "DNA construct," and their grammatical equivalents.

The term "fatty acid derivative," as used herein, refers to a composition that is derived from a metabolic pathway, which pathway includes a thioesterase reaction. Thus, fatty acid derivative products can be products that are, or are derived from, fatty acid or fatty esters that are products of a thioesterase reaction. Fatty acid derivatives thus include, for example, products that are, or that are derived from, fatty acids that are the direct reaction product of a thioesterase, and/or a fatty ester that is a direct reaction product of a thioesterase. Exemplary fatty acid derivatives include, for example, short and long chain alcohols, hydrocarbons, and

fatty alcohols and esters, including waxes, fatty acid esters, and/or fatty esters. Specific non-limiting examples of fatty acid derivatives include fatty acids, fatty acid methyl esters, fatty acid ethyl esters, fatty alcohols, fatty alkyl-acetates, fatty aldehydes, fatty amines, fatty amides, fatty sulfates, fatty ethers, ketones, alkanes, internal olefins, terminal olefins, dicarboxylic acids, w-dicarboxylic acids, diols and terminal and/or internal fatty acids.

The term "fatty acid derivative enzymes" refers to, collectively and individually, enzymes that may be expressed or overexpressed in the production of fatty acid derivatives. These enzymes may be parts of a fatty acid biosynthetic pathway. Non-limiting examples of fatty acid derivative synthases include fatty acid synthases, thioesterases, acyl-CoA synthases, acyl-CoA reductases, alcohol dehydrogenases, alcohol acyltransferases, fatty alcohol-forming acyl-CoA reductase, fatty acid decarbonylases, carboxylic acid reductases, fatty alcohol acetyl transferases, and ester synthases. Fatty acid derivative enzymes convert substrates into fatty acid derivatives. In certain circumstances, a suitable substrate may be a first fatty acid derivative, which is converted by a fatty acid derivative enzyme into a different, second fatty acid derivative.

The term "fatty alcohol" refers to an alcohol having the formula ROH. In certain embodiments, a fatty alcohol is an alcohol made from a fatty acid or fatty acid derivative. In one embodiment, the R group is at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 carbons in length. R can be straight or branched chain. The branched chains may have one or more points of branching. In addition, the branched chains may include cyclic branches, such as cyclopropane or epoxide moieties. Furthermore, R can be saturated or unsaturated. If unsaturated, R can have one or more points of unsaturation. In one embodiment, the fatty alcohol is produced biosynthetically. Fatty alcohols have many uses. For example, fatty alcohols can be used to produce specialty chemicals. Specifically, fatty alcohols can be used as biofuels; as solvents for fats, waxes, gums, and resins; in pharmaceutical salves, emollients and lotions; as lubricating-oil additives; in detergents and emulsifiers; as textile antistatic and finishing agents; as plasticizers; as nonionic surfactants; and in cosmetics, for example as thickeners.

The term "fatty alcohol forming peptides" refers to peptides capable of catalyzing the conversion of acyl-CoA to fatty alcohol, including fatty alcohol forming acyl-CoA reductase (FAR, EC 1.1.1.*), acyl-CoA reductase (EC 1.2.1.50) or alcohol dehydrogenase (EC 1.1.1.1). Additionally, one of ordinary skill in the art will appreciate that some fatty alcohol forming peptides will catalyze other reactions as well. For example, some acyl-CoA reductase peptides will accept substrates other than fatty acids. Such non-specific peptides are, therefore, also included. Polynucleotide sequences encoding fatty alcohol forming peptides are known in the art and such peptides are publicly available.

The term "fatty aldehyde" refers to an aldehyde having the formula RCHO characterized by an unsaturated carbonyl group (C═O). In certain embodiments, a fatty aldehyde is an aldehyde made from a fatty acid or fatty acid derivative. In one embodiment, the R group is at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 carbons in length. R can be straight or branched chain. The branched chains may have one or more points of branching. In addition, the branched chains can be cyclic branches. Furthermore, R can be saturated or unsaturated. If unsaturated, R can have one or more points of unsaturation. In one embodiment, the fatty aldehyde is produced biosynthetically. Fatty aldehydes have many uses. For example, fatty aldehydes can be used to produce specialty chemicals. Specifically, fatty aldehydes can be used to produce polymers, resins, dyes, flavorings, plasticizers, perfumes, pharmaceuticals, and other chemicals. Some are used as solvents, preservatives, or disinfectants. Some natural and synthetic compounds, such as vitamins and hormones, are also aldehydes.

The terms "fatty aldehyde biosynthetic polypeptide," "carboxylic acid reductase," and "CAR" are used interchangeably herein.

The term "fatty ester" refers to an ester having greater than 5 carbon atoms. In certain embodiments, a fatty ester is an ester made from a fatty acid, for example a fatty acid ester. In one embodiment, a fatty ester contains an A side (i.e., the carbon chain attached to the carboxylate oxygen) and a B side (i.e., the carbon chain comprising the parent carboxylate). In a particular embodiment, when a fatty ester is derived from the fatty acid biosynthetic pathway, the A side is contributed by an alcohol, and the B side is contributed by a fatty acid. Any alcohol can be used to form the A side of the fatty esters. For example, the alcohol can be derived from the fatty acid biosynthetic pathway. Alternatively, the alcohol can be produced through non-fatty acid biosynthetic pathways. Moreover, the alcohol can be provided exogenously. For example, the alcohol can be supplied to the fermentation broth in instances where the fatty ester is produced by an organism. Alternatively, a carboxylic acid, such as a fatty acid or acetic acid, can be supplied exogenously in instances where the fatty ester is produced by an organism that can also produce alcohol. The carbon chains comprising the A side or B side can be of any length. In one embodiment, the A side of the ester is at least about 1, 2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16, 18, or 20 carbons in length. The B side of the ester is at least about 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, or 26 carbons in length. The A side and/or the B side can be straight or branched chain. The branched chains may have one or more points of branching. In addition, the branched chains may include cyclic branches, such as cyclopropane or epoxide moieties. Furthermore, the A side and/or B side can be saturated or unsaturated. If unsaturated, the A side and/or B side can have one or more points of unsaturation. In one embodiment, the fatty ester is produced biosynthetically. In this embodiment, first the fatty acid is "activated." Non-limiting examples of activated fatty acids are acyl-CoA, acyl ACP, acyl-AMP, and acyl phosphate. Acyl-CoA can be a direct product of fatty acid biosynthesis or degradation. In addition, acyl-CoA can be synthesized from a free fatty acid, a CoA, and an adenosine nucleotide triphosphate (ATP). An example of an enzyme that produces acyl-CoA is an acyl-CoA synthase. After the fatty acid is activated, it can be readily transferred to a recipient nucleophile. Exemplary nucleophiles are alcohols, thiols, amines, or phosphates. In another embodiment, the fatty ester can be derived from a fatty acyl-thioester and an alcohol. In one embodiment, the fatty ester is a wax. The wax can be derived from a long chain fatty alcohol and a long chain fatty acid. In another embodiment, the fatty ester is a fatty acid thioester, for example fatty acyl Coenzyme A (acyl-CoA). In other embodiments, the fatty ester is a fatty acyl panthothenate, an acyl acyl carrier protein (acyl-ACP), a fatty acyl enzyme ester, or a fatty phosphate ester. An ester can be formed from an acyl enzyme ester intermediate through the alcoholysis of the ester bond to form a new ester and the free enzyme. Fatty esters have many uses. For example, fatty esters can be used as, or as a component of, a biofuel or a surfactant.

The term "fatty ester vs. other fatty acid derivatives" as used herein refers to the proportional yield of fatty ester in comparison with the total amount of other fatty acid deriva-

tives that are not fatty esters. In other words, the amount of fatty esters is compared with the amount of fatty acid derivatives other than fatty esters.

The term "fermentation productivity" or "productivity" refers to the rate of product production and is expressed g $L^{-1}h^{-1}$. Specific Productivity is the productivity normalized for catalyst concentration and is expressed as g/g $L^{-1}h^{-1}g$ $(catalyst)^{-1}$.

The term "fermentation titer" or "titer" refers to the concentration of a reaction product, usually expressed as g/L but also in other units (i.e., molar, mass/mass, mass/volume, or volume/volume).

The term "fermentation yield" or "yield" refers to the amount of product produced from a given amount of raw material and is usually expressed as the ratio of mass of the product produced divided by the mass of raw material consumed (g product/g raw material). It can also be expressed a molar yield (moles product/moles raw material).

The term "fraction of modern carbon" refers to the parameter "f_M" as defined by National Institute of Standards and Technology (NIST) Standard Reference Materials (SRMs) 4990B and 4990C, known as oxalic acids standards HOxI and HOxII, respectively. The fundamental definition relates to 0.95 times the $^{14}C/^{12}C$ isotope ratio HOxI (referenced to AD 1950). This is roughly equivalent to decay-corrected pre-Industrial Revolution wood. For the current living biosphere (plant material), f_M is about 1.1.

The term "functional assay" refers to an assay that provides an indication of a protein's activity. In particularly preferred embodiments, the term refers to an assay system in which a protein is analyzed for its ability to function in its natural capacity. For example, in the case of enzymes, a functional assay involves determining the effectiveness of the enzyme in catalyzing a reaction.

"Gene" refers to a polynucleotide (e.g., a DNA segment), which encodes a polypeptide, and includes regions preceding and following the coding regions as well as intervening sequences (introns) between individual coding segments (exons).

The term "homologous genes" refers to a pair of genes from different but related species, which correspond to each other and which are identical or similar to each other. The term encompasses genes that are separated by the speciation process during the development of new species) (e.g., orthologous genes), as well as genes that have been separated by genetic duplication (e.g., paralogous genes).

The term "endogenous protein" refers to a protein that is native to or naturally occurring in a cell. "Endogeneous polynucleotide" refers to a polynucleotide that is in the cell and was not introduced into the cell using recombinant engineering techniques. For example, a gene that was present in the cell when the cell was originally isolated from nature. A gene is still considered endogenous if the control sequences, such as a promoter or enhancer sequences that activate transcription or translation, have been altered through recombinant techniques. Conversely, the term "heterologous" is also used herein, and refers to a protein or a polynucleotide that does not naturally occur in a host cell.

The term "homologous recombination" refers to the exchange of DNA fragments between two DNA molecules or paired chromosomes at sites of identical or nearly identical nucleotide sequences. In certain embodiments, chromosomal integration is homologous recombination.

The term "homologous sequences" as used herein refers to a polynucleotide or polypeptide sequence having, for example, about 100%, about 99% or more, about 98% or more, about 97% or more, about 96% or more, about 95% or more, about 94% or more, about 93% or more, about 92% or more, about 91% or more, about 90% or more, about 88% or more, about 85% or more, about 80% or more, about 75% or more, about 70% or more, about 65% or more, about 60% or more, about 55% or more, about 50% or more, about 45% or more, or about 40% or more sequence identity to another polynucleotide or polypeptide sequence when optimally aligned for comparison. In particular embodiments, homologous sequences can retain the same type and/or level of a particular activity of interest. In some embodiments, homologous sequences have between 85% and 100% sequence identity, whereas in other embodiments there is between 90% and 100% sequence identity. In particular embodiments, there is 95% and 100% sequence identity.

"Homology" refers to sequence similarity or sequence identity. Homology is determined using standard techniques known in the art (see, e.g., Smith and Waterman, Adv. Appl. Math., 2:482, 1981; Needleman and Wunsch, J. Mol. Biol., 48:443, 1970; Pearson and Lipman, Proc. Natl. Acad. Sci. USA 85:2444, 1988; programs such as GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package (Genetics Computer Group, Madison, Wis.); and Devereux et al., Nucl. Acid Res., 12:387-395, 1984). A non-limiting example includes the use of the BLAST program (Altschul et al., Gapped BLAST and PSI-BLAST: a new generation of protein database search programs, Nucleic Acids Res. 25:3389-3402, 1997) to identify sequences that can be said to be "homologous." A recent version such as version 2.2.16, 2.2.17, 2.2.18, 2.2.19, or the latest version, including sub-programs such as blastp for protein-protein comparisons, blastn for nucleotide-nucleotide comparisons, tblastn for protein-nucleotide comparisons, or blastx for nucleotide-protein comparisons, and with parameters as follows: Maximum number of sequences returned 10,000 or 100,000; E-value (expectation value) of le-2 or le-5, word size 3, scoring matrix BLOSUM62, gap cost existence 11, gap cost extension 1, may be suitable. An E-value of 1e-5, for example, indicates that the chance of a homologous match occurring at random is about 1 in 10,000, thereby marking a high confidence of true homology.

The term "host strain" or "host cell" refers to a suitable host for an expression vector comprising a DNA of the present invention.

The term "hybridization" refers to the process by which a strand of polynucleotide joins with a complementary strand through base pairing, as known in the art. A polynucleotide sequence is considered to be "selectively hybridizable" to a reference polynucleotide sequence if the two sequences specifically hybridize to one another under moderate to high stringency hybridization and wash conditions. Hybridization conditions are based on the melting temperature (T_m) of the polynucleotide binding complex or probe. For example, "maximum stringency" typically occurs at about T_m−5° C. (5° C. below the Tm of the probe); "high stringency" at about 5-10° C. below the T_m; "intermediate stringency" at about 10-20° C. below the T_m of the probe; and "low stringency" at about 20-25° C. below the T_m. Functionally, maximum stringency conditions may be used to identify sequences having strict identity or near-strict identity with the hybridization probe; while an intermediate or a low stringency hybridization can be used to identify or detect polynucleotide sequence homologs. Moderate and high stringency hybridization conditions are well known in the art. An example of high stringency conditions includes hybridization at about 42° C. in 50% formamide, 5×SSC, 5×Denhardt's solution, 0.5% SDS and 100 pg/mL denatured carrier DNA followed by washing two times in 2×SSC and 0.5% SDS at room temperature and

two additional times in 0.1×SSC and 0.5% SDS at 42° C. An example of moderate stringent conditions includes an overnight incubation at 37° C. in a solution comprising 20% formamide, 5×SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5×Denhardt's solution, 10% dextran sulfate and 20 mg/mL denaturated sheared salmon sperm DNA, followed by washing the filters in 1×SSC at about 37° C. to about 50° C. Those of skill in the art know how to adjust the temperature, ionic strength, and other conditions as necessary to accommodate factors such as probe length and the like.

The term "hydrocarbon" refers to chemical compounds that contain the elements carbon (C) and hydrogen (H). All hydrocarbons consist of a carbon backbone and atoms of hydrogen attached to that backbone. Sometimes, the term is used as a shortened form of the term "aliphatic hydrocarbon." There are essentially three types of hydrocarbons: (1) aromatic hydrocarbons, which have at least about one aromatic ring; (2) saturated hydrocarbons, also known as alkanes, which lack double, triple or aromatic bonds; and (3) unsaturated hydrocarbons, which have one or more double or triple bonds between carbon atoms and include, for example, alkenes (e.g., dienes), and alkynes.

The term "identical," in the context of two polynucleotide or polypeptide sequences, means that the residues in the two sequences are the same when aligned for maximum correspondence, as measured using a sequence comparison or analysis algorithm such as those described herein. For example, if when properly aligned, the corresponding segments of two sequences have identical residues at 5 positions out of 10, it is said that the two sequences have a 50% identity. Most bioinformatic programs report percent identity over aligned sequence regions, which are typically not the entire molecules. If an alignment is long enough and contains enough identical residues, an expectation value can be calculated, which indicates that the level of identity in the alignment is unlikely to occur by random chance.

The term "improving mutation" or "performance-enhancing mutation" refers to a mutation in a protein that lead to altered properties, which confer improved performance in terms of a target and/or desired property of a protein as compared to a precursor protein.

The term "insertion," when used in the context of a polypeptide sequence, refers to an insertion in the amino acid sequence of a precursor polypeptide, resulting in a mutant polypeptide having an amino acid that is inserted between two existing contiguous amino acids, i.e., adjacent amino acids residues, which are present in the precursor polypeptide. The term "insertion," when used in the context of a polynucleotide sequence, refers to an insertion of one or more nucleotides in the precursor polynucleotide between two existing contiguous nucleotides, i.e., adjacent nucleotides, which are present in the precursor polynucleotides.

The term "introduced" refers to, in the context of introducing a polynucleotide sequence into a cell, any method suitable for transferring the polynucleotide sequence into the cell. Such methods for introduction include but are not limited to protoplast fusion, transfection, transformation, conjugation, and transduction (see, e.g., Ferrari et al., Genetics, in Hardwood et al, (eds.), *Bacillus*, Plenum Publishing Corp., pp. 57-72, 1989).

The term "isolated" or "purified" means a material that is removed from its original environment, for example, the natural environment if it is naturally occurring, or a fermentation broth if it is produced in a recombinant host cell fermentation medium. A material is said to be "purified" when it is present in a particular composition in a higher or lower concentration than the concentration that exists prior to the purification step(s). For example, with respect to a composition normally found in a naturally-occurring or wild type organism, such a composition is "purified" when the final composition does not include some material from the original matrix. As another example, where a composition is found in combination with other components in a recombinant host cell fermentation medium, that composition is purified when the fermentation medium is treated in a way to remove some component of the fermentation, for example, cell debris or other fermentation products, through, for example, centrifugation or distillation. As another example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated, whether such process is through genetic engineering or mechanical separation. Such polynucleotides can be parts of vectors. Alternatively, such polynucleotides or polypeptides can be parts of compositions. Such polynucleotides or polypeptides can be considered "isolated" because the vectors or compositions comprising thereof are not part of their natural environments. In another example, a polynucleotide or protein is said to be purified if it gives rise to essentially one band in an electrophoretic gel or a blot.

The term "mature," in the context of a protein, means a form of a protein or peptide that is in its final functional form. To exemplify, a mature form of a thioesterase of the present invention comprises the amino acid residues 2-183 of SEQ ID NO:31 in FIG. **57**.

The term "modified fatty acid derivatives" refers to products made, at least in part, from a part of the fatty acid biosynthetic pathway of a recombinant host cell, wherein the product differs from the product made by such host cell in the absence of the mutant thioesterase of the invention. Thus, where a mutant thioesterase (or naturally-occurring equivalent thereof) is introduced into a recombinant host cell, resulting in the production of a fatty acid derivative that has a different product profile, for example, a higher or lower concentration of certain fatty acid derivatives having a specific chain length, or a higher or lower concentration of a certain type of fatty acid derivative, that fatty acid material is "modified" within the context of this invention.

The term "mutant thioesterase" or "variant thioesterase" refers to a thioesterase that comprises a mutation with reference to a precursor thioesterase.

The term "mutation" refers to, in the context of a polynucleotide, a modification to the polynucleotide sequence resulting in a change in the sequence of a polynucleotide with reference to a precursor polynucleotide sequence. A mutant polynucleotide sequence can refer to an alteration that does not change the encoded amino acid sequence, for example, with regard to codon optimization for expression purposes, or that modifies a codon in such a way as to result in a modification of the encoded amino acid sequence. Mutations can be introduced into a polynucleotide through any number of methods known to those of ordinary skill in the art, including random mutagenesis, site-specific mutagenesis, oligonucleotide directed mutagenesis, gene shuffling, directed evolution techniques, combinatorial mutagenesis, site saturation mutagenesis among others.

"Mutation" or "mutated" means, in the context of a protein, a modification to the amino acid sequence resulting in a change in the sequence of a protein with reference to a precursor protein sequence. A mutation can refer to a substitution of one amino acid with another amino acid, an insertion or a deletion of one or more amino acid residues. Specifically, a

mutation can also be the replacement of an amino acid with a non-natural amino acid, or with a chemically-modified amino acid or like residues. A mutation can also be a truncation (e.g., a deletion or interruption) in a sequence or a subsequence from the precursor sequence. A mutation may also be an addition of a subsequence (e.g., two or more amino acids in a stretch, which are inserted between two contiguous amino acids in a precursor protein sequence) within a protein, or at either terminal end of a protein, thereby increasing the length of (or elongating) the protein. A mutation can be made by modifying the DNA sequence corresponding to the precursor protein. Mutations can be introduced into a protein sequence by known methods in the art, for example, by creating synthetic DNA sequences that encode the mutation with reference to precursor proteins, or chemically altering the protein itself. A "mutant" as used herein is a protein comprising a mutation. For example, it is also possible to make a mutant by replacing a portion of a thioesterase with a wild type sequence that corresponds to such portion but includes a desired variation at a specific position that is naturally-occurring in the wild type sequence.

A "naturally-occurring equivalent," in the context of the present invention, refers to a naturally-occurring thioesterase, or a portion thereof, that comprises a naturally-occurring residue, wherein the naturally-occurring residue corresponds to a mutation in 'TesA (e.g., a mutation in SEQ ID NO:31 of FIG. **57**) that has introduced a desirable altered property to 'TesA.

The term "operably linked," in the context of a polynucleotide sequence, refers to the placement of one polynucleotide sequence into a functional relationship with another polynucleotide sequence. For example, a DNA encoding a secretory leader (e.g., a signal peptide) is operably linked to a DNA encoding a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide. A promoter or an enhancer is operably linked to a coding sequence if it affects the transcription of the sequence. A ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in the same reading frame.

The term "operon region" refers to a group of contiguous genes that are transcribed as a single transcription unit from a common promoter, and are thereby subject to co-regulation. In some embodiments, the operon includes a regulator gene.

The term "optimal alignment" refers to the alignment giving the highest overall alignment score.

The term "orthologs" or "orthologous genes" refers to genes in different species that have evolved from a common ancestral gene by speciation. Typically, orthologs retain the same function during the course of evolution. Identification of orthologs finds use in the reliable prediction of gene function in newly sequenced genomes.

"Overexpressed" or "overexpression" in a host cell occurs if the enzyme is expressed in the cell at a higher level than the level at which it is expressed in a corresponding wild-type cell.

The term "paralog" or "paralogous genes" refers to genes that are related by duplication within a genome. While orthologs retain the same function through the course of evolution, paralogs evolve new functions, even though some functions are often related to the original one. Examples of paralogous genes include, but are not limited to, genes encoding myoglobin and hemoglobin, which arose from the same ancient ancestor but evolved to have different functions.

The term "partition coefficient" means the equilibrium concentration of a compound in an organic phase divided by the concentration at equilibrium in an aqueous phase (e.g., in a fermentation broth). In one embodiment of the bi-phasic system described herein, the organic phase is formed by the fatty acid derivative during the production process. In certain circumstances, an organic phase can also be provided, for example, a layer of octane can be provided to the fermentation broth to facilitate product separation. When describing a two phase system, the partition coefficient, P, is usually discussed in terms of log P. A compound with a log P of 1 would partition 10:1 to the organic phase. A compound with a log P of −1 would partition 1:10 to the organic phase. By choosing an appropriate fermentation broth and organic phase, a fatty acid derivative with a high log P value will separate into the organic phase even at very low concentrations in the fermentation vessel.

The terms "percent sequence identity," "percent amino acid sequence identity," "percent gene sequence identity," and/or "percent polynucleotide sequence identity," with respect to two polypeptides, polynucleotides and/or gene sequences (as appropriate), refer to the percentage of residues that are identical in the two sequences when the sequences are optimally aligned. Thus, 80% amino acid sequence identity means that 80% of the amino acids in two optimally aligned polypeptide sequences are identical.

The term "plasmid" refers to a circular double-stranded (ds) DNA construct used as a cloning vector, and which forms an extrachromosomal self-replicating genetic element in some eukaryotes or prokaryotes, or integrates into the host chromosome.

The term "precursor thioesterase" refers a thioesterase protein from which the mutant thioesterase of the invention can be derived, through, for example, recombinant or chemical means. Examples of precursor thioesterases are naturally-occurring or wildtype thioesterases from plant, animal or microbial sources. A precursor thioesterase can also be a thioesterase that is non-naturally-occurring. An example of a non-naturally-occurring thioesterase is a thioesterase made through, for example, random mutation, chemical synthesis, molecular evolution, or site directed mutagenesis, which can serve as a useful starting point from which to design and/or make the mutant thioesterases of the invention.

A "primer" is an oligonucleotide, whether occurring naturally as in a purified restriction digest sample, or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which the synthesis of a primer extension product that is complementary to a reference polynucleotide strand is induced. Suitable conditions include, for example, the presence of nucleotides and an inducing agent such as a DNA polymerase, and a suitable temperature and pH. A primer is preferably single stranded for maximum efficiency in amplification, but can alternatively be double stranded. If double stranded, a primer can be first treated to separate its strands before it is used to prepare extension products. In particular embodiments, a primer is an oligodeoxyribonucleotide. In certain preferred embodiments, a primer is sufficiently long to prime the synthesis of extension products in the presence of an inducing agent. The exact lengths of primers will depend on a number of factors, including temperature, source of primer, and the methods used for amplification.

The term "probe" refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, recombinantly or by PCR amplification, which is capable of hybridizing to another oligonucleotide of interest. A probe may be single-stranded or double-stranded.

Probes are useful in the detection, identification and isolation of particular gene sequences. It is contemplated that any probe used in the present invention will be labeled with any "reporter molecule," so that is detectable in any detection system, including, but not limited to enzyme (e.g., ELISA or other enzyme-based histochemical assays), fluorescent, radioactive, and luminescent systems. It is not intended that the present invention be limited to any particular detection system or label.

A "production host" is a cell used to produce products. As disclosed herein, a production host is modified to express or overexpress selected genes, or to have attenuated expression of selected genes. Non-limiting examples of production hosts include plant, animal, human, bacteria, yeast, cyanobacteria, algae, and/or filamentous fungi cells.

A "promoter" is a polynucleotide sequence that functions to direct transcription of a downstream gene. In preferred embodiments, the promoter is appropriate to the host cell in which the target gene is being expressed. The promoter, together with other transcriptional and translational regulatory polynucleotide sequences (also termed "control sequences") is necessary to express a given gene. In general, the transcriptional and translational regulatory sequences include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences.

The term "promoters" or "enhancers" refers to transcriptional control signals in eukaryotes. Promoters and enhancers consist of short arrays of DNA sequences that interact specifically with cellular proteins involved in transcription (Maniatis et al., Science, 236:1237, 1987). Promoter and enhancer elements have been isolated from a variety of eukaryotic sources including genes in yeast, insect, mammalian and plant cells. Promoter and enhancer elements have also been isolated from viruses. Analogous control elements, such as promoters and enhancers, are also found in prokaryotes. The selection of a particular promoter and enhancer depends on the cell type used to express the protein of interest. Some eukaryotic and prokaryotic promoters and enhancers have a broad production host cell range while others are functional in a limited subset of production host cells (see, e.g., Voss et al., Trends Biochem. Sci., 11:287, 1986; Maniatis et al., 1987, supra). The term "promoter element," "promoter," or "promoter sequence" refers to a DNA sequence that functions as a switch which activates the expression of a gene. If the gene is activated, it is said to be transcribed, or participating in transcription. Transcription involves the synthesis of mRNA from the gene. The promoter, therefore, serves as a transcriptional regulatory element and also provides a site for initiation of transcription of the gene into mRNA.

The term "property" refers to, in the context of a polynucleotide, any characteristic or attribute of a polynucleotide that can be selected or detected. These properties include, but are not limited to, a property affecting binding to a polypeptide, a property conferred on a cell comprising a particular polynucleotide, a property affecting gene transcription (e.g., promoter strength, promoter recognition, promoter regulation, enhancer function), a property affecting RNA processing (e.g., RNA splicing, RNA stability, RNA conformation, and post-transcriptional modification), a property affecting translation (e.g., level, regulation, binding of mRNA to ribosomal proteins, post-translational modification). For example, a binding site for a transcription factor, polymerase, regulatory factor, and the like, of a polynucleotide may be altered to produce desired characteristics or to identify undesirable characteristics.

The term "property" refers to, in the context of a protein, any characteristic or attribute of a protein that can be selected or detected.

The terms "protein" and "polypeptide" are used interchangeably herein. The 3-letter code as well as the 1-letter code for amino acid residues as defined in conformity with the IUPAC-IUB Joint Commission on Biochemical Nomenclature (JCBN) is used throughout this disclosure. It is also understood that a polypeptide may be coded for by more than one polynucleotide sequence due to the degeneracy of the genetic code. An enzyme is a protein.

The terms "proportional yield" and "percentage yield" are used interchangeably herein. It refers to the amount of a desired product in relation to other products that are within the same mixture produced by a recombinant host of the present invention. For example, the proportional yield of a desired product can be improved such that it is more predominant over the other components in the product mixture to reduce the burden of purification. In another example, the proportional yield of an undesired product (i.e., a component that will need to be removed from the desired product) can be reduced such that it is less predominant over the desired component in the product mixture to achieve the same end. Proportional yields are expressed herein in the form of "X vs. other fatty acid derivatives," which compares the amount of X, which is a type of fatty acid derivative (e.g., a fatty ester, a fatty acid derivative of a particular chain length), and the term "other fatty acid derivatives" means the aggregate amount of all other fatty acid derivatives other than X that are produced in the same experiment, culture, or fermentation run.

The term "prosequence" refers to an amino acid sequence between the signal sequence and mature protein that is necessary for the secretion of the protein. Cleavage of the prosequence can lead to a mature active protein/enzyme under certain circumstances and suitable conditions.

The term "recombinant," when used to modify the term "cell" or "vector" herein, refers to a cell or a vector that has been modified by the introduction of a heterologous polynucleotide sequence, or that the cell is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found in identical form within the native (non-recombinant) form of the cells or express, as a result of deliberate human intervention, native genes that are otherwise abnormally expressed, underexpressed or not expressed at all. The terms "recombination," "recombining," and generating a "recombined" polynucleotide refer generally to the assembly of two or more polynucleotide fragments wherein the assembly gives rise to a chimeric polynucleotide made from the assembled parts.

The term "regulatory segment," "regulatory sequence," or "expression control sequence" refers to a polynucleotide sequence that is operatively linked with another polynucleotide sequence that encodes the amino acid sequence of a polypeptide chain to effect the expression of that encoded amino acid sequence. The regulatory sequence can inhibit, repress, promote, or even drive the expression of the operably-linked polynucleotide sequence encoding the amino acid sequence.

The term "selectable marker" or "selective marker" refers to a polynucleotide (e.g., a gene) capable of expression in a host cell, which allows for ease of selection of those hosts containing the vector. Examples of selectable markers include but are not limited to antimicrobial markers. Thus, the term "selectable marker" refers to a gene that provides an

indication when a host cell has taken up an incoming sequence of interest or when some other reaction has taken place. Typically, selectable markers are genes that confer antimicrobial resistance or a metabolic advantage on the host cells to allow the cells containing the exogenous sequences to be distinguished from the cells that have not received the exogenous sequences. A "residing selectable marker" is one that is located on the chromosome of the microorganism to be transformed. A residing selectable marker encodes a gene that is different from the selectable marker on the transforming construct. Selective markers are known to those of skill in the art. As indicated above, suitably the marker is an antimicrobial resistant marker, including, for example, amp^R; $phleo^R$; $spec^R$; kan^R; ery^R; tet^R; cmp^R; and neo^R. See, e.g., Guerot-Fleury, Gene, 167:335-337, 1995; Palmeros et al., Gene, 247: 255-264, 2000; and Trieu-Cuot et al., Gene, 23:331-341, 1983. Other markers useful in accordance with the invention include, but are not limited to, auxotrophic markers, such as tryptophan; and detection markers, such as 6-galactosidase.

The term "selectable marker-encoding nucleotide sequence" refers to a polynucleotide sequence that is capable of expression in the host cells and where the expression of the selectable marker confers to the cells containing the expressed gene the ability to grow in the presence of a corresponding selective agent or in the absence of one or more essential nutrients.

A "signal sequence" or "signal peptide" refers to a polynucleotide or amino acid sequence that participates in the secretion of the mature or precursor forms of a protein. This definition of signal sequence is a functional one, meant to include all those amino acid sequences encoded by the N-terminal portion of the protein gene, which participate in the effectuation of the secretion of protein. They are often, but not universally, bound to the N-terminal portion of a protein or to the N-terminal portion of a precursor protein. The signal sequence can be endogenous or exogenous. The signal sequence can be one that is normally associated with the protein (e.g., thioesterase), or can be one originated or derived from a gene encoding another secreted protein. An exemplary exogenous signal sequence comprises the first seven amino acid residues of the signal sequence from *Bacillus subtilis* subtilisin fused to the remainder of the signal sequence of the subtilisin from *Bacillus lentos* (ATCC 21536). Another exemplary signal sequence comprises the signal sequence for TesA that is removed to produce 'TesA.

The term "substantially identical," in the context of two polynucleotides or two polypeptides refers to a polynucleotide or polypeptide that comprises at least 70% sequence identity, for example, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity as compared to a reference sequence using the programs or algorithms (e.g., BLAST, ALIGN, CLUSTAL) using standard parameters. One indication that two polypeptides are substantially identical can be that the first polypeptide is immunologically cross-reactive with the second polypeptide. Typically, polypeptides that differ by conservative amino acid substitutions are immunologically cross-reactive. Thus, a polypeptide is substantially identical to a second polypeptide, for example, when the two peptides differ only by a conservative substitution. Another indication that two polynucleotide sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions (e.g., within a range of medium to maximum stringency).

"Substantially purified" means molecules that are at least about 60% free, preferably at least about 75% free, about 80% free, about 85% free, and more preferably at least about 90% free from other components with which they are naturally associated. As used herein, the term "purified" or "to purify" also refers to the removal of contaminants from a sample. For example, the removal of contaminants can result in an increase in the percentage of fatty acid derivatives of interest in a sample. For example, after fatty acid derivatives are expressed in plant, bacterial, yeast, or mammalian production host cells, the fatty acid derivatives can be purified by, e.g., the removal of production host cell proteins. This step, also called recovery, involves separating and processing the fatty acid derivative composition such that the composition is useful in industrial applications, for example, as a fuel or a chemical. After purification, the percentage of fatty acid derivatives in the sample is increased. The term purified does not require absolute purity; rather, it is intended as a relative term. Thus, for example, a purified fatty acid derivative preparation is one in which the product is more concentrated than the product is in its environment within a cell. For example, a purified fatty ester is one that is substantially separated from cellular components (e.g., polynucleotides, lipids, carbohydrates, and other peptides) that can accompany it. In another example, a purified fatty ester preparation is one in which the fatty ester is substantially free from contaminants, such as those that might be present following fermentation. For example, a fatty ester is said to be "purified" when at least about 50% by weight of a sample is composed of the fatty ester. In another example when at least about 60%, 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more by weight of a sample is composed of the fatty ester.

"Substitution" means replacing an amino acid in the sequence of a precursor protein with another amino acid at a particular position, resulting in a mutant of the precursor protein. The amino acid used as a substitute can be a naturally-occurring amino acid, or can be a synthetic or non naturally-occurring amino acid.

The term "surfactants" refers to substances that are capable of reducing the surface tension of a liquid in which they are dissolved. They are typically composed of a water-soluble head and a hydrocarbon chain or tail. The water-soluble head is hydrophilic and can be either ionic or nonionic. The hydrocarbon chain is hydrophobic. Surfactants are used in a variety of products, including detergents and cleaners, and are also used as auxiliaries for textiles, leather and paper, in chemical processes, in cosmetics and pharmaceuticals, in the food industry, in agriculture, and in oil recovery. In addition, they can be used to aid in the extraction and isolation of crude oils which are found in hard-to-access environments or in water emulsions. There are four types of surfactants characterized by varying uses. Anionic surfactants have detergent-like activity and are generally used for cleaning applications. Cationic surfactants contain long chain hydrocarbons and are often used to treat proteins and synthetic polymers or are components of fabric softeners and hair conditioners. Amphoteric surfactants also contain long chain hydrocarbons and are typically used in shampoos. Non-ionic surfactants are often used in cleaning products.

The term "synthase" refers to an enzyme that catalyzes a synthesis process. As used herein, the term "synthase" includes synthases and synthetases.

The term "target property" refers to a property of the starting gene that is intended to be altered.

The term "thioesterase" refers to an enzyme that has thioesterase activity. Thioesterases include thioester hydrolases, which are identified as members of Enzyme Classification E.C. 3.1.2 and are obtainable from a variety of sources. Plant thioesterases are described in, for example, Voelker and

Davies, J. Bact., Vol., 176, No. 23, pp. 7320-27, 1994, U.S. Pat. No. 5,667,997, and U.S. Pat. No. 5,455,167. Thioesterases are also obtainable from microbial sources, such as those described in Akoh et al., Prog. Lipid Res., vol. 43, no. 6, pp. 534-52, 2004; Diczfalusy and Alexson, Arch. Biochem. Biophys., vol. 334, no. 1, pp. 104-12, 1996; Larson and Kolalttukudy, Arch. Biochem. Biophys., vol. 237, no. 1, pp. 27-37, 1985; Lawson et al., Biochemistry, vol. 33, no. 32, pp. 9382-88, 1994; Lee et al., Eur. J. Biochem., vol. 184, no. 1, pp. 21-28, 1989; Naggert et al., J. Biol. Chem., vol. 266, no. 17, pp. 11044-50, 1991; Nie et al., Biochemistry, vol. 47, no. 29, pp. 7744-51, 2008; Seay and Lueking, Biochemistry, vol. 25, no. 9, pp. 2480-85, 1986; Spencer et al., J. Biol. Chem., vol. 253, no. 17, pp. 5922-26, 1978; and Zhuang et al., Biochemistry, vol. 47, no. 9, pp. 2789-96, 2008. Thioesterases are also obtainable from, for example, cyanobacterial, algal, mammalian, insect, and fungal sources. A thioesterase can have activity other than thioesterase activity, for example proteolytic activity or oxygen ester hydrolysis activity. A particularly useful thioesterase is the 'TesA (or thioesterase I) enzyme from *E. coli*, which is a truncated version of the full-length TesA serine thioesterase enzyme that is described in Cho and Cronan, J. Biol. Chem., vol., 268, no. 13, pp. 9238-45, 1993. An *E. coli* 'TesA polypeptide comprises 182 amino acids, and is the product of a cleavage reaction wherein the 26 amino acid leader sequence of *E. coli* TesA is removed. *E. coli* 'Tes A, for example, has the amino acid sequence of SEQ ID NO:31 in FIG. **57**, which comprises the 182 amino acid mature polypeptide sequence at residues 2-183, and an initiator methionine residue at residue 1. The 182 amino acid *E. coli* 'TesA mature polypeptide sequence is also identified herein as SEQ ID NO: 73.

The term "thioesterase activity" refers to the capacity to catalyze a thioester cleavage reaction, which usually involves the hydrolysis of a thioester at a thiol group into an acid and a thiol, but can also include a transesterification step in which a thioester bond is cleaved and a new ester bond is formed. In general, an acyl-ACP thioesterase is capable of catalyzing the hydrolytic cleavage of fatty acyl-acyl carrier protein thioesters and/or fatty acyl-coenzyme A thioesters. Examples of enzymes having thioesterase activity include acetyl-CoA hydrolase, palmitoyl-CoA hydrolase, succinyl-CoA hydrolase, formyl-CoA hydrolase, acyl-CoA hydrolase, palmitoyl-protein thioesterase, and ubiquitin thiolesterase. Thioesterase activity can be established by any of the following assays:

Acyl-CoA Hydrolysis Assay:

A Tris-HCl buffer, 0.1 M, pH 8.0; Palmitoyl-CoA, 5 μM; DTNB, 0.01 M in 0.1 M potassium phosphate buffer, pH 7.0 are used to prepare a complete assay mixture. The assay mixture thus contains a final concentration of 10 μmol of Tris-HCl buffer, pH 8.0, 0.05 μmol of DTNB, and 0.01 μmol of palmitoyl-CoA. The complete assay mixture is then mixed with the thioesterase, in a final volume of 2.0 mL.

The rate of cleavage of the acyl-CoA substrate is measured by monitoring the change in absorbance at 405 nm, using a molar extinction coefficient of 13,600 M^{-1} cm^{-1}.

In vivo Assay:

The thioesterase of interest is expressed in a suitable host, such as an *E. coli*. Following expression of the protein, the culture is acidified with 1 N HCl to a final pH of about 2.5 and then extracted with an equal volume of ethyl acetate. Free fatty acids in the organic phase are derivatized with tetramethylammonium hydroxide (TMAH) to generate the respective methyl esters, which are then analyzed on a gas chromatograph equipped with a flame ionization detector.

Thiolactone Hydrolysis Assay:

A reagent solution containing 25 mM L-homocysteine thiolactone (L-HcyT) and 0.5 mM 5,5-dithio-bis-2-nitrobenzoic acid (DTNB) in 0.1 M HEPES buffer (pH 7.3) is first prepared. Enzyme is then added to the reagent solution and L-HcyT hydrolysis is monitored by detecting the free thiol group with DTNB at 412 nm (∈=13,600 M^{-1} cm^{-1} for 5-thio-2-nitrobenzoic acid).

4-MU-6S-Palm-βGlc Assay:

A reaction mixture containing 10 μL of thioesterase enzyme and 20 μL of substrate solution is first prepared. The substrate solution contains 0.64 mM MU-6S-Palm-β-Glc, 15 mM dithiothreitol (DTT), 0.375% (w/v) Triton X-100, and 0.1 U β-glucosidase from almonds in McIlvain's phosphate/citrate buffer, pH 4.0. The reaction mixture is incubated for 1 hour at 37° C. Exogenous almond β-glucosidase is added to hydrolyze the reaction intermediate, MU-6-thio-β-glucoside, quantitatively. The hydrolysis reaction is terminated by the addition of 200 μL of 0.5 M sodium carbonate, pH 10.7, containing 0.025% Triton X-100, and the fluorescence of the released 4-methylumbelliferone (MU) is measured in a fluorometer (λ_{ex}=372, λ_{em}=445 nm).

Lysophospholipase Assay:

A reaction mixture containing 10 μL of thioesterase mixed with 10 μL of 3 mM 1-oleoyl-phosphatidylethanolamine, 25 μL of 100 mM Tris-HCl (pH 7.0), and 5 μL of 5 mM EDTA is prepared. The reaction is terminated with the addition of 1.5 mL $CHCl_3$:CH_3OH (1:2), followed by the addition of water to bring the total aqueous volume to 0.9 mL. The organic phase is then analyzed by thin layer chromatography together with suitable standards, using plates prepared from 40 g Silica Gel H suspended in 95 mL of 1 mM sodium tetraborate. The solvent system consists of $CHCl_3$:CH_3OH:H_2O (95:35:5).

Protease Substrate Assay:

A reaction mixture containing 10 μL of enzyme mixed with 800 μL 12.5 mM Tris-HCl (pH 8.0) containing 0.25% Triton X-100 and 10 μL of Cbz-Phe-ONp dissolved in DMSO is prepared. The p-nitrophenol released via cleavage of the substrate is measured by monitoring the absorbance at 405 nm.

Fatty Acyl-PNP Hydrolysis Assay:

A reagent solution containing 2% Triton X-100 in 50 mM sodium phosphate, pH 7.0, and 10 mM C_{12}-p-nitrophenol (acyl-PNP) in acetone is first prepared. Then a C_{12}-PNP working solution is prepared by mixing 600 μL 10 mM C_{12}-PNP into a 9.4-mL phosphate buffer.

The assay is performed by adding 40 μL of the acyl-PNP working solution to each well of a 96-well plate, followed by the rapid addition of 40 μL of enzyme. The solution is mixed for 15 seconds, and the absorbance change is read at 405 nm in a microtiter plate reader at 25° C.

Ester Formation from Thioester:

A reaction mixture containing 1.5 μM thioesterase enzyme, 100 μM myristoyl-CoA, 10% (v/v) methanol, and 50 mM sodium phosphate, pH 7.0 is prepared. The reaction mixture is incubated for 1 hour at 20° C. and terminated with the addition of 1 N HCl to decrease the pH to about 2.5. The mixture is extracted with an equal volume of ethyl acetate and the amount of fatty ester produced is determined via GC-MS or other standard methods such as GC-FID, LC-MS, or thin layer chromatography.

Ester Formation from Ester:

A reaction mixture containing 1.5 μM thioesterase enzyme, 300 μM lauroyl-CoA, 10% (v/v) methanol, and 50 mM sodium phosphate, pH 7.0 is prepared. The reaction mixture is incubated for 1 hour at 20° C. and terminated with the addition of 1 N HCl to decrease the pH to about 2.5. The mixture is extracted with an equal volume of ethyl acetate and the amount of lauryl ester produced is determined via GC-MS or other standard methods such as GC-FID, LC-MS, or thin layer chromatography.

The term "transformed" or "stably transformed" cell refers to a cell that has a non-native (heterologous) polynucleotide sequence integrated into its genome or as an episomal plasmid that is maintained for at least two generations.

The term "transport protein" refers to a protein that facilitates the movement of one or more compounds in and/or out of an organism or organelle. In some embodiments, an exogenous DNA sequence encoding an ATP-Binding Cassette (ABC) transport protein will be functionally expressed by the production host so that the production host exports the fatty acid derivative into the culture medium. ABC transport proteins are found in many organisms, such as *Caenorhabditis elegans, Arabidopsis thalania, Alcaligenes eutrophus* (later renamed *Ralstonia eutropha*), or *Rhodococcus erythropolis*. Non-limiting examples of ABC transport proteins include CER5, AtMRP5, AmiS2 and AtPGP1. In a preferred embodiment, the ABC transport protein is CER5 (e.g., AY734542). In other embodiments, the transport protein is an efflux protein selected from: AcrAB, To1C, or AcrEF from *E. coli* or tll1618, tll1619, and tll0139 from *Thermosynechococcus elongatus* BP-1. In further embodiments, the transport protein is a fatty acid transport protein (FATP) selected from *Drosophila melanogaster, Caenorhabditis elegans, Mycobacterium tuberculosis*, or *Saccharomyces cerevisiae* or any one of the mammalian FATPs known in the art. Transport proteins are useful, for example, for enhancing the secretion or release of products that are otherwise not capable of spontaneously secret the product. They are also useful when the engineered host cells are capable of spontaneously secret or release the product, but either release it slowly or incompletely. Under those circumstances, the transport proteins can enhance the secretion by accelerating the secretion step or driving the secretion to completion.

"Variant" is used interchangeably herein with "mutant."

"Vector" refers to a polynucleotide construct designed to introduce polynucleotides into one or more cell types. Vectors include cloning vectors, expression vectors, shuttle vectors, plasmids, cassettes and the like. In some embodiments, the polynucleotide construct comprises a polynucleotide sequence encoding a thioesterase (e.g., a precursor or a mature thioesterase) that is operably linked to a suitable prosequence (e.g., a secretory pro-sequence) capable of effecting the expression of the polynucleotide or gene in a suitable host.

A "wax" is a substance comprising, at least in part, fatty esters. In certain embodiments, a fatty ester has an A side and a B side, each comprising medium to long carbon chains. In addition to fatty esters, a wax may comprise other components. For example, a wax can comprise hydrocarbons, sterol esters, aliphatic aldehydes, alcohols, ketones, beta-diketones, triacylglycerols and the like. Typically a wax is a solid at room temperature, for example, at 20° C.

"Wild-type" means, in the context of gene or protein, a polynucleotide or protein sequence that occurs in nature. In some embodiments, the wild-type sequence refers to a sequence of interest that is a starting point for protein engineering.

Production of Fatty Acid Derivatives

According to an embodiment of the present invention, the novel thioesterases of the invention are expressed in a host cell that is capable of converting a carbon source to a fatty acid derivative. The invention pertains to two distinct embodiments: (1) the discovery that a mutant thioesterase can be used to optimize and/or "design" a fatty acid derivative composition so as to make such compositions more useful and that different mutations will provide different target properties; and (2) the discovery that thioesterase will act in a recombinant host cell to directly produce fatty ester products, without the presence of a wax synthase or ester synthase enzyme.

According to an embodiment of the invention, the fatty acid derivative compositions produced in accordance with the methods, vectors, and cells herein have modified or altered properties as compared to the fatty acid derivatives produced using host cells that do not comprise the thioesterase variants of the invention. For example, as also described herein, using the thioesterases of the present invention, it is possible to develop manufacturing processes that produce fatty acid derivatives, which, in comparison with a similar process involving a wildtype thioesterase, have altered compositional profiles, for example, altered percentages of a range of or a specific carbon chain length acyl group, saturated or unsaturated acyl groups, position of unsaturations, branched acyl groups, position of branching, hydroxyl-acyl groups, keto-acyl groups, proportion of esters or free fatty acids in the product, proportion of short-chain (e.g., C_8, C_9, C_{10}, C_{11}, C_{12}, C_{13}, and/or C_{14}) vs. long-chain (e.g., C_{15}, C_{16}, C_{17}, C_{18}, C_{19}, and/or C_{20}) fatty acid derivatives, or yield of fatty acid derivatives. Accordingly, products with various desirable properties can be engineered such that they have optimized cetane numbers, octane ratings, oxidative stability, lubricity, flash points, viscosity, boiling points, melting points, pour points, cloud points, cold filter plugging points, cold flow characteristics, aromaticity, and/or iodine numbers.

Fatty acid derivatives are useful as, or as components of, biofuels and specialty chemicals. Fatty acid derivatives and products made therefrom include fuels, fuel additives, fuel blends, detergents and surfactants, nutritional supplements, polymers, paraffin replacements, lubricants, solvents, personal care products, rubber processing additives, corrosion inhibitors, emulsifiers, plastics, textiles, cosmetics, paper products, coatings, metalworking fluids, dielectrics, oiling agents and emollients. The methods and compositions disclosed herein allow for the production of fatty acid derivatives with particular branch points, levels of saturation, and carbon chain length. The methods and compositions herein also allow for the production of a higher proportion of fatty esters vs. other products, or alternatively, a lower proportion of fatty esters vs. other products, depending on whether a higher proportional or percentage yield of fatty esters or a lower proportional or percentage yield of fatty esters is desirable. Specifically, for example, the methods and compositions herein allow for the production of a larger proportion of fatty acid esters vs. free fatty acids, or in other words, allows for a higher proportional or percentage yield of fatty acid esters vs. free fatty acids. Alternatively, for example, the methods and compositions herein allow for the production of a smaller proportion of fatty acid esters vs. free fatty acids, when large amounts of fatty acid esters are undesirable. Furthermore, the methods and compositions herein allow for the production of an improved yield of fatty acid derivatives.

Non-limiting examples of microorganisms which can be used as production hosts to produce fatty acid derivatives include cyanobacteria, algae, bacteria, yeast, or filamentous

fungi. Further non-limiting examples of suitable production hosts include plant, animal, or human cells.

Alcohols (short chain, long chain, branched, or unsaturated) can be produced by the production hosts described herein. Such alcohols can be used as fuels directly or they can be used to create a fatty ester. Fatty esters, alone or in combination with other fatty acid derivatives described herein, are also useful as, or as components of, fuels.

Similarly, hydrocarbons produced from the production hosts described herein can be used as, or as components of, biofuels. Such hydrocarbon-based fuels can be designed to contain branch points, defined degrees of saturation, and specific carbon lengths utilizing the teachings provided herein. When used as biofuels alone or in combination with other fatty acid derivatives, the hydrocarbons can be combined with suitable additives or other traditional fuels (e.g., alcohols, diesel derived from triglycerides, and petroleum-based fuels).

The cetane number (CN), viscosity, melting point, and heat of combustion for various fatty esters have been characterized in Knothe, Fuel Processing Technology 86:1059-1070, 2005, which is herein incorporated by reference in its entirety. A production host can be engineered to produce any of the fatty esters described in Knothe, using the teachings provided herein.

I. Production of Fatty Acid Derivatives and Modifications for Improving Production/Yield

The production host used to produce acyl-CoA and/or fatty acid derivatives can be recombinantly modified to include polynucleotide sequences that over-express peptides. For example, the production host can be modified to increase the production of acyl-CoA and reduce the catabolism of fatty acid derivatives and intermediates in the fatty acid biosynthetic pathway, or to reduce feedback inhibition at specific points in the fatty acid biosynthetic pathway. In addition to modifying the genes described herein, additional cellular resources can be diverted to over-produce fatty acids. For example, the lactate, succinate, and/or acetate pathways can be attenuated, and acetyl-CoA carboxylase (acc) can be over-expressed. The modifications to the production host described herein can be through genomic alterations, addition of recombinant expression systems, or combinations thereof. For example, one or more endogenous thioesterases of a particular production host can be modified using suitable techniques such that the mutant thioester has at least one altered property as compared to the endogenous thioesterase precursor, or such that the host cell exhibits at least one altered property, as compared to the same host cell before it is subject to the genomic alteration steps.

The fatty acid biosynthetic pathways involved are illustrated in FIGS. **2-5**. Subsections A-G below describe the steps in these pathways. Various enzymes catalyze various steps in the pathway. Accordingly, each step is a potential place for overexpression of the gene to produce more enzyme(s) and thus drive the production of more fatty acids and fatty acid derivatives. Genes encoding the enzymes required for the pathway may also be recombinantly added to a production host lacking such enzymes. Finally, steps that would compete with the pathway leading to production of fatty acids and fatty acid derivatives can be attenuated or blocked in order to increase the production of the desired products.

According to the disclosures herein, a person of ordinary skill in the art can use the thioesterases of the invention to prepare microorganisms that produce fatty acid derivatives and to manufacture various fatty acid derivatives using such microorganisms, wherein such fatty acid derivatives have altered properties. It is further possible to prepare microorganisms that produce such fatty acid derivatives more efficiently by having the desired levels of yield, productivity, or titer during fermentations.

A. Acetyl-CoA-Malonyl-CoA to Acyl-ACP

Fatty acid synthase (FAS) is a group of peptides that catalyze the initiation and elongation of acyl chains (Marrakchi et al., Biochemical Society, 30:1050-1055, 2002). The acyl carrier protein (ACP) along with the enzymes in the FAS pathway control the length, degree of saturation, and branching of the fatty acids produced. The steps in this pathway are catalyzed by enzymes of the fatty acid biosynthesis (fab) and acetyl-CoA carboxylase (acc) gene families. Depending upon the desired product, one or more of these genes can be attenuated or over-expressed.

I. Fatty Acid Biosynthetic Pathway: Acetyl-CoA or Malonyl-CoA to Acyl-ACP

The fatty acid biosynthetic pathway in the production host uses the precursors acetyl-CoA and malonyl-CoA. The steps in this pathway are catalyzed by enzymes of the fatty acid biosynthesis (fab) and acetyl-CoA carboxylase (acc) gene families. This pathway is described in Heath et al., Prog. Lipid Res., 40(6):467-97, 2001, which is incorporated herein by reference.

Acetyl-CoA is carboxylated by acetyl-CoA carboxylase (Acc, a multi-subunit enzyme encoded by four separate genes, accABCD) to form malonyl-CoA. The malonate group is transferred to ACP by malonyl-CoA:ACP transacylase (FabD) to form malonyl-ACP. A condensation reaction then occurs, where malonyl-ACP merges with acetyl-CoA, resulting in β-ketoacyl-ACP. β-ketoacyl-ACP synthase III (FabH) initiates the FAS cycle, while β-ketoacyl-ACP synthase I (FabB) and β-ketoacyl-ACP synthase II (FabF) are involved in subsequent cycles.

Next, a cycle of steps is repeated until a saturated fatty acid of the appropriate length is made. First, the β-ketoacyl-ACP is reduced by NADPH to form β-hydroxyacyl-ACP. This step is catalyzed by β-ketoacyl-ACP reductase (FabG). β-hydroxyacyl-ACP is then dehydrated to form trans-2-enoyl-ACP. β-hydroxyacyl-ACP dehydratase/isomerase (FabA) or β-hydroxyacyl-ACP dehydratase (FabZ) catalyze this step. NADPH-dependent trans-2-enoyl-ACP reductase I, II, or III (FabI, FabK, or FabL, respectively) reduces trans-2-enoyl-ACP to form acyl-ACP. Subsequent cycles are started by the condensation of malonyl-ACP with acyl-ACP by β-ketoacyl-ACP synthase I or β-ketoacyl-ACP synthase II (FabB or FabF, respectively).

II. Modifying the Fatty Acid Biosynthetic Pathway to Increase Acyl-ACP Production

Production host organisms may be engineered to overproduce acetyl-CoA and malonyl-CoA. Such production host organisms include plant, animal, or human cells. Microorganisms such as cyanobacteria, algae, bacteria, yeast, or filamentous fungi can be used as production hosts. Non-limiting examples of microorganisms that may be used as production hosts include *E. coli, Saccharomyces cerevisiae, Candida lipolytica, Synechococcus, Synechocystis, Clamydomonas, Arthrobacter* AK 19, *Rhodotorula glutinins, Acinetobacter* sp. strain M-1, *Candida lipolytica*, and other oleaginous microorganisms. Several different modifications can be made, either in combination or individually, to the production host to obtain increased acetyl-CoA/malonyl-CoA/fatty acid and fatty acid derivative production.

For example, to increase acetyl-CoA production, one or more of the following genes can be expressed in a production host: pdh, panK, aceEF (which encodes the E1p dehydrogenase component and the E2p dihydrolipoamide acyltransferase component of the pyruvate and 2-oxoglutarate dehy-

drogenase complexes), fabH, fabD, fabG, acpP, and fabF. In other examples, additional genes encoding fatty-acyl-CoA reductases and aldehyde decarbonylases can be expressed in the production host. It is known in the art that a plasmid containing one or more of the aforementioned genes, all under the control of a constitutive, or otherwise controllable promoter, can be constructed. Exemplary GenBank Accession numbers for these genes are listed in the parentheticals: pdh (BAB34380, AAC73227, AAC73226), panK (also known as coaA, AAC76952), aceEF (AAC73227, AAC73226), fabH (AAC74175), fabD (AAC74176), fabG (AAC74177), acpP (AAC74178), and fabF (AAC74179).

Additionally, the expression levels of fadE, gpsA, ldhA, pflb, adhE, pta, poxB, ackA, and/or ackB can be attenuated or knocked-out in the engineered microorganism by transformation with conditionally replicative or non-replicative plasmids containing null or deletion mutations of the corresponding genes, or by substituting the promoter or enhancer sequences. Exemplary GenBank Accession numbers for these genes are listed in the parentheticals: fadE (AAC73325), gspA (AAC76632), ldhA (AAC74462), pflb (AAC73989), adhE (AAC74323), pta (AAC75357), poxB (AAC73958), ackA (AAC75356), and ackB (BAB81430). The resulting engineered production hosts have increased acetyl-CoA production levels when grown in an appropriate environment.

Moreover, malonyl-CoA overproduction can be affected by engineering the production host as described above with accABCD (e.g., GenBank Accession number AAC73296, EC 6.4.1.2) included in the plasmid synthesized de novo. Fatty acid overproduction can be achieved by further including a gene encoding lipase (e.g., GenBank Accession Nos. CAA89087 and CAA98876) in the plasmid synthesized de novo.

As a result, in some examples, an acetyl-CoA carboxylase is overexpressed to increase the intracellular concentration thereof by at least about 2-fold, at least about 5-fold, or at least about 10-fold, relative to the native expression levels.

In addition, a PlsB (e.g., GenBank Accession number AAC77011) D311E mutant can be used to increase the amount of available acyl-CoA.

In addition, overexpression of an sfa gene (suppressor of FabA, e.g., GenBank Accession No. AAN79592) can be included in the production host to increase production of monounsaturated fatty acids (Rock et al., J. Bacteriology, 178:5382-5387, 1996).

B. Acyl-ACP and/or Acyl-CoA to Fatty Ester Using Thioesterase

In a typical microbial process model for fatty acid synthesis, acetyl-CoA and malonyl-CoA are converted through a series of steps to form the acyl-ACP chains. Acyl-ACP is then converted via a series of alternative enzymatic steps to various end products, including fatty acid derivatives. For example, typically acyl-ACP is converted to fatty esters by the combined consecutive reactions of a thioesterase, an acyl-CoA ligase/synthetase and an ester synthase. A limitation to the commercial use of these enzymes in a metabolic pathway is the need to produce the fatty acyl CoA substrate from a fatty acyl ACP precursor, which requires at least two enzymatic steps and the expenditure of metabolic energy from two phosphoanhydride bonds. Direct production of fatty esters with thioesterase mitigates the loss of ATP caused by these two enzymatic steps. Recently it has been demonstrated that lipases (whose natural "alcohol" substrate is water) can also be used in vitro to catalyze the transesterification reaction that makes biodiesel (i.e. the conversion of triacyl glyceride and methanol to fatty acid methyl ester and glycerol). However, lipases are generally toxic to the cells when produced intracellularly.

Despite having a published specificity for water, the present invention describes the discovery that, in the presence of a sufficient amount of an alcohol, the alcohol can become an acceptable substrate for a thioesterase. In that case, thioesterases can catalyze the alcoholysis of the fatty acyl enzyme intermediates, just like a lipase does in vitro. Thus, under the right conditions, an enzyme that accepts a fatty ester as substrate to form a fatty enzyme intermediate that is subsequently cleaved through either hydrolysis or transesterification can be used to synthesize desired fatty acid esters if a sufficient level of a suitable alcohol is provided to drive alcoholysis. Examples of enzymes having this capability, which can produce esters directly from acyl-ACP include, in addition to thioesterases, acyltransferases, lipases, esterases, and proteases. Useful thioesterases can be naturally-occurring and/or precursor thioesterases as defined herein, or can be mutant thioesterases prepared in accordance with the disclosures herein. One of ordinary skill in the art is capable of determining the fitness of using a particular enzyme to directly produce fatty esters from Acyl-ACP. For example, the assays provided in Example 32 are useful in determining direct ester production.

According to this aspect of the invention, the thioesterase can be utilized to directly produce fatty esters either in the presence or the absence of an ester synthase and/or a fatty acyl CoA ligase/synthetase. For example, expression of a thioesterase that can catalyze the direct production of fatty esters in a recombinant host strain can be used to supplement fatty ester production where the strain also expresses an ester synthase. Additionally, expression of a thioesterase that can catalyze the direct production of fatty esters in a recombinant host cell can be used where there is no or low ester synthase expression.

A mutant thioesterase can be utilized that has been modified to have altered properties compared to the precursor thioesterase.

C. Acyl-ACP to Fatty Acid

I. Fatty Acid Biosynthetic Pathway: Acyl-ACP to Fatty Acids

As described above, acetyl-CoA and malonyl-CoA are processed in several steps to form acyl-ACP chains. The enzyme sn-glycerol-3-phosphate acyltransferase (PlsB) catalyzes the transfer of an acyl group from acyl-ACP or acyl-CoA to the sn-1 position of glycerol-3-phosphate. Thus, PlsB is a key regulatory enzyme in phospholipid synthesis, which is a part of the fatty acid pathway Inhibiting PlsB leads to an increase in the levels of long chain acyl-ACP, which feedback will inhibit early steps in the pathway, which involve genes such as, for example, accABCD, fabH, and fabI. Uncoupling of this regulation, for example by thioesterase overexpression, leads to increased fatty acid production.

II. Modifying the Fatty Acid Biosynthetic Pathway to Produce the Desired Types or Proportions of Fatty Acids

According to the invention, the expressed thioesterase has altered properties as compared to the native or endogenous thioesterase in the host strain. To engineer a production host for the production of a homogeneous population of fatty acid derivatives, one or more endogenous genes can be attenuated or functionally deleted and, as a result, one or more thioesterases according to the invention can be expressed. For example, C_{10} fatty acid derivatives (i.e., fatty acid derivatives each comprising a carbon chain that is 10 carbons long) can

be produced by attenuating thioesterase C_{18} (e.g., GenBank Accession Nos. AAC73596 and P0ADA1), which uses $C_{18:1}$-ACP, and by expressing an altered thioesterase that has increased specificity for and/or activity (e.g., catalytic rate) with regard to C_{10} substrates (i.e., substrates each comprising a carbon chain that is 10 carbons long). This results in a more homogeneous population of fatty acid derivatives that have an increase in fatty acids having a carbon chain length of 10. In another example, C_{12} fatty acid derivatives can be produced by attenuating endogenous thioesterases that produce non-C_{12} fatty acids and expressing an altered thioesterase that has increased specificity for and/or activity (i.e., catalytic rate) with regard to C_{12} substrates. In another example, C_{14} fatty acid derivatives can be produced by attenuating endogenous thioesterases that produce non-C_{14} fatty acids and expressing an altered thioesterase that has increased specificity for and/or activity (i.e., catalytic rate) with regard to C_{14} substrates. In another example, a higher proportional yield of short-chain (e.g., C_8, C_9, C_{10}, C_{11}, C_{12}, C_{13}, and/or C_{14}) fatty acid derivatives vs. other non-short-chain fatty acid derivatives in the product mixture. In yet another example, a lower proportional yield of short chain (e.g., C_8, C_9, C_{10}, C_{11}, C_{12}, C_{13}, and/or C_{14}) fatty acid derivatives vs. other non-short-chain fatty acid derivatives in the product mixture can also be achieved. In a further example, a higher and/or improved yield of free fatty acid derivatives can be produced by expressing an altered thioesterase that has improved catalytic rate and/or production or yield in vivo. In yet another example, a higher or lower proportional or percentage yield of fatty esters vs. other products, such as free fatty acids, can be produced by applying one or more of certain thioesterase mutants. Acetyl-CoA, malonyl-CoA, and fatty acid overproduction can be verified using methods known in the art, for example by radioactive precursors, HPLC, LC-MS, and GC-MS subsequent to cell lysis.

In an alternative embodiment, a thioesterase of the invention can be expressed within the host strain in combination with an endogenous thioesterase. In yet another alternative embodiment, one or more endogenous thioesterases can be modified using suitable genomic alternation techniques that are known to those skilled in the art, such that the mutant thioesterases has at least one altered property as compared to the endogenous thioesterase precursors, and/or such that the host cell exhibits at least one altered property as compared to the host cell before such genomic alteration techniques are applied.

D. Fatty Acid to Acyl-CoA

I. Conversion of Fatty Acids to Acyl-CoA

Acyl-CoA synthase (ACS) esterifies free fatty acids to acyl-CoA by a two-step mechanism. The free fatty acid first is converted to an acyl-AMP intermediate (an adenylate) through the pyrophosphorolysis of ATP. The activated carbonyl carbon of the adenylate is then coupled to the thiol group of CoA, releasing AMP and the acyl-CoA final product. See Shockey et al., Plant Physiol. 129:1710-1722, 2002.

The *E. coli* ACS enzyme FadD and the fatty acid transport protein FadL are typically important components of a fatty acid uptake system. FadL mediates the transportation of fatty acids into the bacterial cell, and FadD mediates the formation of acyl-CoA esters. When no other carbon source is available, exogenous fatty acids are taken up by bacteria and converted to acyl-CoA esters, which bind to the transcription factor FadR and derepress the expression of the fad genes that encode proteins responsible for fatty acid transport (FadL), activation (FadD), and β-oxidation (FadA, FadB, FadE, and FadII). When alternative sources of carbon are available, bacteria synthesize fatty acids as acyl-ACPs, which are then used for phospholipid synthesis, rather than serving as substrates for β-oxidation. Thus, acyl-CoA and acyl-ACP are independent sources of fatty acids that lead to different end-products. See Caviglia et al., J. Biol. Chem., 279(12):1163-1169, 2004.

II. Modifying the Fatty Acid Biosynthetic Pathway to Increase Conversion of Fatty Acids to Acyl-CoA

Production hosts can be engineered using known peptides to produce fatty acids of various lengths which can be converted to acyl-CoA. One method of making fatty acid derivatives involves increasing the expression of, or expressing more active forms of, one or more acyl-CoA synthase peptides (EC 6.2.1.-).

A list of acyl-CoA synthases that can be expressed to produce acyl-CoA and fatty acid derivatives is shown in Table 1. These Acyl-CoA synthases can be examined to optimize any pathway that uses fatty-acyl-CoAs as substrates. Using bioinformatics and synthetic genes, heterologous fadD genes can be expressed in production strains and evaluated for their capacity to produce biodiesel and potentially biocrude.

TABLE 1

Acyl-CoA synthases

Gene Name/ Locus	Source	GenBank Accession No.	% Identity to *E. coli* FadD	% Similarity to *E. coli* FadD
fadD	*E. coli*	NP_416319	—	—
fadK	*E. coli*	YP_416216	28	46
fadD	*Acinetobacter* sp. ADP1	YP_045024	51	70
fadD	*Haemophilus influenza* RdKW20	NP_438551	64	78
BH3103	*Bacillus halodurans* C-125	NP_243969	40	58
yhfL	*Bacillus subtilis*	NP_388908	39	57
pfl-4354	*Pseudomonas fluorescens* Pfo-1	YP_350082	52	71
EAV15023	*Comamonas testosterone* KF-1	ZP_01520072	55	72
fadD1	*Pseudomonas aeruginosa*	NP_251989	54	72
fadD2	*Pseudomonas aeruginosa* PAO1	NP_251990	55	72
fadD	*Rhizobium etli* CFN42	YP_533919	55	72
RPC_4074	*Rhodopseudomonas palustris* Bis B18	YP_533919	56	72
fadD1	*Rasltonia solanacearum* GMI 1000	NP_520978	56	72
fadDD35	*Mycobacterium tuberculosis* H37Rv	NP_217021	28	46
fadDD22	*Mycobacterium tuberculosis* H37Rv	NP_217464	23	42
PRK0059	*Stenotrophomonas maltophilia* R551-3	ZP_01644857	59	75

Based on their degree of similarity to *E. coli* fadD, the following homologous genes are selected to be synthesized and evaluated:

fadDD35 from *M. tuberculosis* HR7Rv [NP_217021].

yhfL from *B. subtilis* [NP_388908].

fadD1 from *P. aeruginosa* PAO1 [NP_251989].

fadD homolog, encoding Faa3p from *Saccharomyces cerevisiae* [NP_012257].

Additional fatty acid acyl-CoA synthases from eukaryotic organisms, which can be used to produce acyl-CoA as well as fatty acid derivatives, include those described in Shockey et al., Plant Physiol., 129: 1710-1722, 2002 (Arabidopsis), Caviglia et al., J. Biol. Chem., 279: 1163-1169, 2004 (rat), and Knoll et al., J. Biol. Chem., 269(23):16348-56, 1994 (yeast). Gene sequences encoding these synthetases are known in the art. See, e.g., Johnson et al., J. Biol. Chem., 269: 18037-18046, 1994; Shockey et al., Plant Physiol., 129: 1710-1722, 2002; Black et al., J. Biol. Chem., 267: 25513-25520, 1992. These eukaryotic acyl-CoA synthases, despite lacking in high homology to *E. coli* FadD sequences, can complement FadD activity in *E. coli* FadD knockouts.

A. Acyl-CoA to Fatty Alcohol

1. Conversion of Acyl-CoA to Fatty Alcohol

Acyl-CoA is reduced to a fatty aldehyde by an NADH-dependent acyl-CoA reductase (e.g., Acr1). The fatty aldehyde is then reduced to a fatty alcohol by an NADPH-dependent alcohol dehydrogenase (e.g., YqhD). Alternatively, fatty alcohol forming acyl-CoA reductase (FAR) catalyzes the reduction of an acyl-CoA into a fatty alcohol and CoASH. FAR uses NADH or NADPH as a cofactor in this four-electron reduction. Although the alcohol-generating FAR reactions proceed through an aldehyde intermediate, a free aldehyde is not released. Thus, the alcohol-forming FARs are distinct from the enzymes that carry out two-electron reductions of acyl-CoA and yield free fatty aldehyde as a product. (See Cheng and Russell, J. Biol. Chem., 279(36):37789-37797, 2004; Metz et al., Plant Physiol., 122:635-644, 2000).

2. Modifying the Fatty Acid Biosynthetic Pathways to Increase Conversion of Acyl-CoA to Fatty Alcohol

Production hosts can be engineered using known polypeptides to produce fatty alcohols from acyl-CoA. One method of making fatty alcohols involves increasing the expression of, or expressing more active forms of, fatty alcohol forming acyl-CoA reductases (encoded by a gene such as acr1, EC 1.2.1.50/1.1.1), acyl-CoA reductases (EC 1.2.1.50), and/or alcohol dehydrogenases (EC 1.1.1.1).

Fatty alcohols are often described as hydrocarbon-based surfactants. They also serve as suitable components of surfactants. For surfactant production, the production host is modified so that it produces a surfactant from a renewable carbon source. Such a production host includes a first exogenous polynucleotide sequence encoding a protein capable of converting a fatty acid to a fatty aldehyde and a second exogenous polynucleotide sequence encoding a protein capable of converting a fatty aldehyde to an alcohol. In some examples, the first exogenous polynucleotide sequence encodes a fatty acid reductase. In one embodiment, the second exogenous polynucleotide sequence encodes mammalian microsomal aldehyde reductase or long-chain aldehyde dehydrogenase. In a further example, the first and second exogenous polynucleotide sequences are from *Arthrobacter* AK 19, *Rhodotorula glutinins, Acinetobacter* sp. strain M-1, or *Candida lipolytica*. In one embodiment, the first and second heterologous polynucleotide sequences form a multienzyme complex from *Acinetobacter* sp. strain M-1 or from *Candida lipolytica.*

Additional sources of heterologous DNA sequences encoding fatty acid to long chain alcohol converting proteins that can be used in surfactant production include, but are not limited to, *Mortierella alpina* (ATCC 32222), *Cryptococcus curvatus*, (also referred to as *Apiotricum curvatum*), *Alcanivorax jadensis* (T9T=DSM 12718=ATCC 700854), *Acinetobacter* sp. HO1-N (ATCC 14987) and *Rhodococcus opacus* (PD630 DSMZ 44193).

In one example, the fatty acid derivative is a saturated or unsaturated surfactant product having a carbon chain length of about 6 to about 36 carbon atoms, about 8 to about 30 carbon atoms, about 10 to about 26 carbon atoms, about 12 to about 20 carbon atoms, or about 12 to about 16 carbon atoms. In another example, the surfactant product has a carbon chain length of about 10 to about 18 carbon atoms, or about 12 to about 14 carbon atoms.

Suitable production hosts for producing surfactants include eukaryotic or prokaryotic microorganisms. Exemplary production hosts include Arthrobacter AK 19, *Rhodotorula glutinins, Acinetobacter* sp. strain M-1, *Arabidopsis thalania, Candida lipolytica, Saccharomyces cerevisiae*, cyanobacteria such as *Synechocystis* spp. and *Synechococcus* spp., Algae such as *Clamydomonas*, and *E. coli* engineered to overexpress acetyl-CoA carboxylase. Production hosts that demonstrate an innate ability to synthesize high levels of surfactant precursors in the form of lipids and oils, such as *Rhodococcus opacus, Arthrobacter* AK 19, *Rhodotorula glutinins, E. coli* engineered to express acetyl CoA carboxylase, and other oleaginous cyanobacteria, bacteria, yeast, and fungi can also be used.

B. Fatty Alcohols to Fatty Esters

Production hosts can be engineered using known polypeptides to produce fatty esters of various lengths. One method of making fatty esters includes increasing the expression of, or expressing more active forms of, one or more alcohol O-acetyltransferase peptides (EC 2.3.1.84). These peptides catalyze the acetylation of an alcohol by converting an acetyl-CoA and an alcohol to a CoA and an ester. In some examples, the alcohol O-acetyltransferase peptides can be expressed in conjunction with selected thioesterase peptides, FAS peptides, and fatty alcohol forming peptides, thus allowing the control of carbon chain lengths, saturation levels, and degrees of branching. In some cases, the bkd operon can be coexpressed in order to produce branched fatty acid precursors.

As used herein, alcohol O-acetyltransferase peptides include peptides in enzyme classification number EC 2.3.1.84, as well as any other peptides capable of catalyzing the conversion of an acetyl-CoA and an alcohol to form a CoA and an ester. Additionally, one of ordinary skill in the art will appreciate that alcohol O-acetyltransferase peptides can also catalyze other reactions.

For example, some alcohol O-acetyltransferase peptides can accept other substrates in addition to fatty alcohols and/or acetyl-CoA thioesters, such as other alcohols and other acyl-CoA thioesters. Such non-specific or divergent-specificity alcohol O-acetyltransferase peptides are, therefore, also included. Various alcohol O-acetyltransferase peptide sequences are publicly available. Assays for measuring the activity of alcohol O-acetyltransferase peptides are known in the art. Moreover, O-acyltransferases can be engineered to impart new activities and/or specificities for the donor acyl group or acceptor alcohol moiety. Engineered enzymes can be generated through well documented rational and evolutionary approaches.

C. Acyl-CoA to Fatty Esters

1. Production of Fatty Esters

Fatty esters are synthesized by an acyl-CoA:fatty alcohol acyltransferase (e.g., ester synthase), which conjugates a long chain fatty alcohol to a fatty acyl-CoA via an ester linkage. Ester synthases and the encoding genes are known from the jojoba plant and the bacterium *Acinetobacter* sp. strain ADP1 (formerly *Acinetobacter calcoaceticus* ADP1). The bacterial ester synthase is a bifunctional enzyme, exhibiting ester synthase activity and the ability to form triacylglycerols from diacylglycerol substrates and fatty acyl-CoAs (acyl-CoA:diglycerol acyltransferase (DGAT) activity). The gene wax/dgat encodes both ester synthase and DGAT. See Cheng et al., J. Biol. Chem., 279(36):37798-37807, 2004; Kalscheuer and Steinbuchel, J. Biol. Chem., 278:8075-8082, 2003. Ester synthases can also be used to produce certain fatty esters that can be used as a fuel, such as biodiesel, as described herein.

2. Modifying the Fatty Acid Biosynthetic Pathway to Produce Fatty Esters Using Ester Synthase

The production of fatty esters, including waxes, from acyl-CoA and alcohols, can be engineered using known polypeptides. One method of making fatty esters includes increasing the expression of, or expressing more active forms of, one or more ester synthases (EC 2.3.1.20, 2.3.1.75). Various ester synthase peptide sequences are publicly available. Methods of determining ester synthase activity are provided in U.S. Pat. No. 7,118,896, which is herein incorporated by reference in its entirety.

In certain embodiments, if the desired product is an ester-based biofuel, a production host can be modified such that it produces an ester from a renewable energy source. Such a production host includes an exogenous genes encoding an ester synthase that is expressed so as to confer upon said production host the ability to synthesize a saturated, unsaturated, or branched fatty ester from a renewable energy source. In some embodiments, the organism can also express genes encoding the following exemplary proteins: fatty acid elongases, acyl-CoA reductases, acyltransferases, ester synthases, fatty acyl transferases, diacylglycerol acyltransferases, thioesterases, and/or acyl-coA wax alcohol acyltransferases. In an alternate embodiment, the organism expresses a gene encoding a bifunctional ester synthase/acyl-CoA:diacylglycerol acyltransferase. For example, the bifunctional ester synthase/acyl-CoA:diacylglycerol acyltransferase can be selected from the multi-enzyme complexes from *Simmondsia chinensis, Acinetobacter* sp. strain ADP1 (formerly *Acinetobacter calcoaceticus* ADP1), *Alcanivorax borkumensis, Pseudomonas aeruginosa, Fundibacter jadensis, Arabidopsis thaliana*, or *Alcaligenes eutrophus* (later renamed *Ralstonia eutropha*). In one embodiment, the fatty acid elongases, acyl-CoA reductases, or wax synthases are obtained and/or derived from a multi-enzyme complex from *Alcaligenes eutrophus* (later renamed *Ralstonia eutropha*) or other organisms known in the literature to produce esters such as wax or fatty esters.

Additional sources of heterologous DNA sequences encoding ester synthesis proteins useful in fatty ester production include, but are not limited to, *Mortierella alpina* (e.g., ATCC 32222), *Cryptococcus curvatus* (also referred to as *Apiotricum curvatum*), *Alcanivorax jadensis* (e.g., T9T=DSM 12718=ATCC 700854), *Acinetobacter* sp. HO1-N, (e.g., ATCC 14987) and *Rhodococcus opacus* (e.g., PD630, DSMZ 44193).

Useful production hosts for producing fatty esters can be eukaryotic or prokaryotic microorganisms. Non-limiting examples of production hosts for producing fatty esters include *Saccharomyces cerevisiae, Synechococcus, Synechocystis, Clamydomonas, Candida lipolytica, E. coli, Arthrobacter* AK 19, *Rhodotorula glutinins, Acinetobacter* sp. strain M-1, *Candida lipolytica*, and other oleaginous microorganisms.

In one example, the ester synthase from *Acinetobacter* sp. ADP1 at locus AAO17391 (described in Kalscheuer and Steinbuchel, J. Biol. Chem., 278:8075-8082, 2003, herein incorporated by reference) is used. In another example, the ester synthase from *Simmondsia chinensis* at locus AAD38041 is used.

In certain embodiments, the esters produced in accordance with the methods and compositions herein are secreted or released from the host cells, and thus can be recovered extracellularly. Optionally, an ester exporter such as a member of the FATP family can be used to facilitate the release of esters into the extracellular environment. A non-limiting example of a suitable ester exporter is fatty acid (long chain) transport protein CG7400-PA, isoform A, from *Drosophila melanogaster*, at locus NP_524723.

D. Acyl-ACP, Acyl-CoA to Hydrocarbon

1. Hydrocarbons from Particular Microorganisms

A diverse set of microorganisms are known to produce hydrocarbons, such as alkanes, olefins, and isoprenoids. Many of these hydrocarbons are derived from fatty acid biosynthesis. The production of these hydrocarbons can be controlled by controlling the genes associated with fatty acid biosynthesis in the native production hosts.

For example, hydrocarbon biosynthesis in the algae *Botryococcus braunii* occurs via the decarbonylation of fatty aldehydes. The fatty aldehydes are produced by the reduction of fatty acyl thioesters by an enzyme such as a fatty acyl-CoA reductase. Thus, the structure of the final alkanes can be controlled by engineering *B. braunii* to express specific genes, such as thioesterases, which control the chain length of the fatty acids being channeled into alkane biosynthesis. Expressing the enzymes that result in branched chain fatty acid biosynthesis in *B. braunii* will result in the production of branched chain alkanes. Introduction of genes affecting the production of desaturated fatty acids will result in the production of olefins. Further combinations of these genes can provide further control over the final structure of the hydrocarbons that will be produced.

To produce higher levels of native or engineered hydrocarbons, the genes involved in the biosynthesis of fatty acids and their precursors, or the degradation of other products can be expressed, overexpressed, or attenuated. Each of these approaches can be applied to the production of alkanes in *Vibrio fumissii* M1 and other *Vibrio fumissii* strains, which produce alkanes through the reduction of fatty alcohols. In addition to *Vibrio fumissii*, other alkane producing organisms that utilize the fatty acid pathway can be used.

Each of these approaches can also be applied to the production of the olefins produced by strains of *Micrococcus leuteus, Stenotrophomonas maltophilia*, and related microorganisms. These microorganisms produce long chain olefins that are derived from the head-to-head condensation of fatty acid precursors. Controlling the structure and level of the fatty acid precursors using the methods described herein will result in the formation of olefins of different chain lengths, branching characteristics, and levels of saturation.

Cyanobacteria can also be used as suitable production hosts for the production of fatty acid derivatives such as fatty alcohols, fatty esters, and hydrocarbons. For example, *Synechocystis* sp. PCC6803 and *Synechococcus elongates* PCC7942 can serve as production hosts and can be engineered using standard molecular biology techniques (Thiel, Genetic analysis of cyanobacteria, in THE MOLECULAR BIOLOGY

OF CYANOBACTERIA, ADVANCES IN PHOTOSYNTHESIS AND RESPIRATION 581-611 (Kluwer Academic Publishers), 1994; Koksharova and Wolk, Appl. Microbiol. Biotechnol., 58: 123-137, 2002, the contents of which are incorporated by reference herein. Fatty acid biosynthesis genes can be readily identified and isolated in these organisms.

Furthermore, many cyanobacteria are natural producers of hydrocarbons, such as heptadecane, and therefore contain hydrocarbon biosynthesis genes that can be deregulated and overexpressed in conjunction with manipulating their fatty acid biosynthesis genes, in order to increase hydrocarbon production.

Unlike other bacteria, some cyanobacteria (e.g., *Synechocystis* sp. PCC6803) contain polyunsaturated fatty acids in their lipids (Murata, Plant cell Physiol., 33: 933-941, 1992), and thus have the inherent capability to produce polyunsaturated fatty acid derivatives. Most importantly, cyanobacteria are photosynthetic organisms that synthesize all cellular carbon by harvesting sun light and fixing carbon dioxide. Therefore, fatty acid derivatives produced in cyanobacteria are directly derived from CO_2.

2. Producing Hydrocarbons from Reduction of Primary Alcohols

Hydrocarbons can also be produced using evolved oxidoreductases for the reduction of primary alcohols. Using primary fatty alcohols to produce alkanes in microorganisms, such as *Vibrio fumissii* M1, is known. See, e.g., Park, J. Bacteriol., 187:1426-1429, 2005, the content of which is incorporated herein by reference. One example of an oxidoreductase that can be used to produce hydrocarbons from fatty alcohols is NAD(P)H-dependent oxidoreductase. Synthetic NAD(P)H dependent oxidoreductases can be produced through the use of evolutionary engineering and can be expressed in production hosts to produce fatty acid derivatives.

The process of "evolving" a fatty alcohol reductase to have the desired activity is known and practiced by those skilled in the art (Kolkman and Stemmer, Nat. Biotechnol., 19:423-8, 2001; Ness et al., Adv. Protein Chem., 55:261-92, 2000; Minshull and Stemmer, Curr. Opin. Chem. Biol., 3:284-90, 1999; Huisman and Gray, Curr. Opin. Biotechnol., 13:352-8, 2002; U.S. Patent Publication No. 2006/0195947), the contents of all of which are incorporated herein by reference.

A library of NAD(P)H-dependent oxidoreductases is generated by standard methods, such as error-prone PCR, site-specific random mutagenesis, site-specific saturation mutagenesis, or site-directed specific mutagenesis. Additionally, a library can be created through the "shuffling" of naturally-occurring NAD(P)H-dependent oxidoreductase encoding sequences. The library is expressed in a suitable production host, such as an *E. coli*. Individual colonies expressing a different member of the oxidoreductase library are then analyzed for expression of an oxidoreductase that can catalyze the reduction of a fatty alcohol.

For example, each cell can be assayed as a whole cell bioconversion, a cell extract, or a permeabilized cell. Enzymes purified from the cell can be analyzed as well. Fatty alcohol reductases are identified by spectrophotometrically or fluorometrically monitoring the fatty alcohol-dependent oxidation of NAD(P)H. Production of alkanes is monitored by GC-MS, TLC, or other suitable methods.

An oxidoreductase identified in this manner is used to produce alkanes, alkenes, and related branched hydrocarbons. This is achieved either in vitro or in vivo. The latter is achieved by expressing the evolved fatty alcohol reductase gene in an organism that produces fatty alcohols, such as the ones described herein. The fatty alcohols act as substrates for the alcohol reductase, which produces alkanes. Other oxidoreductases can also be engineered to catalyze this reaction, such as those that use molecular hydrogen, glutathione, FADH, or other reductive coenzymes.

3. Conversion of Acyl-ACP to Ketone and/or Olefins

Acyl-ACP can be converted to a ketone and/or an internal olefin by the action of acyl condensing enzymes, as described in PCT Publication No. 2008/147781 A2, the disclosures of which are incorporated herein by reference. As described in the '781 publication, acyl-condensing peptides include peptides that are capable of catalyzing the condensation of acyl-ACP, acyl-CoA, acyl-AMP, fatty acids, and mixtures thereof using the methods described therein. In some embodiments, these acyl-condensing peptides have high, medium, or low substrate specificity. In certain examples, the acyl-condensing peptides are more substrate specific and will only accept substrates of a specific chain length. Additionally, one of ordinary skill in the art will appreciate that some acyl-condensing peptides will catalyze other reactions as well. Examples of acyl-condensing enzymes are disclosed in the '781 publication. In addition, the '781 publication describes adenylating proteins, dehydratases, and dehydrogenases that can be used in the production of hydrocarbons such as internal olefins.

Recombinant organisms can be engineered using polynucleotides and proteins, for example, those disclosed in the '781 publication, to produce hydrocarbons and aliphatic ketones that have defined structural characteristics (e.g., degrees of branching, levels of saturation, or carbon chain lengths). One method of making hydrocarbons involves increasing the expression of, or expressing more active forms of, one or more acyl-condensing enzymes (enzymes that condense two or more of acyl-CoA, acyl-ACP, acyl-AMP, acyl-ester, fatty acid, or mixtures thereof). One of ordinary skill in the art will appreciate that the products produced from such condensation reactions vary depending on the acyl chain that is condensed. Products that can be produced include, for example, hydrocarbons and hydrocarbon intermediates, such as aliphatic ketones. The aliphatic ketones, hydrocarbons, and hydrocarbon intermediates can be engineered to have specific carbon chain characteristics by expressing various enzymes or attenuating the expression of various enzymes in the recombinant organism. According to the present invention, the mutant thioesterases of the invention can be used to manipulate the range of acyl species carbon chain lengths. Thus, by using a mutant thioesterase having a particular substrate specificity or selectivity, it is possible to affect the downstream reactions so as to result in a predetermined olefin or ketone product profile.

4. Conversion of Fatty Acid to Aldehyde

Fatty acids resulting from thioesterase cleavage can be converted to an aldehyde by the action of the carboxylic acid reductase gene. Aldehydes can be useful products in themselves, or they can serve as substrates for further enzymatic catalysis reactions, for example, in the production of fatty alcohols via an enzymatic reaction of alcohol dehydrogenase, or in the production of alkanes via an enzymatic reaction of decarbonylases. According to the compositions and methods herein, the fatty acid substrates of the carboxylic acid reductase can be manipulated so as to achieve a predetermined product profile in the aldehyde or fatty alcohol product.

E. Release of Fatty Acid Derivatives—With or Without Transport Proteins

As described herein, the fatty acid derivatives produced in accordance with the methods, compositions, vectors, and host cells herein can be secreted or spontaneously released so as to allow the recovery of the fatty acid derivative products extra-

cellularly. The speed of spontaneous secretion may or may not be sufficiently fast, and the level of release may or may not be sufficiently complete. Therefore, optionally, transport proteins can be used to facilitate export of fatty acid derivatives out of the production host. Transport and efflux proteins are known to excrete a large variety of compounds, and can naturally be modified to be selective for particular types of fatty acid derivatives. Non-limiting examples of suitable transport proteins are ATP-Binding Cassette (ABC) transport proteins, efflux proteins, and fatty acid transporter proteins (FATP). Additional non-limiting examples of suitable transport proteins include the ABC transport proteins from organisms such as *Caenorhabditis elegans, Arabidopsis thalania, Alkaligenes eutrophus*, and *Rhodococcus erythropolis*. Exemplary ABC transport proteins include CER5, AtMRP5, AmiS2, or AtPGP1. In a preferred embodiment, the ABC transport protein is a CER5 (e.g., AY734542)). Vectors containing genes that express suitable transport proteins can be inserted into protein production hosts to increase or drive the release of fatty acid derivatives.

Production of fatty acid derivative products according to the present invention does not require transport or efflux protein modification and it is possible to select production hosts for their endogenous ability to release fatty acid derivatives. Furthermore, simply by constructing host cells according to the present disclosure, for example, fatty acid derivative products that are otherwise not known to be secreted can be secreted or spontaneously released. The efficiency of product production and release into the fermentation broth can be expressed as a ratio of intracellular product to extracellular product. In some examples, the ratio can be about 100:1, 50:1, 20:1, 10:1, 5:1, 4:1, 3:1, 2:1, 1:1, 1:2, 1:3, 1:4, 1:5, 1:10, 1:20, 1:30, 1:40 or 1:50.

II. Selection of Carbon Chain Characteristics of Fatty Acid Derivatives

Fatty acid derivatives with particular branch points, levels of saturation, carbon chain lengths, and ester characteristics can be produced as desired. Microorganisms that naturally produce particular derivatives can be selected as production hosts, and in certain circumstances, endogenous enzymes therein can be manipulated to produce fatty acid derivatives of desirable characteristics. Alternatively, genes that express enzymes that will produce particular fatty acid derivatives can be suitably inserted into the production host microorganisms.

In some examples, expression of exogenous FAS genes originating from different species or engineered variants can be achieved in a production host, resulting in the biosynthesis of fatty acids that are structurally different (in, for example, lengths, levels of branching, degrees of unsaturation, etc.) from those of the native production host. These heterologous gene products can also be selected or engineered to be unaffected by the natural regulatory mechanisms in the production host cells, and as such allowing control of the production of the desired commercial product. For example, the FAS enzymes from *Bacillus subtilis, Saccharomyces cerevisiae, Streptomyces* spp., *Ralstonia, Rhodococcus, Corynebacteria, Brevibacteria, Mycobacteria*, oleaginous yeast, or the like can be expressed in a suitable production host. The expression of such exogenous enzymes will alter the structure of the fatty acid produced.

When a production host is engineered to produce a fatty acid with a specific level of unsaturation, branching, or carbon chain length, the resulting engineered fatty acid can be used in the production of fatty acid derivatives. Fatty acid derivatives generated from such production hosts can display the characteristics of the engineered fatty acid.

For example, a production host can be engineered to make branched, short chain fatty acids, which can then be used by the production host to produce branched, short chain fatty alcohols. Similarly, a hydrocarbon can be produced by engineering a production host to produce a fatty acid having a defined level of branching, unsaturation, and/or carbon chain length, and thus producing a homogeneous hydrocarbon population. Additional steps can be employed to improve the homogeneity of the resulting product. For example, when an unsaturated alcohol, fatty ester, or hydrocarbon is desired, the production host organism can be engineered to produce low levels of saturated fatty acids, and in addition can be modified to express an additional desaturase and thus lessen the production of saturated product.

A. Branched and Cyclic Moieties

1. Engineering Branched and Cyclic Fatty Acid Derivatives

Fatty acids are key intermediates in the production of fatty acid derivatives. Fatty acid derivatives containing branch points, cyclic moieties, and combinations thereof can be prepared using branched or cyclic fatty acids.

For example, *E. coli* naturally produces straight chain fatty acids (sFAs). To engineer *E. coli* to produce branched chain fatty acids (brFAs), several genes that provide branched precursors (e.g., a bkd operon) can be introduced into the production host and expressed to allow initiation of fatty acid biosynthesis from branched precursors (e.g., fabH). The bkd, ilv, icm, and fab gene families can be expressed or overexpressed to produce branched chain fatty acid derivatives. Similarly, to produce cyclic fatty acids, genes that provide cyclic precursors can be introduced into the production host and expressed to allow initiation of fatty acid biosynthesis from cyclic precursors. The ans, chc, and plm gene families can be expressed or overexpressed to produce cyclic fatty acids.

Additionally, a production host can be engineered to express genes encoding proteins for the elongation of brFAs (e.g., genes encoding ACP, FabF, etc.) and/or to delete or attenuate the corresponding *E. coli* genes that normally lead to sFAs. In this regard, endogenous genes that would compete with the introduced genes (e.g., fabH, fabF) are deleted or attenuated.

The branched acyl-CoA (e.g., 2-methyl-butyryl-CoA, isovaleryl-CoA, isobutyryl-CoA, etc.) are the precursors of brFA. In most microorganisms containing brFA, the brFA are synthesized in two steps from branched amino acids (e.g., isoleucine, leucine, or valine) (Kadena, Microbiol. Rev., 55:288, 1991). A production host can be engineered to express or overexpress one or more of the enzymes involved in these two steps to produce brFAs, or to over-produce brFAs. For example, the production host may have an endogenous enzyme that can accomplish one step leading to brFA, therefore only genes encoding enzymes involved in the second step need to be introduced recombinantly.

The mutant thioesterases of the invention can be engineered to have one or more altered properties, for example, altered specificity and/or increased activity (e.g., catalytic rate), with regard to branched or cyclic chain acyl-CoA or acyl-ACP compounds described herein. Accordingly the recombinant cell producing fatty acid derivatives can be made to preferentially produce a desired branched or cyclic chain fatty acid derivative product that may have high value as an end product.

2. Formation of Branched Fatty Acids and Branched Fatty Acid Derivatives

The first step in forming brFAs is the production of the corresponding α-keto acids by a branched-chain amino acid

aminotransferase. Production hosts can endogenously include genes encoding such enzymes, or alternatively, such genes can be recombinantly introduced. *E. coli*, for example, endogenously expresses such an enzyme, IlvE (EC 2.6.1.42; GenBank Accession No. YP_026247). In some production hosts, a heterologous branched-chain amino acid aminotransferase may not be expressed. However, *E. coli* IlvE or any other branched-chain amino acid aminotransferase (e.g., IlvE from *Lactococcus lactis* (GenBank Accession No. AAF34406), IlvE from *Pseudomonas putida* (GenBank Accession No. NP_745648), or IlvE from *Streptomyces coelicolor* (GenBank Accession No. NP_629657)), if not endogenous, can be introduced. If the aminotransferase reaction is rate limiting in brFA biosynthesis in the chosen production host organism, then the aminotransferase can be over-expressed.

The second step is the oxidative decarboxylation of the α-keto acids to the corresponding branched-chain acyl-CoA. This reaction can be catalyzed by a branched-chain α-keto acid dehydrogenase complex (bkd; EC 1.2.4.4.) (Denoya et al., J. Bacteriol., 177:3504, 1995), which consists of E1α/β (decarboxylase), E2 (dihydrolipoyl transacylase) and E3 (dihydrolipoyl dehydrogenase) subunits. These branched-chain α-keto acid dehydrogenase complexes are similar to pyruvate and α-ketoglutarate dehydrogenase complexes. Every microorganism that possesses brFAs and/or grows on branched-chain amino acids can be used as a source to isolate bkd genes for expression in production hosts such as, for example, *E. coli*. Furthermore, *E. coli* has the E3 component as part of its pyruvate dehydrogenase complex (encoded by, for example, lpd, EC 1.8.1.4, GenBank Accession No. NP_414658), thus it can be sufficient to only express the E1 α/β and E2 bkd genes. Table 2 recites non-limiting examples of bkd genes from several microorganisms that can be recombinantly introduced and expressed in a production host to provide branched-chain acyl-CoA precursors. Microorganisms having such bkd genes can also be used as production hosts.

TABLE 2

Bkd genes from selected microorganisms

Organism	Gene	GenBank Accession No.
Streptomyces coelicolor	bkdA1 (E1α)	NP_628006
	bkdB1 (E1β)	NP_628005
	bkdC1 (E2)	NP_638004
Streptomyces coelicolor	bkdA2 (E1α)	NP_733618
	bkdB2 (E1β)	NP_628019
	bkdC2 (E2)	NP_628018
Streptomyces avermitilis	bkdA (E1a)	BAC72074
	bkdB (E1b)	BAC72075
	bkdC (E2)	BAC72076
Streptomyces avermitilis	bkdF (E1α)	BAC72088
	bkdG (E1β)	BAC72089
	bkdH (E2)	BAC72090
Bacillus subtilis	bkdAA (E1α)	NP_390288
	bkdAB (E1β)	NP_390288
	bkdB (E2)	NP_390288
Pseudomonas putida	bkdA1 (E1α)	AAA65614
	bkdA2 (E1β)	AAA65615
	bkdC (E2)	AAA65617

In another example, isobutyryl-CoA can be made in a production host, for example in *E. coli*, through the coexpression of a crotonyl-CoA reductase (Ccr, EC 1.6.5.5, 1.1.1.1) and isobutyryl-CoA mutase (large subunit IcmA, EC 5.4.99.2; small subunit IcmB, EC 5.4.99.2) (Han and Reynolds, J. Bacteriol., 179:5157, 1997). Crotonyl-CoA is an intermediate in fatty acid biosynthesis in *E. coli* and other microorganisms. Non-limiting examples of ccr and icm genes from selected microorganisms are given in Table 3.

TABLE 3

ccr and icm genes from selected microorganisms

Organism	Gene	GenBank Accession No.
Streptomyces coelicolor	ccr	NP_630556
	icmA	NP_629554
	icmB	NP_630904
Streptomyces cinnamonensis	ccr	AAD53915
	icmA	AAC08713
	icmB	AJ246005

In addition to expression of the bkd genes, the initiation of brFA biosynthesis utilizes β-ketoacyl-acyl-carrier-protein synthase III (FabH, EC 2.3.1.41) with specificity for branched chain acyl-CoAs (Li et al., *J. Bacteriol.*, 187:3795-3799, 2005). Non-limiting examples of such FabH enzymes are listed in Table 4. fabH genes that are involved in fatty acid biosynthesis of any brFA-containing microorganism can be expressed in a production host. The Bkd and FabH enzymes from production hosts that do not naturally make brFA may not support brFA production, therefore Bkd and FabH can be expressed recombinantly. Vectors containing the bkd and fabH genes can be inserted into such a production host. Similarly, the endogenous level of Bkd and FabH production may not be sufficient to produce brFA, therefore, they can be over-expressed. Additionally, other components of fatty acid biosynthesis pathway can be expressed or over-expressed, such as acyl carrier proteins (ACPs) and β-ketoacyl-acyl-carrier-protein synthase II (encoded by fabF, EC 2.3.1.41) (non-limiting examples of candidates are listed in Table 4). In addition to expressing these genes, some genes in the endogenous fatty acid biosynthesis pathway may be attenuated in the production host. Genes encoding enzymes that compete for substrate(s) with the enzymes of the pathway that result in brFA production can be attenuated to increase brFA production. For example, in *E. coli* the most likely candidates to interfere with brFA biosynthesis are fabH (GenBank Accession No. NP_415609) and/or fabF genes (GenBank Accession No. NP_415613).

TABLE 4

fabH, ACP and fabF genes from selected microorganisms with brFAs

Organism	Gene	GenBank Accession No.
Streptomyces coelicolor	fabH1	NP_626634
	ACP	NP_626635
	fabF	NP_626636
Streptomyces avermitilis	fabH3	NP_823466
	fabC3 (ACP)	NP_823467
	fabF	NP_823468
Bacillus subtilis	fabH_A	NP_389015
	fabH_B	NP_388898
	ACP	NP_389474
	fabF	NP_389016
Stenotrophomonas maltophilia	SmalDRAFT_0818 (fabH)	ZP_01643059
	SmalDRAFT_0821 (ACP)	ZP_01643063
	SmalDRAFT_0822 (fabF)	ZP_01643064
Legionella pneumophila	FabH	YP_123672
	ACP	YP_123675
	fabF	YP_123676

As mentioned above, branched chain alcohols can be produced through the combination of expressing genes that support brFA synthesis and alcohol synthesis. For example, when

a gene encoding an alcohol reductase, such as acr1 from *Acinetobacter baylyi* ADP1, is coexpressed with a bkd operon in an *E. coli* host cell, the host cell can synthesize isopentanol, isobutanol, or 2-methyl butanol. Similarly, when acr1 is coexpressed with ccr/icm genes in an *E. coli* host cell, the host cell can synthesize isobutanol.

3. Formation of Cyclic Fatty Acids and Cyclic Fatty Acid Derivatives

To convert a production host such as an *E. coli* into an organism capable of synthesizing ω-cyclic fatty acids (cyFA), a gene that provides the cyclic precursor cyclohexylcarbonyl-CoA (CHC-CoA) (Cropp et al., Nature Biotech., 18:980-983, 2000) is introduced and expressed in the production host. A similar conversion is possible for other production hosts, for example, bacteria, yeast and filamentous fungi.

Non-limiting examples of genes that provide CHC-CoA in *E. coli* include: ansJ, ansK, ansL, chcA, and ansM from the ansatrienin gene cluster of *Streptomyces collinus* (Chen et al., Eur. J. Biochem., 261: 98-107, 1999), or plmJ, plmK, plmL, chcA, and plmM from the phoslactomycin B gene cluster of *Streptomyces* sp. HK803 (Palaniappan et al., J. Biol. Chem., 278:35552-35557, 2003) together with the chcB gene (Patton et al., Biochem., 39:7595-7604, 2000) from *S. collinus, S. avermitilis*, or *S. coelicolor* (see Table 5 for GenBank Accession numbers). The genes listed above in Table 4 can then be expressed to allow initiation and elongation of ω-cyclic fatty acids. Alternatively, the homologous genes can be isolated from microorganisms that make cyFA and expressed in *E. coli*.

TABLE 5

Genes for the synthesis of CHC-CoA

Organism	Gene	GenBank Accession No.
Streptomyces collinus	ansJK	U72144*
	ansL	
	chcA	
	ansM	
	chcB	AF268489
Streptomyces sp. HK803	pmlJK	AAQ84158
	pmlL	AAQ84159
	chcA	AAQ84160
	pmlM	AAQ84161
Streptomyces coelicolor	chcB/caiD	NP_629292
Streptomyces avermitilis	chcB/caiD	NP_629292

*Only chcA is annotated in GenBank entry U72144, ansJKLM are according to Chen et al., Eur. J. Biochem., 261: 98-107, 1999.

The genes listed in Table 4 (fabH, ACP, and fabF) are sufficient to allow initiation and elongation of co-cyclic fatty acids because they typically have broad substrate specificity. If the coexpression of any of these genes with the ansJKLM/chcAB or pmlJKLM/chcAB genes from Table 5 does not yield cyFA, then fabH, ACP, and/or fabF homologs from microorganisms that make cyFAs can be isolated (e.g., by using degenerate PCR primers or heterologous DNA sequence probes) and coexpressed. Table 6 lists non-limiting examples of microorganisms that contain ω-cyclic fatty acids.

TABLE 6

Non-limiting examples of microorganisms that contain ω-cyclic fatty acids

Organism	Reference
Curtobacterium pusillum	ATCC19096
Alicyclobacillus acidoterrestris	ATCC49025
Alicyclobacillus acidocaldarius	ATCC27009
*Alicyclobacillus cycloheptanicus**	Moore, J. Org. Chem., 62: pp. 2173, 1997.

*Uses cycloheptylcarbonyl-CoA and not cyclohexylcarbonyl-CoA as precursor for cyFA biosynthesis.

B. Saturation

Fatty acids are key intermediates in the production of fatty acid derivatives. The degrees of saturation in fatty acid derivatives can be controlled by regulating the degrees of saturation of the fatty acid intermediates. The sfa, gns, and fab families of genes can be expressed or overexpressed to control the saturation of fatty acids.

Production hosts can be engineered to produce unsaturated fatty acids by engineering the production host to overexpress fabB, or by growing the production host at low temperatures (e.g., less than 37° C.). FabB has preference for cis-δ^3 decenoyl-ACP, and results in unsaturated fatty acid production in *E. coli*. Overexpression of the fabB gene results in the production of a significant percentage of unsaturated fatty acids (de Mendoza et al., J. Biol. Chem., 258:2098-101, 1983). The fabB gene can be inserted into and expressed in production hosts not naturally having the gene. These unsaturated fatty acids can then be used as intermediates in the production hosts that are engineered to produce fatty acid derivatives, such as fatty alcohols, fatty esters, waxes, olefins, alkanes, and the like.

Alternatively, repressors of fatty acid biosynthesis, for example, a repressor (GenBank Accession No. NP_418398) encoded by fabR, can be deleted. This will also result in increased unsaturated fatty acid production in *E. coli* (Zhang et al., J. Biol. Chem., 277:15558, 2002). Similar deletions can be made in other production hosts. Further increase in unsaturated fatty acids may be achieved, for example, by overexpression of fabM (encoding trans-2, cis-3-decenoyl-ACP isomerase, GenBank Accession No. DAA05501) and controlled expression of fabK (encoding trans-2-enoyl-ACP reductase II, GenBank Accession No. NP_357969) from *Streptococcus pneumoniae* (Marrakchi et al., J. Biol. Chem., 277: 44809, 2002), while deleting *E. coli* fabI (encoding trans-2-enoyl-ACP reductase, GenBank Accession No. NP_415804). Additionally, to increase the percentage of unsaturated fatty esters, the production host can also overexpress fabB (encoding β-ketoacyl-ACP synthase I, GenBank Accession No. BAA16180, EC:2.3.1.41), sfa (encoding a suppressor of fabA, GenBank Accession No. AAC44390), and gnsA and gnsB (both encoding secG null mutant suppressors, GenBank Accession No. ABD18647.1 and GenBank Accession No. AAC74076.1, respectively). In some examples, the endogenous fabF gene can be attenuated, thus increasing the percentage of palmitoleate ($C_{16:1}$) produced.

The mutant thioesterases of the invention can be engineered to have altered properties, for example, altered specificity and/or increased activity, with regard to substituted or unsubstituted acyl-CoA or acyl-ACP compounds that are prepared as described herein. Accordingly the recombinant cell producing the fatty acid derivatives can be made to preferentially produce a desired saturation profile in a fatty acid derivative product that may have high value as an end product.

C. Chain Lengths and Ester Characteristics

1. Chain Lengths and Production of Odd-Numbered Chains

The methods described herein permit production of fatty esters and fatty acid derivatives of varied chain lengths by selecting a suitable mutant thioesterase that has specificity and/or selectivity for a substrate of a specific carbon chain length. By expressing the specific thioesterases, fatty acids and fatty acid derivatives having desired carbon chain lengths can be produced. In some embodiments, an endogenous thioesterase can be mutated using known genomic alteration techniques. Or, a gene encoding a particular thioesterase can be heterologously introduced into a production host such that a fatty acid or fatty acid derivative of a particular carbon chain length is produced. In certain embodiments, expression of endogenous thioesterases is suppressed. The mutant thioesterases of the invention can be engineered to have altered properties, for example, altered specificity and/or increased activity, with regard to specific chain lengths of acyl-CoA or acyl-ACP compounds described herein. Accordingly, the recombinant cell producing the fatty acid derivatives can be made to preferentially produce a fatty acid derivative product with the desired chain length and/or high value as an end product.

In one embodiment, the fatty acid derivative contains a carbon chain of about 4 to 36 carbon atoms, about 6 to 32 carbon atoms, about 10 to 30 carbon atoms, about 10 to 18 carbon atoms, about 24 to 32 carbon atoms, about 26 to 30 carbon atoms, about 26 to 32 carbon atoms, about 5 to 10 carbon atoms, about 10 to 16 carbon atoms, or about 12 to 18 carbon atoms. In an alternate embodiment, the fatty acid derivative contains a carbon chain less than about 20 carbon atoms, less than about 18 carbon atoms, or less than about 16 carbon atoms. In another embodiment, the fatty ester product is a saturated or unsaturated fatty ester product having a carbon atom content between 24 and 46 carbon atoms. In one embodiment, the fatty ester product has a carbon atom content between 24 and 32 carbon atoms. In another embodiment, the fatty ester product has a carbon content of 14 and 20 carbons. In another embodiment, the fatty ester is the methyl ester of $C_{18:1}$. In another embodiment, the fatty ester is the ethyl ester of $C_{16:1}$. In another embodiment, the fatty ester is the methyl ester of $C_{16:1}$. In yet another embodiment, the fatty ester is octadecyl ester of octanol.

Certain microorganisms preferentially produce even- or odd-numbered carbon chain fatty acids and fatty acid derivatives. For example, *E. coli* normally produce even-numbered carbon chain fatty acids and fatty acid ethyl esters (FAEE). Surprisingly, the methods disclosed herein can be used to alter that production. For example, *E. coli* can be made to produce odd-numbered carbon chain fatty acids and FAEE under certain circumstances.

2. Ester Characteristics

An ester typically includes what may be designated an "A" side and a "B" side. The B side may be contributed by a fatty acid produced from de novo synthesis in the production host organism. In some embodiments, where the production host is additionally engineered to make alcohols, including fatty alcohols, the A side is also produced by the production host organism. In yet other embodiments, the A side can be provided by the growth medium. By selecting the desired thioesterase genes, the B side (and the A side when fatty alcohols are being made) can be designed to be have certain desirable carbon chain characteristics. These characteristics include, for example, points of branching, points of unsaturation, and desired carbon chain lengths. Thus, the mutant thioesterases of the invention can be engineered to have altered properties, for example, altered specificity and/or increased activity, with regard to preference for accepting certain acyl-CoA or acyl-ACP compounds as an A side chain as described herein. Accordingly the recombinant cell producing the fatty acid derivatives can be made such that it preferentially produces a desired fatty acid derivative product that is valuable as an end product.

When particular thioesterase genes are selected, the A and B sides will have similar carbon chain characteristics when they are both contributed by the production host using fatty acid biosynthetic pathway intermediates. For example, at least about 50%, 60%, 70%, or 80% of the fatty esters produced will have A and B sides that vary by about 2, 4, 6, 8, 10, 12, or 14 carbons in length. The A side and the B side can also display similar branching and saturation levels.

In addition to producing fatty alcohols that contribute to the A side, the production host can produce other short chain alcohols such as ethanol, propanol, isopropanol, isobutanol, and butanol for incorporation on the A side using techniques well known in the art. For example, butanol can be made by the production host organism. To create butanol producing cells, the LS9001 strain, for example, can be further engineered to express atoB (acetyl-CoA acetyltransferase) from *Escherichia coli* K12, β-hydroxybutyryl-CoA dehydrogenase from *Butyrivibrio fibrisolvens*, crotonase from *Clostridium beijerinckii*, butyryl CoA dehydrogenase from *Clostridium beijerinckii*, CoA-acylating aldehyde dehydrogenase (ALDH) from *Cladosporium falvum*, and adhE encoding an aldehyde-alcohol dehydrogenase of *Clostridium acetobutylicum* in the pBAD24 expression vector under the prpBCDE promoter system. Other production host organisms may be similarly modified to produce butanol or other short chain alcohols. For example, ethanol can be produced in a production host using the methods described by Kalscheuer et al., Microbiology, 152:2529-2536, 2006, which is herein incorporated by reference.

III. Genetic Engineering of Production Strain to Increase/Improve Fatty Acid Derivative Production/Yield

Heterologous polynucleotide sequences involved in a biosynthetic pathway for the production of fatty acid derivatives can be introduced stably or transiently into a production host cell using techniques known in the art. Non-limiting examples of such techniques include electroporation, calcium phosphate precipitation, DEAE-dextran mediated transfection, liposome-mediated transfection, conjugation, transduction, and genomic integration. For stable transformation, a DNA sequence can further include a selectable marker, including, for example, markers for antibiotic resistance, and genes that complement auxotrophic deficiencies. On the other hand, endogenous polynucleotides involved in the biosynthetic pathway for the production of fatty acid derivatives can also be mutated using known genomic alteration techniques. These strategies can be applied separately or in combination.

Various embodiments herein utilize an expression vector that includes a heterologous DNA sequence encoding a protein involved in a metabolic or biosynthetic pathway. Suitable expression vectors include, but are not limited to, viral vectors (such as baculovirus vectors), phage vectors (such as bacteriophage vectors), plasmids, phagemids, cosmids, fosmids, bacterial artificial chromosomes, viral vectors (e.g., viral vectors based on vaccinia virus, poliovirus, adenovirus, adeno-associated virus, SV40, herpes simplex virus, and the like), P1-based artificial chromosomes, yeast plasmids, yeast artificial chromosomes, and any other vectors for specific production hosts of interest (such as *E. coli, Pseudomonas pisum*, and *Saccharomyces cerevisiae*).

Useful expression vectors can include one or more selectable marker genes to provide a phenotypic trait for selection of transformed production host cells. The selectable marker gene encodes a protein necessary for the survival or growth of transformed production host cells grown in a selective culture medium. Production host cells not transformed with the vector containing the selectable marker gene will not survive in the culture medium. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins (e.g., ampicillin, neomycin, methotrexate, or tetracycline); (b) complement auxotrophic deficiencies; or (c) supply critical nutrients not available from complex media (e.g., the gene that encodes D-alanine racemate for Bacilli). In alternative embodiments, the selectable marker gene is one that encodes dihydrofolate reductase or confers neomycin resistance (for use in eukaryotic cell culture), or one that confers tetracycline or ampicillin resistance (for use in a prokaryotic production host cell, such as in *E. coli*).

In the expression vector, the DNA sequence encoding the gene in the biosynthetic pathway is operably linked to an appropriate expression control sequence (e.g., promoters, enhancers, and the like) to direct synthesis of the encoded gene product. Such promoters can be derived from microbial or viral sources, including, for example, from CMV and SV40. Depending on the production host/vector system utilized, any number of suitable transcription and translation control elements can be used in the expression vector, including constitutive and inducible promoters, transcription enhancer elements, transcription terminators, and the like. See, e.g., Bitter et al., Methods in Enzymology, 153:516-544, 1987.

Suitable promoters for use in prokaryotic production host cells include, but are not limited to, promoters capable of recognizing the T4, T3, Sp6 and T7 polymerases, the P_R and P_L promoters of bacteriophage lambda, the trp, recA, heat shock, and lacZ promoters of *E. coli*, the alpha-amylase and the sigma-specific promoters of *B. subtilis*, the promoters of the bacteriophages of *Bacillus, Streptomyces* promoters, the int promoter of bacteriophage lambda, the bla promoter of the beta-lactamase gene of pBR322, and the CAT promoter of the chloramphenicol acetyl transferase gene. Prokaryotic promoters are reviewed by Glick, J. Indust. Microbiol., 1:277, 1987; Watson et al., Molecular Biology of the Gene, 4th Ed. (1987), Benjamin Cummins (1987); and Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed. (Cold Spring Harbor Laboratory Press, 1989), the disclosures of which are incorporated herein by reference. Non-limiting examples of suitable eukaryotic promoters for use within a eukaryotic production host are viral in origin and include the promoter of the mouse metallothionein I gene (Hamer et al., J. Mol. Appl. Gen., 1:273, 1982); the TK promoter of herpes virus (McKnight, Cell, 31:355, 1982); the SV40 early promoter (Benoist et al., Nature, 290:304, 1981); the cytomegalovirus promoter (Foecking et al., Gene, 45:101, 1980); the yeast gal4 gene promoter (Johnston et al., PNAS (USA), 79:6971, 1982; Silver et al., PNAS (USA), 81:5951, 1984); and the IgG promoter (Orlandi et al., PNAS (USA), 86:3833, 1989), the contents of which are incorporated herein by reference.

The production host can be genetically modified with a heterologous gene sequence encoding a biosynthetic pathway gene product that is operably linked to an inducible promoter. Inducible promoters are known in the art. Non-limiting examples of suitable inducible promoters include promoters that are affected by proteins, metabolites, or chemicals. These include, but are not limited to: a bovine leukemia virus promoter, a metallothionein promoter, a dexamethasone-inducible MMTV promoter, an SV40 promoter, an MRP polIII promoter, a tetracycline-inducible CMV promoter (such as the human immediate-early CMV promoter) as well as those from the trp and lac operons.

In some examples, a production host is genetically modified with a heterologous gene sequence encoding a biosynthetic pathway gene product that is operably linked to a constitutive promoter. Suitable constitutive promoters are known in the art and include constitutive adenovirus major late promoter, a constitutive MPSV promoter, or a constitutive CMV promoter.

In some examples, a modified production host is one that is genetically modified with an exogenous gene sequence encoding a single protein involved in a biosynthesis pathway. In other embodiments, a modified production host is one that is genetically modified with exogenous gene sequences encoding two or more proteins involved in a biosynthesis pathway, for example, the first and second enzymes in a biosynthetic pathway.

When a production host is genetically modified to express two or more proteins involved in a biosynthetic pathway, those gene sequences can each be contained in a single or in separate expression vectors. When those gene sequences are contained in a single expression vector, in some embodiments, the polynucleotide sequences will be operably linked to a common control element wherein the common control element controls expression of all of the biosynthetic pathway protein-encoding gene sequences in the single expression vector (e.g., a promoter).

When a modified production host is genetically modified with heterologous DNA sequences encoding two or more proteins involved in a biosynthesis pathway, one of the DNA sequences can be operably linked to an inducible promoter, and one or more of the DNA sequences can be operably linked to a constitutive promoter.

In some embodiments, the intracellular concentration (i.e., the concentration within the genetically modified production host) of a biosynthetic pathway intermediate can be increased to further boost the yield of the final product. The intracellular concentration of the intermediate can be increased in a number of ways, including, but not limited to, increasing the concentration in the culture medium of a substrate for a biosynthetic pathway; increasing the catalytic activity of an enzyme that is active in the biosynthetic pathway; increasing the intracellular amount of a substrate (e.g., a primary substrate) for an enzyme that is active in the biosynthetic pathway; and the like.

In some examples, the fatty acid derivative or intermediate is produced in the cytoplasm of the production host. The cytoplasmic concentration can be increased in a number of ways, including, but not limited to, binding of the fatty acid to coenzyme A to form an acyl-CoA thioester. Additionally, the concentration of acyl-CoA can be increased by increasing the biosynthesis of CoA in the cell, such as by over-expressing genes associated with pantothenate biosynthesis (e.g., panD) or knocking out genes associated with glutathione biosynthesis (e.g., glutathione synthase).

Regulatory sequences, coding sequences, and combinations thereof, can be introduced or altered in the chromosome of the production host. In some examples, the integration of the desired recombinant sequence into the production host genomic sequence does not require the use of a selectable marker such as an antibiotic. In some examples, the genomic alterations include changing the control sequence of the target genes by replacing the native promoter(s) with a promoter that is insensitive to regulation. There are numerous approaches for doing this. For example, Valle and Flores, in

Methods Mol. Biol., 267:113-122, 2006, describe a PCR-based method to overexpress chromosomal genes in *E. coli*. The content of Valle and Flores is incorporated by reference herein. Another approach is based on the use of single-stranded oligonucleotides to create specific mutations directly in the chromosome, using the technique developed by Court et al., PNAS (USA), 100:15748-15753, 2003, the content of which is also incorporated herein by reference. This technique is based on the use of the overexpression of the Beta protein from the bacteriophage lambda to enhance genetic recombination. The advantages of this approach include that synthetic oligonucleotides 70 bases long (or more) can be used to create point mutations, insertions, and deletions, thus eliminating any cloning steps. Furthermore, the system is sufficiently efficient that no markers are necessary to isolate the desired mutations.

With this approach the regulatory region of a gene can be changed to create a stronger promoter and/or eliminate the binding site of a repressor. Accordingly, a desired gene can be overexpressed in the production host organism.

IV. Fermentation

A. Maximizing Production Efficiency

Production and isolation of fatty acid derivatives can be enhanced by employing specific fermentation techniques. One method for maximizing production while reducing costs is increasing the percentage of the carbon source that is converted to hydrocarbon products.

During normal cellular lifecycles, carbon is used in cellular functions to produce lipids, saccharides, proteins, organic acids, and polynucleotides. Reducing the amount of carbon necessary for growth-related activities can increase the efficiency of carbon source conversion to output. This can be achieved by first growing microorganisms to a desired density, which is achieved at the peak of the growth log phase. Then, replication checkpoint genes can be harnessed to stop the growth of cells. Specifically, quorum sensing mechanisms (as reviewed in Camilli and Bassler, Science, 311:1113, 2006; Venturi, FEMS Microbio. Rev., 30:274-291, 2006; and Reading and Sperandio, FEMS Microbiol. Lett., 254:1-11, 2006, the disclosures of which are incorporated by reference herein) can be used to activate genes associated with the stationary phase.

Genes that can be activated to stop cell replication and growth in *E. coli* include umuDC genes, the over-expression of which stops the progression from stationary phase to exponential growth (Murli et al., J. of Bact., 182:1127, 2000). UmuC is a DNA polymerase that can carry out translesion synthesis over non-coding lesions—the mechanistic basis of most UV and chemical mutagenesis. The umuDC gene products are used for the process of translesion synthesis and also serve as polynucleotide sequence damage checkpoints. The umuDC gene products include UmuC, UmuD, umuD', $UmuD'_2C$, $UmuD'_2$, and/or $UmuD_2$. In the mean time, the product-producing genes can be activated, thus minimizing the need for replication and maintenance pathways to be used while the fatty acid derivative is being made. Production host microorganisms can also be engineered to express umuC and/or umuD from *E. coli* in pBAD24 under the prpBCDE promoter system through de novo synthesis of these genes with the appropriate end-product production genes.

The percentage of input carbons converted to fatty esters or hydrocarbon products is a cost driver. The more efficient the process is (i.e., the higher the percentage of input carbons converted to fatty esters or hydrocarbon products), the less expensive the process is. For oxygen-containing carbon sources (e.g., glucose and other carbohydrate based sources), the oxygen is released in the form of carbon dioxide. For every 2 oxygen atoms released, a carbon atom is also released, leading to a maximal theoretical metabolic efficiency of about 34% (w/w) (for fatty acid derived products). This figure, however, changes for other hydrocarbon products and carbon sources. Typical efficiencies in the literature are about <5%. Production hosts engineered to produce hydrocarbon products can have greater than about 1%, for example, greater than about 3%, 5%, 10%, 15%, 20%, 25%, or 30% efficiency. In one example, production hosts will exhibit an efficiency of about 10% to about 25%. In other examples, such production hosts will exhibit an efficiency of about 25% to about 30%. In other examples, such production hosts will exhibit >30% efficiency.

The production host can be additionally engineered to express recombinant cellulosomes, such as those described in PCT application number PCT/US2007/003736, incorporated herein by reference in its entirety, which can allow the production host to use cellulosic material as a carbon source. For example, the production host can be additionally engineered to express invertases (EC 3.2.1.26) so that sucrose can be used as a carbon source.

Similarly, the production host can be engineered using the teachings described in U.S. Pat. Nos. 5,000,000; 5,028,539; 5,424,202; 5,482,846; and 5,602,030, all incorporated herein by reference in their entirety, so that the production host can assimilate carbon efficiently and use cellulosic materials as carbon sources.

In one example, the fermentation chamber encloses a fermentation run/mixture that is undergoing a continuous reduction. In this instance, a stable reductive environment is created. The electron balance is maintained by the release of carbon dioxide (in gaseous form). Efforts to augment the NAD/H and NADP/H balance can also facilitate in stabilizing the electron balance.

The availability of intracellular NADPH can also be enhanced by engineering the production host to express an NADH:NADPH transhydrogenase. The expression of one or more NADH:NADPH transhydrogenases converts the NADH produced in glycolysis to NADPH which enhances the production of fatty acid derivatives.

B. Small-Scale Hydrocarbon Production

For small scale hydrocarbon product production, *E. coli* BL21(DE3) cells harboring pBAD24 (with ampicillin resistance and the end-product synthesis pathway) as well as pUMVC1 (with kanamycin resistance and the acetyl CoA/malonyl CoA over-expression system) are incubated overnight in 2 Liter flasks at 37° C., shaken at >200 rpm in 500 mL LB medium supplemented with 75 μg/mL ampicillin and 50 μg/mL kanamycin until the cultures reach an OD_{600} of >0.8. Upon achieving an OD_{600} of >0.8, cells are supplemented with 25 mM sodium propionate (at pH 8.0) to activate the engineered gene systems for production, and to stop cellular proliferation by activating UmuC and UmuD proteins. The induction step is performed for 6 hours at 30° C. After incubation, the medium is examined for hydrocarbon product using GC-MS.

C. Large-Scale Hydrocarbon Production

For large scale product production, the engineered production hosts are grown in batches of 10 Liter, 100 Liter, or larger; fermented; and induced to express the desired products based on the specific genes encoded in the appropriate plasmids therein.

For example, *E. coli* BL21(DE3) cells harboring pBAD24 (with ampicillin resistance and the end-product synthesis pathway) as well as pUMVC1 (with kanamycin resistance and the acetyl-CoA/malonyl-CoA overexpression) are incubated from a 500-mL seed culture for a 10-Liter fermentation

run (or a 5-Liter seed culture for a 100-Liter fermentation) in an LB medium (glycerol free) containing 50 μg/mL kanamycin and 75 μg/mL ampicillin at 37° C., which is shaken at >200 rpm until the culture reaches an OD_{600} of >0.8, a process that typically takes about 16 hours. The fermentation medium is continuously supplemented so as to maintain a sodium pohosphate of 25 mM, at pH 8.0, in order to activate the engineered gene systems for production, and to stop cellular proliferation by activating UmuC and UmuD proteins. The medium is also continuously supplemented with glucose to maintain a concentration of 25 g/100 mL.

After the first hour of induction, an aliquot of no more than 10% of the total cell volume is removed each hour and allowed to settle without agitation, which in turn allows the hydrocarbon product(s) to rise to the surface, undergoing a spontaneous phase separation. The hydrocarbon component is collected and the aqueous phase returned to the reaction chamber. The reaction chamber is operated continuously. When the OD_{600} drops below about 0.6, the cells are replaced with a new batch grown from a seed culture.

For wax ester production, the wax esters are isolated, washed briefly in 1 M HCl, and returned to pH 7 through extensive washing with distilled water.

V. Post-Production Processing

The fatty acid derivatives produced during fermentation can be separated from the fermentation media. Any technique known for separating fatty acid derivatives from aqueous media can be used. An exemplary separation process is a two-phase (bi-phasic) separation process. This process involves fermenting the genetically engineered production hosts under conditions sufficient to produce a fatty acid derivative, allowing the derivative to collect in an organic phase, and separating the organic phase from the aqueous fermentation broth. This method can be practiced in both a batch and continuous fermentation setting.

Bi-phasic separation takes advantage of the relative immiscibility of fatty acid derivatives to facilitate separation. "Immiscibility" refers to the relative inability of a compound to dissolve in water and is defined and/or determined by the compounds partition coefficient. One or ordinary skill in the art will appreciate that by choosing a fermentation broth and organic phase such that the fatty acid derivative being produced has a high log P value, the fatty acid derivative will separate into the organic phase in the fermentation vessel, even at low concentrations.

The fatty acid derivatives produced in accordance to the compositions, vectors, cells, and methods herein will be relatively immiscible in the fermentation broth, as well as in the cytoplasm. Therefore, the fatty acid derivative will collect in an organic phase either intracellularly and/or extracellularly. The collection of the products in the organic phase will lessen the impact of the fatty acid derivatives on cellular function, and will allow the production host to produce greater amount of product for longer.

The fatty alcohols, fatty esters, waxes, and hydrocarbons produced in accordance to the disclosures herein allow for the production of homogeneous compounds wherein at least about 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, or 95% of the fatty alcohols, fatty esters, and waxes produced suitably have carbon chain lengths that vary by less than about 6, less than about 4 carbons, or less than about 2 carbons. These compounds can also be produced so that they have a relatively uniform degree of saturation, for example, at least about 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, or 95% of the fatty alcohols, fatty esters, hydrocarbons and waxes are monounsaturated, diunsaturated, or triunsaturated. These compounds can be used directly as products or components of products, for example, as fuels, detergents, lubricants, personal care additives, nutritional supplements etc. These compounds can also be used as feedstock for subsequent reactions to make other products, including, for example transesterification, hydrogenation, catalytic cracking (via hydrogenation, pyrolysis, or both), or epoxidation reactions.

The fatty alcohols, fatty esters, waxes, and hydrocarbons produced in accordance to the compositions, vectors, cells, and methods herein contain low levels of unwanted or undesired elements, including, but not limited to, heavy metals. In some embodiments, the fatty alcohols, fatty esters, waxes, and hydrocarbons produced as described herein suitably contain less than about 50 ppm arsenic; less than about 300 ppm calcium; less than about 200 ppm chlorine; less than about 50 ppm cobalt; less than about 50 ppm copper; less than about 300 ppm iron; less than about 2% by weight of water; less than about 50 ppm lead; less than about 50 ppm manganese; less than about 0.2 ppm mercury; less than about 50 ppm molybdenum; less than about 1% by weight of nitrogen; less than about 200 ppm potassium; less than about 300 ppm sodium; less than about 3% by weight of sulfur; less than 50 ppm zinc; and/or less than 700 ppm phosphorus.

In some embodiments, the fatty alcohols, fatty esters, waxes, and hydrocarbons produced in accordance to the disclosures herein contain between about 50% and about 90% carbon; between about 5% and about 25% hydrogen; or between about 5% and about 25% oxygen. In other embodiments, the fatty alcohols, fatty esters, waxes, and hydrocarbons produced as described herein contain between about 65% and about 85% carbon; between about 10% and about 15% hydrogen; or between about 10% and about 20% oxygen.

VI. Fuel Compositions

As provided herein, certain fatty acid derivatives made according to the methods and compositions described herein possess various advantageous characteristics for use as a fuel. One of ordinary skill in the art will appreciate that, depending upon the intended purpose of the fuel, different fatty acid derivatives may have advantages as compared to others fatty acid derivatives. For example, branched fatty acid derivatives may be more desirable as automobile fuels or components of automobile fuels that are intended for uses in cold climates. Similarly, for certain applications, it may be advantageous to produce a fuel that is either more or less oxygenated or more or less saturated.

Using the methods described herein, fuels comprising relatively homogeneous fatty acid derivatives that at the same time have the desired characteristics/qualities can be produced. Such fatty acid derivative-based fuels can be characterized by carbon fingerprinting, and their lack of impurities, when compared to petroleum derived fuels or biodiesel derived from triglyceride, is also advantageous. The fatty acid derivative-based fuels can be combined with other fuels or fuel additives to produce fuels having desired properties.

The production hosts and methods disclosed herein can be used to produce free fatty acids and fatty esters. In some embodiments, the production hosts and methods disclosed herein can be used to produce a higher and/or improved titer or yield of fatty acid derivatives, including, for example, free fatty acids and/or fatty esters. In some embodiments, the percentage of free fatty acids in the product produced by the production host is at least about 1%, for example, at least about 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, or 25%. In some embodiments, the percentage of fatty esters in the product produced by the production host is at least about 50%, for example, at least about 55%, 60%, 65%, 70%, 75%, 80%, 85%, or 90%. In some embodiments, the ratio of fatty

esters to free fatty acids in the product produced by the production host is about 10:1, 9:1, 8:1, 7:1, 5:1, 2:1, or 1:1. In certain embodiments, the fatty ester produced by the production host is ethyl dodecanoate, ethyl tridecanoate, ethyl tetradecanoate, ethyl pentadecanoate, ethyl cis-9-hexadecenoate, ethyl hexadecanoate, ethyl heptadecanoate, ethyl cis-11-octadecenoate, ethyl octadecanoate, or combinations thereof. In certain other embodiments, the fatty ester produced by the production is methyl dedecanoate, methyl tridecanoate, methyl tetradecanoate, methyl pentadecanoate, methyl cis-9-hexadecenoate, methyl hexadecanoate, methyl heptadecanoate, methyl cis-11-octadecenoate, methyl octadecanoate, or combinations thereof. In certain embodiments, the free fatty acid produced by the production host is dodecanoic acid, tetradecanoic acid, pentadecanoic acid, cis-9-hexadecenoic acid, hexadecanoic acid, cis-11-octadecenoic acid, or combinations thereof.

The production hosts and methods disclosed herein can be used to produce different proportions of free fatty acids and fatty esters. In some embodiments, the proportion of free fatty acids in the product can be modified according to the methods, compositions, vectors and cells described herein such that the proportion is higher or lower vs. the fatty esters that are produced. In certain related embodiments, the proportion of fatty esters in the product can also be modified according to the disclosures herein, such that the proportion is higher or lower vs. the other products, for example, the free fatty acids, that are produced. In certain other embodiments, the proportional yield of fatty acid derivative with certain carbon chain lengths can be increased or decreased.

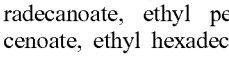
A. Carbon Fingerprinting

Biologically produced fatty acid derivatives represent a new source of fuels, such as alcohols, diesel, and gasoline. Biofuels made according to the methods and compositions described herein have not heretofore been produced from renewable sources and are new compositions of matter. These new fuels can be distinguished from fuels derived from petrochemical carbon on the basis of dual carbon-isotopic fingerprinting. Additionally, the specific source of biosourced carbon (e.g., glucose vs. glycerol) can be determined by dual carbon-isotopic fingerprinting (see U.S. Pat. No. 7,169,588, which is herein incorporated by reference in its entirety, in particular, at col. 4, line 31, to col. 6, line 8).

The fatty acid derivatives and the associated biofuels, chemicals, and mixtures can be distinguished from their petrochemical derived counterparts on the basis of ^{14}C (f_M) and dual carbon-isotopic fingerprinting.

The fatty acid derivatives described herein have utility in the production of biofuels and chemicals. The new fatty acid derivative-based products provided by the instant invention additionally can be distinguished on the basis of dual carbon-isotopic fingerprinting from those materials derived solely from petrochemical sources. The ability to distinguish these products is beneficial in tracking these materials in commerce. For example, fuels or chemicals comprising both "new" and "old" carbon isotope profiles can be distinguished from fuels and chemicals made only of "old" materials. Thus, the instant materials can be followed or "tracked" in commerce or identified in commerce as a biofuel on the basis of their unique profile. In addition, other competing materials can be identified as being biologically derived or derived from a petrochemical source.

In some examples, a biofuel composition is made, which includes a fatty acid derivative having $\delta^{13}C$ of from about −10.9 to about −15.4, wherein the fatty acid derivative accounts for at least about 85% of biosourced material (i.e., derived from a renewable resource such as, for example, cellulosic materials and sugars) in the composition. In other examples, the biofuel composition includes a fatty acid derivative having the formula:



wherein

X═CH_3, —CH_2OR^1; —C(O)OR^2; or —C(O)NR^3R^4;

R=for each n, independently absent, an H, or a lower aliphatic;

n=an integer from about 8 to about 34, preferably an integer from about 10 to about 24;

R^1, R^2, R^3, R^4=independently selected from an H or a lower alkyl.

Typically, when R is a lower aliphatic group, R represents a branched, unbranched or cyclic lower alkyl or lower alkenyl moiety. Exemplary R groups include, without limitation, methyl, isopropyl, isobutyl, sec-butyl, cyclopentenyl, and the like. The fatty acid derivative is additionally characterized as having a $\delta^{13}C$ of from about −10.9 to about −15.4, and the fatty acid derivative accounts for at least about 85% of biosourced material in the composition. In some examples the fatty acid derivative in the biofuel composition is characterized by having a fraction of modern carbon ($F_M{}^{14}C$) of at least about 1.003, 1.010, or 1.5.

B. Impurities

The fatty acid derivatives prepared in accordance with the disclosures herein are useful as components of or for making biofuels as well as other industrial chemicals. These fatty acid derivatives are made directly from fatty acids and not from the chemical processing of triglycerides. Accordingly, fuels and other industrial chemicals comprising the disclosed fatty acid derivatives often contain fewer impurities than are normally associated with, for example, products derived from triglycerides such as fuels derived from vegetable oils and fats.

The crude fatty acid derivative biofuels prepared in accordance with the disclosures herein (prior to mixing the fatty acid derivative with other fuels such as petroleum-based fuels) contain less transesterification catalysts than petroleum-based diesel or other biodiesel produced via one or more transesterification steps. The fatty acid derivative can contain less than about 2.0%, for example, less than about 1.5%, 1.0%, 0.5%, 0.3%, 0.1%, 0.05%, or 0% of a transesterification catalyst or an impurity resulting from a transesterification catalyst. Non-limiting examples of transesterification catalysts include hydroxide catalysts, such as NaOH, KOH, and LiOH; and acidic catalysts, such as mineral acid catalysts and Lewis acid catalysts. Non-limiting examples of catalysts and impurities resulting from transesterification catalysts include tin, lead, mercury, cadmium, zinc, titanium, zirconium, hafnium, boron, aluminum, phosphorus, arsenic, antimony, bismuth, calcium, magnesium, strontium, uranium, potassium, sodium, lithium, and combinations thereof.

The crude fatty acid derivative biofuels prepared in accordance with the disclosures herein (prior to mixing the fatty acid derivatives with one or more other fuels) tend to have a low gelling point, especially when the fatty acid derivative product comprises a $C_{16:1}$ ethyl ester or a $C_{18:1}$ ethyl ester, as compared to the gelling points of other types of biofuels.

Similarly, the crude fatty acid derivative biofuels prepared in accordance with the disclosures herein (prior to mixing the fatty acid derivative(s) with one or more other fuels such as petroleum-based diesels or other biodiesels) contain less glycerol (or glycerin) than biofuels made from triglycerides. The fatty acid derivative(s) can contain less than about 2.0%, for example, less than about 1.5%, 1.0%, 0.5%, 0.3%, 0.1%, 0.05%, or 0% by weight of glycerol.

Crude biofuels derived from the fatty acid derivatives herein also contain less free alcohol(s) (e.g., alcohols that are used to create the ester) than biodiesels made from triglycerides. This is due in part to the efficiency of utilization of the alcohols by the production hosts of the present disclosure. For example, the fatty acid derivative(s) can contain less than about 2.0%, 1.5%, 1.0%, 0.5%, 0.3%, 0.1%, 0.05%, or 0% by weight of free alcohol.

Biofuel derived from the disclosed fatty acid derivatives can be additionally characterized by its low concentration of sulfur as compared to petroleum-derived diesel. Biofuel derived from fatty acid derivatives herein can have less than about 2.0%, for example, less than about 1.5%, 1.0%, 0.5%, 0.3%, 0.1%, 0.05%, or 0% by weight of sulfur.

C. Additives and Fuel Compositions

Fuel additives are used to enhance the performance of a fuel or engine. For example, fuel additives can be used to alter the freezing/gelling points, cloud points, lubricity, viscosity, oxidative stability, ignition quality, octane levels, and flash points. In the United States, all fuel additives must be registered with Environmental Protection Agency. The names of fuel additives and the companies that sell the fuel additives are publicly available by contacting the EPA or by viewing the agency's website. One of ordinary skill in the art will appreciate that the fatty acid derivatives described herein can be mixed with one or more fuel additives to impart a desired quality.

The fatty acid derivatives described herein can be formulated into suitable fuel additives, which enhances the performance of fuels or engines. For example, the fatty acid derivatives described herein can be formulated into lubricity improvers, which impart desirable properties such as wear protection to the engine parts. Accordingly, additive compositions comprising the fatty acid derivatives produced in accordance with the disclosures herein are provided. In another example, the fatty acid derivatives described herein can be formulated into corrosion inhibitors.

The fatty acid derivatives described herein can be mixed with other fuels such as one or more biodiesels derived from triglycerides, various alcohols such as ethanol and butanol, and petroleum-derived products such as gasoline or diesel. Under certain circumstances, a fatty acid derivative with a low gelling point, such as a $C_{16:1}$ ethyl ester or a $C_{18:1}$ ethyl ester, is produced. This low gelling point fatty acid derivative can be mixed with one or more biodiesels made from triglycerides to reduce gelling point of the resulting fuel when compared to a fuel containing only the one or more biodiesels made from triglycerides. Similarly, a fatty acid derivative, such as a $C_{16:1}$ ethyl ester or a $C_{18:1}$ ethyl ester, can be mixed with a petroleum-derived diesel to provide a mixture that contains at least about, and often greater than about, 5% by weight of biodiesel. In some examples, the fuel mixture includes at least about 10%, 15%, 20%, 30%, 40%, 50%, and 60% by weight of the fatty acid derivative.

In some embodiments, the fuel composition can further comprise a synthetic fuel. Any synthetic fuel obtained from coal, natural gas, or biomass can be suitably used. In a further embodiments, the synthetic fuel comprises a Fischer-Tropsch based fuel, a Bergius-based fuel, a Mobil-based fuel, a Karrick-based fuel, or a combination thereof. In still further embodiments, the synthetic fuel comprises a Coal-To-Liquids based fuel (CTL-based fuel), a Gas-To-Liquids based fuel (GTL-based fuel), a Biomass-To-Liquids based fuel (BTL-based fuel), a Coal and Biomass-To-Liquids based fuel (CBTL-based fuel), or a combination thereof. In an exemplary embodiment, the synthetic fuel comprises a Fischer-Tropsch-based fuel.

The amount of synthetic fuel in the fuel composition disclosed herein may be from about 5% to about 90%, from about 5% to about 80%, from about 5% to about 70%, from about 5% to about 60%, or from about 5% to about 50%.

In certain embodiments, a biofuel composition can be made that includes at least about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90% or 95% of a fatty acice derivative that includes a carbon chain that is 8:0, 10:0, 12:0, 14:0, 14:1, 16:0, 16:1, 18:0, 18:1, 18:2, 18:3, 20:0, 20:1, 20:2, 20:3, 22:0, 22:1 or 22:3. Such biofuel compositions can additionally include at least one additive selected from a cloud point lowering additive that can lower the cloud point to less than about 5° C., or less than about 0° C.; a surfactant; a microemulsion; at least about 5%, 10%, 15%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, or 95% diesel fuel from triglycerides; a petroleum-derived gasoline; or a diesel fuel from petroleum.

In some embodiments, the fuel composition comprising the fatty esters produced in accordance with the methods, vectors, cells and compositions herein further comprises one or more diesel fuel additives. Suitable additives are desirably those that afford improved performance but also compatibility with the components in the fuel composition and devices that are typically associated with diesel engines. Illustrative examples of other suitable fuel additives include ignition improvers or cetane number improvers, detergents, dispersants, antiwear agents, viscosity index modifiers, friction modifiers, lubricity improvers, stabilizers, antioxidants, corrosion inhibitors, biocides, metal deactivators, and minor amounts of other optional additives, including, without limitation, antifoaming agents and seal fixes.

In particular embodiments, ignition improvers or cetane number improvers are often added to improve diesel engine performance. Exemplary cetane number improvers include 2'-ethylhexyl nitrate, and other alkyl nitrates. Cetane number improvers can be added to a fuel composition in an amount that is about 0.01 wt. % to about 1.0 wt. %, for example, about 0.05 wt. % to about 0.5 wt. %, based on the total weight of the fuel composition.

In certain embodiments, various detergents and/or dispersants can be included in the fuel composition comprising the fatty ester produced in accordance with the present disclosures to associate and disperse or remove harmful deposits from diesel engine parts. Suitable detergents typically comprise a polar head comprising a metal salt of an acidic organic compound and a long hydrophobic tail. Exemplary detergents include borated carbonate salts, borated sulfonate salts, which are preferably overbased. See, e.g., U.S. Pat. Nos. 4,744,920, 4,965,003, the disclosures of which are incorporated herein. Exemplary dispersants include, without limitation, carboxylic dispersants, succinimide dispersants, amine dispersants, and Mannich dispersants. See, e.g., U.S. Pat. Nos. 3,172,892, 3,438,757, 3,980,569, and 6,165,235, the disclosures of which are incorporated by reference herein. Dispersants can be present in the fuel composition in an amount of about 0.01 wt. % to about 0.1 wt. %, for example, 0.03 to about 0.05 wt. %, based on the total weight of the fuel composition.

In certain embodiments, antiwear agents, including for example, dihydrocarbyl dithiophosphate metal salts, can be added to the fuel composition to provide both antiwear and antioxidation benefits. See, e.g., U.S. Pat. No. 5,898,023, the disclosures of which are incorporated herein by reference.

In particular embodiments, the amount of lubricity improver in the fuel composition can range from about 1 ppm to about 50,000 ppm, for example, about 10 ppm to about 20,000 ppm, or about 25 ppm to about 10,000 ppm. Non-

limiting examples of lubricity improvers include esters and fatty acids, which may or may not be the same as those produced in accordance to the methods described herein.

In particular embodiments, the amount of stabilizers, which improves the storage stability of the fuel composition, can range from about 0.001 wt. % to about 2 wt. %, for example about 0.01 wt. % to about 1 wt. %, based on the total weight of the fuel composition. An exemplary stabilizer is a tertiary alkyl primary amine.

Antioxidants prevent the formation of gum depositions on fuel system components due to oxidation of the fuels in storage and/or inhibit the formation of peroxide compounds in certain fuel compositions. The amount of antioxidants can be ranged from about 0.001 wt. % to about 5 wt. %, for example, from about 0.01 wt. % to about 1 wt. %, based on the total weight of the fuel composition.

Corrosion inhibitors protect ferrous metals in fuel handling systems, such as pipelines and storage tanks, from corrosion. Certain corrosion inhibitors are also known to impart additional lubricity, and as such are particularly suitable when additional lubricity is desired. The corrosion inhibitor may be present in the fuel composition in an amount of about 0.001 wt. % to about 5 wt. %, for example, from about 0.01 wt. % to about 1 wt. %, based on the total weight of the fuel composition.

Biocides are used to combat microbial growth in the fuel composition, which may be present in the fuel composition at a concentration of about 0.001 wt. % to about 5 wt. %, for example, from about 0.01 wt. % to about 1 wt. %, based on the total weight of the fuel composition.

Metal deactivators suppress the catalytic effects of some metals, particularly copper, have on fuel oxidation, which can be present in the fuel composition in an amount of about 0.001 wt. % to about 5 wt. %, for example, at 0.01 wt. % to about 1 wt. %, based on the total weight of the fuel composition.

In addition, viscosity improvers, which are typically polymeric materials of number average molecular weights of from about 5,000 to about 250,000, and friction modifiers, which are typically sulfur-containing organo-molybdenum compounds can be added in minor amounts. Foam inhibitors, which typically include alkyl methacrylate polymers or dimethyl silicon polymers, can also be added to the fuel composition in an amount of less than about 10 ppm. Furthermore, seal fixes can be added to insure proper elastomer sealing and prevent premature seal failure can be included in the fuel composition.

EXAMPLES

The examples that follow illustrate the engineering of production hosts to produce specific fatty acid derivatives. The biosynthetic pathways involved in the production of fatty acid derivatives are illustrated in the figures.

For example, FIG. **3** is a diagram of the FAS pathway depicting the enzymes directly involved in the synthesis of acyl-ACP. To increase the production of fatty acid derivatives, such as waxes, fatty esters, fatty alcohols, and hydrocarbons, one or more of the enzymes described therein can be over expressed or mutated to reduce feedback inhibition, in order to increase the amount of acyl-ACP produced. Additionally, enzymes that metabolize the intermediates to make non-fatty acid based products (e.g., side reactions) can be functionally deleted or attenuated to increase the flux of carbon through the fatty acid biosynthetic (FAS) pathway. In the examples below, many production hosts are described that have been modified to increase fatty acid production.

FIGS. **4** and **5** depict biosynthetic pathways that can be engineered to make fatty esters and fatty alcohols, respectively. The conversion of each substrate (e.g., acetyl-CoA, malonyl-CoA, acyl-ACP, fatty acid, and acyl-CoA) to each product (e.g., acetyl-CoA, malonyl-CoA, acyl-ACP, fatty acid, acyl-CoA, fatty aldehydes, fatty esters, and fatty alcohols) can be accomplished using several different polypeptides that are members of the enzyme classes indicated.

The examples below describe microorganisms that have been engineered or can be engineered to produce specific fatty alcohols, fatty esters, and hydrocarbons.

Example 1

Production Host Construction

An exemplary production host is LS9001. LS9001 was produced by modifying C41(DE3) from Overexpress (Saint Beausine, France) to knockout the fadE gene (acyl-CoA dehydrogenase).

Briefly, the fadE knockout strain of *E. coli* was prepared using primers YafV_NotI and Ivry_O1 to amplify about 830 by upstream of fadE and primers Lpcaf of and LpcaR_Bam to amplify about 960 by downstream of fadE. Overlap PCR was used to create a construct for in-frame deletion of the complete fadE gene. The fadE deletion construct was cloned into the temperature-sensitive plasmid pKOV3, which contained a sacB gene for counterselection, and a chromosomal deletion of fadE was made according to the method of Link et al., J. Bact. 179:6228-6237, 1997. The resulting strain was not capable of degrading fatty acids and fatty acyl-CoAs. This knockout strain is herein designated as *E. coli* (DE3, ΔfadE).

Another fadE deletion strain, MG1655, was construted according to the procedures described by Datsenko et al., PNAS(USA), 97:6640-6645 (2000), with the modifications described below. The two primers used to create the deletion were:

Del-fadE-F:
(SEQ ID NO: 69)
5'-AAAAACAGCAACAATGTGAGCTTTGTTGTAATTATATTGTAAACATA

TTGATTCCGGGGATCCGTCGACC;
and

Del-fadE-R:
(SEQ ID NO: 70)
5'-AAACGGAGCCTTTCGGCTCCGTTATTCATTTACGCGGCTTCAACTTT

CCTGTAGGCTGGAGCTGCTTC.

The Del-fadE-F and Del-fadE-R primers each contain 50 bases of homology to the *E. coli* fadE gene and were used to amplify the Kanamycin resistance cassette from plasmid pKD13 by PCT as described. The resulting PCR product was used to transform electrocompetent *E. coli* MG1655 cells containing pKD46. The cells were previously induced with arabinose for 3-4 hours as described by Datsenko, supra. Following 3 hours of outgrowth in an SOC medium at 37° C., the cells were plated on Luria agar plates containing 50 μg/mL of Kanamycin. Resistant colonies were isolated after an overnight incubation at 37° C. Disruption of the fadE gene was confirmed in some of the colonies by PCR amplication using primers fadE-L2 and fadE-R1, which were designed to flank the fadE gene.

(SEQ ID NO: 71)
fadE-L2 5'-CGGGCAGGTGCTATGACCAGGAC;
and

(SEQ ID NO: 72)
fadE-R1 5'-CGCGGCGTTGACCGGCAGCCTGG

After the proper fadE deletion was confirmed, one colony was used to remove the Km^R marker using the pCP20 plasmid. The resulting strain is designaed as MG1655 (ΔfadE).

The fadE-deleted hosts were subject to further adjustments. A plasmid carrying the four genes that are responsible for acetyl-CoA carboxylase activity in *E. coli* (accA, accB, accC, and accD, GenBank Accession Nos: NP_414727, NP_417721, NP_417722, NP_416819, EC 6.4.1.2) were introduced. The accABCD genes were cloned in two steps as bicistronic operons into the NcoI/HindIII and NdeI/AvrII sites of pACYCDuet-1 (Novagen, Madison, Wis.), and the resulting plasmid was designated as pAS004.126. Alternatively, the production host was engineered to express accABCD from *Lactobacillus plantarum.*

Additional modifications that were included in a production host included the following: overexpression of aceEF (encoding the E1p dehydrogenase component and the E2p dihydrolipoamide acyltransferase component of the pyruvate and 2-oxoglutarate dehydrogenase complexes); and fabH/fabD/fabG/acpP/fabF (encoding FAS) from *E. coli, Nitrosomonas europaea* (ATCC 19718), *Bacillus subtilis, Saccharomyces cerevisiae, Streptomyces* spp, *Ralstonia, Rhodococcus, Corynebacteria, Brevibacteria, Mycobacteria*, and oleaginous yeast. Similarly, production hosts were engineered to express accABCD (encoding acetyl CoA carboxylase) from *Pisum savitum*. However, when the production host was also producing butanol it was found less desirable to express the *Pisum savitum* homolog.

In some production hosts, genes were knocked out or attenuated using the method of Link, et al., J. Bacteriol. 179:6228-6237, 1997. Genes that were knocked out or attenuated included gpsA (encoding biosynthetic sn-glycerol 3-phosphate dehydrogenase, GenBank Accession No. NP_418065, EC: 1.1.1.94); ldhA (encoding lactate dehydrogenase, GenBank Accession No. NP_415898, EC: 1.1.1.28); pflb (encoding formate acetyltransferase 1, GenBank Accession No. P09373, EC: 2.3.1.54); adhE (encoding alcohol dehydrogenase, GenBank Accession No. CAA47743, EC: 1.1.1.1, 1.2.1.10); pta (encoding phosphotransacetylase, GenBank Accession No. NP_416800, EC: 2.3.1.8); poxB (encoding pyruvate oxidase, GenBank Accession No. NP_415392, EC: 1.2.2.2); ackA (encoding acetate kinase, GenBank Accession No. NP_416799, EC: 2.7.2.1), and combinations thereof.

Similarly, the P1sB1D311E] mutation was introduced into LS9001 to attenuate plsB for the fadE deletion. This mutation decreased the amount of carbon diverted to phospholipid production. An allele encoding P1sB[D311E] was made by replacing the GAC codon for aspartate 311 with a GAA codon for glutamate. The altered allele was prepared by gene synthesis and the chromosomal plsB wildtype allele was exchanged for the mutant plsB [D311E] allele using the method of Link et al. (see supra).

Example 2

Production Host Modifications

The following plasmids were constructed for the expression of various proteins that are used in the synthesis of fatty acid derivatives. The constructs were prepared using standard molecular biology methods. All the cloned genes were put under the control of IPTG-inducible promoters (e.g., a T7 promoter, a tac promoter, or a lac promoter).

The 'tesA gene (thioesterase A gene, GenBank Accession No. NP_415027 without leader sequence (SEQ ID NO:31) (Cho and Cronan, J. Biol. Chem., 270:4216-9, 1995, EC: 3.1.1.5, 3.1.2.-)) of *E. coli* was cloned into an NdeI/AvrII digested pETDuet-1 vector (pETDuet-1 described herein is available from Novagen, Madison, Wis.). Genes encoding FatB-type plant thioesterases (TEs) from *Umbellularia californica, Cuphea hookeriana*, and *Cinnamonum camphorum* (GenBank Accession Nos: UcFatB1=AAA34215, ChFatB2=AAC49269, ChFatB3=AAC72881, CcFatB=AAC49151) were individually cloned into three different vectors: (i) NdeI/AvrII digested pETDuet-1; (ii) XhoI/HindIII digested pBluescript KS+ (Stratagene, La Jolla, Calif., to create N-terminal lacZ::TE fusion proteins); and (iii) XbaI/HindIII digested pMAL-c2X (New England Lab, Ipswich, Mass.) (to create n-terminal malE::TE fusions). The fadD gene (encoding acyl-CoA synthase) from *E. coli* was cloned into a NcoI/HindIII digested pCDFDuet-1 derivative, which contained the acr1 gene (acyl-CoA reductase) from *Acinetobacter baylyi* ADP1 within its NdeI/AvrII sites.

Table 7 provides a summary of the plasmids generated to make several exemplary production hosts.

TABLE 7

Summary of plasmids used in production hosts

Plasmid	Source Organism Gene Product	GenBank Accession No. & EC number
pETDuet-1-'TesA	*E. coli* 'TesA	Accessions: NP_415027, EC: 3.1.1.5, 3.1.2.—
pETDuet-1-TEuc	*Umbellularia californica*	Q41635
pBluescript-TEuc	UcFatB1	
pMAL-c2X-TEuc		AAA34215
pETDuet-1-TEch	*Cuphea hookeriana*	ABB71581
pBluescript-TEch	ChFatB2	AAC49269
pMAL-c2X-TEch	ChFatB3	AAC72881
pETDuet-1-TEcc	*Cinnamonum camphorum*	AAC49151
pBluescript-TEcc TEci	CcFabB	
pETDuet-1-atFatA3	*Arabidopsis thaliana*	NP_189147
pETDuet-1-HaFatA1	*Helianthus annuus*	AAL769361
pCDFDuet-1-fadD-acr1	*E. coli*	fadD: Accessions NP_416319, EC 6.2.1.3

TABLE 7-continued

Summary of plasmids used in production hosts

Plasmid	Source Organism Gene Product	GenBank Accession No. & EC number
		acr1: Accessions YP_047869
pETDuet-1-'TesA	*E. coli*	Accessions: NP_415027,
	'TesA	EC: 3.1.1.5, 3.1.2.—
pETDuet-1-TEuc	*Umbellularia californica*	Q41635
pBluescript-TEuc	UcFatB1	AAA34215
pMAL-c2X-TEuc		
pETDuet-1-TEch	*Cuphea hookeriana*	ABB71581
pBluescript-TEch	ChFatB2	AAC49269
pMAL-c2X-TEch	ChFatB3	AAC72881
pETDuet-1-TEcc	*Cinnamonumcamphorum*	
pBluescript-TEcc	CcFatB	AAC49151
TEci		
pCDFDuet-1-fadD-acr1	*E. coli*	fadD: Accessions NP_416319, EC 6.2.1.3 acr1: Accessions YP_047869

One of ordinary skill in the art will appreciate that different plasmids and genomic modifications can be used to achieve similar strains.

The selected expression plasmids contained compatible replicons and antibiotic resistance markers to produce a four-plasmid expression system.

In some embodiments, LS9001 can be co-transformed with: (i) any of the TE-expressing plasmids; (ii) the fadD-expressing plasmid, which also expresses acr1; and (iii) ester synthase expression plasmid.

As will be clear to one of ordinary skill in the art, when LS9001 is induced with IPTG, the resulting strain will produce increased concentrations of fatty alcohols from carbon sources such as glucose.

Example 3

Production of Fatty Alcohol in the Recombinant *E. coli* Strain

Fatty alcohols were produced by expressing a thioesterase gene and an acyl-CoA reductase gene exogenously in a production host. More specifically, plasmids pCDFDuet-1-fadD-acr1 (acyl-CoA reductase) and pETDuet-1-'TesA (thioesterase) were transformed into *E. coli* strain LS9001 and corresponding transformants were selected using LB plates supplemented with 100 mg/L spectinomycin and 50 mg/L carbenicillin. Four transformants of LS9001/pCDF-Duet-1-fadD-acr1 were independently inoculated into 3 mL of an M9 medium supplemented with 50 mg/L carbenicillin and 100 mg/L spectinomycin. The samples containing the transformants were cultured at 25° C. in a shaker (shaking at about 250 rpm) until they reached 0.5 OD_{600}. Next, 1.5 mL of each sample was transferred into a 250 mL flask containing 30 mL of the M9 medium described above. The resulting culture was grown at 25° C. in a shaker until it reached an OD_{600} of between 0.5-1.0. IPTG was then added to a final concentration of 1 mM. Cell growth continued for 40 hours.

The cells were then centrifuged and pelleted at 4,000 rpm. The cell pellet was suspended in 1.0 mL of methanol. 3 mL of ethyl acetate was then mixed with the suspended cells, followed by the addition of 3 mL of H_2O. Next, the mixture was sonicated for 20 minutes. The resulting sample was centrifuged at 4,000 rpm for 5 minutes. Then the organic phase (the upper phase), which contained fatty alcohol(s), was subjected to GC/MS analysis. The total alcohol (including tetradecanol, hexadecanol, hexadecenol, and octadecenol) titer was about 1-10 mg/L. When an *E. coli* strain carrying only empty vectors was cultured under the same conditions and following the same protocol, a fatty alcohols titer of only 0.2-0.5 mg/L was obtained.

Example 4

Production of Fatty Acids (FA) and Fatty Acide Ethyl Esters (FAEE) Containing Odd-Numbered Carbon Chains Without Heavy Metals

1. Production of biodiesel sample #23-30

Biodiesel sample #23-30 ("sample #23-30") was produced by bioreactor cultivation of an *E. coli* strain (C41 DE3 ΔfadE ΔfabR 'TesA fadD adplws) engineered to produce fatty esters. A two-stage inoculum protocol was utilized for expansion of the culture. The first stage consisted of the inoculation of a 50 mL LB medium (supplemented with 100 μg/L carbenicillin and 100 μg/L spectinomycin) in a 250 mL baffled shake flask with a 1 mL frozen stock vial of the *E. coli* ester production strain. This seed flask was incubated at 37° C. for about 7 hours (final OD_{600}=4.5, pH 6.7), after which 3 mL of the primary culture was transferred to each of three 2 L baffled flasks containing 350 mL buffered F1 minimal medium that also contained 100 μg/L carbenicillin and 100 μg/L spectinomycin. The shake flask buffer used was Bis-Tris propane at a final concentration of 200 mM (pH 7.2). These secondary seed flasks were incubated at 37° C. for about 18 hours (final OD_{600}=12, pH 5.5) and the contents were used to inoculate three 14 L bioreactors with a starting volume of 6.5 liters of buffered F1 minimal medium following inoculation. These bioreactors also contained 100 μg/L carbenicillin and 100 g/L spectinomycin.

These 14 L bioreactors were initially cultivated at 37° C., and the dissolved oxygen levels were maintained at 30% of saturation, using the agitation and oxygen enrichment cascade loops. The pH of the fermentation mix was maintained at 7.2, using 1 M H_2SO_4 and anhydrous ammonia gas. A nutrient feed consisting primarily of 43% (w/v) glucose was initiated in each bioreactor when the original 5 g/L glucose charge in the basal medium was exhausted. The glucose solution feed rate was then manually adjusted for the duration of the fermentation run to keep the residual glucose at a low (but

non-zero) value for the duration of the fermentation run. Cultures were induced with a final concentration of 1 mM IPTG when the OD_{600} of the cultures reached 30. At this induction point, the bioreactor cultivation temperature was reduced to 30° C., and about 15 mL/L (on a 6.5 to 7-Liter volume basis) of ethanol was added to the culture and monitored by HPLC throughout. Additional ethanol was added periodically to the bioreactors to maintain the residual concentrations at about 20 mL/L. The contents of the bioreactors were harvested after about 60 hours of cultivation, with about 10 L of the broth harvested from each of the three bioreactors.

These harvest broths were combined and extracted with an equivalent volume of ethyl acetate with stirring at room temperature for two hours. The broth extracts were then centrifuged (3,500 rpm, 30 minutes) to separate the liquid layers, followed by the removal of the organic layer for further processing. Ethyl acetate was almost completely removed (<0.3% residual, as determined by GC/FID) from the organic layer using rotary evaporation (Büchi, R-200), leaving about 90 mL of a dark, oily liquid. This liquid was referred to as sample #23-30.

2. Quantification of FA and FAEE in Sample #23-30

GC-MS was performed using an Agilent 5975B MSD system equipped with a 30 m×0.25 mm (0.10 μm film) DB-5 column. The column temperature was 3-minute isothermal at 100° C. The temperature of the column was programmed to rise from 100° C. to 320° C. at a rate of 20° C./min. When the final temperature of 320° C. was reached, the column remained isothermal for 5 minutes at that temperature. The injection volume was 1 μL. The carrier gas, helium, was released at 1.3 mL/min. The mass spectrometer was equipped with an electron impact ionization source. The ionization source temperature was set at 300° C. FAEE standards (e.g., ethyl dodecanoate, ethyl tetradecanoate, ethyl cis-9-hexadecenoate, ethyl hexadecanoate, ethyl octadecanoate, all >99%); fatty acid methyl ester (FAME) standards (e.g., methyl dodecanoate, methyl tetradecanoate, methyl pentadecanoate, methyl cis-9-hexadecenoate, methyl hexadecanoate, methyl cis-11-octadecenoate, all >99%); trimethylsilyl diazomethane (TMSD, 2 M in hexane); hydrochloric acid (37%); methanol (>99.9%); and ethyl acetate (>99.9%) were purchased from Sigma-Aldrich and applied without prior purification.

Sample #23-30 was derivatized by adding 50 μL trimethylsilyldiazomethane (TMSD), 8 μl HCl, and 36 μl methanol to 1 mL of sample (1 mg/mL in ethyl acetate). The mixture was incubated at room temperature for 1 hour.

Prior to quantitation, the FAEE and FAME in sample #23-30 were identified using two methods. First, the GC retention time of each compound was compared to the retention time of a known standard. Second, identification of each compound was confirmed by matching the compound's mass spectrum to a standard's mass spectrum in the mass spectra library.

When a standard for a FAEE or FAME was available, the quantification of the FAEE or FAME was determined by generating a calibration curve (concentration vs. instrument response). A linear relationship between the instrument response and the analyte concentration was then obtained. The concentration of the compound in the sample was determined by taking its instrument response and referring to the calibration curve.

When a standard for an FAEE was not available, an average instrument response was used to determine the compound's concentrations. The slope and the intercept for all existing calibration curves were averaged. From these averages, a linear relationship between concentration and instrument response was determined. The concentrations of unknown compounds were then determined by referencing the instrument responses to the linear relationship between instrument response and concentration using Equation 1.

$$\text{concentration}=(\text{instrument response}-\text{average intercept})/\text{average slope} \quad \text{Equation 1:}$$

After identifying and quantifying the FAME, the concentration of the associated free fatty acids was determined based upon the concentration of FAME and the molecular weight ratio of FA to FAME. Finally, the concentration of FAEE and FA in mg/L was converted into percentage in the biodiesel sample (w/w %).

The concentrations of FAEE and FA in sample #23-30 are listed in Table 8. The total concentration of FAEEs and FAs was 80.7%. The rest of the unknown compounds may be analyzed by LC/MS/MS method. Ethyl pentadecanoate, ethyl cis-9-hexadecenoate, ethyl hexadecanoate and ethyl cis-11-octadecenoate were the major component of sample #23-30.

TABLE 8

Percentage of FAEE and FA in sample #23-30

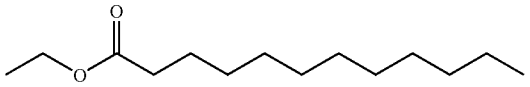
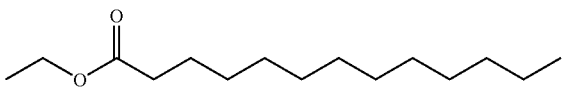
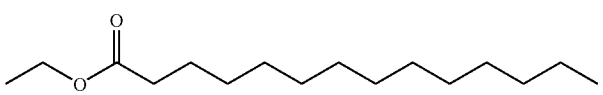
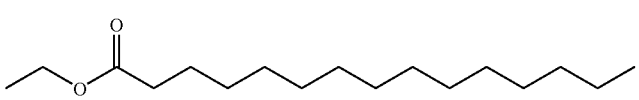
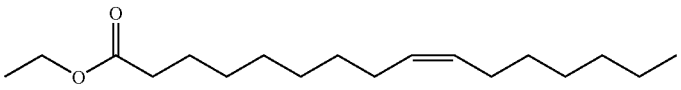
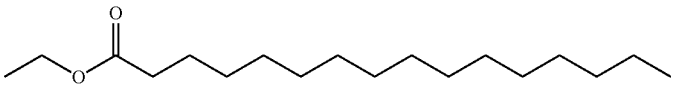
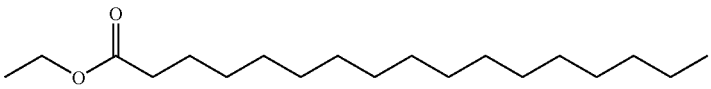
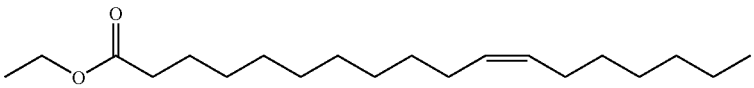
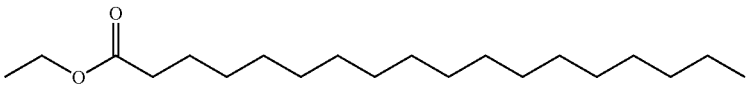
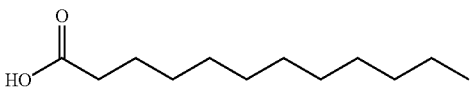
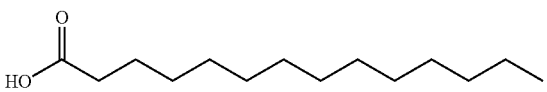
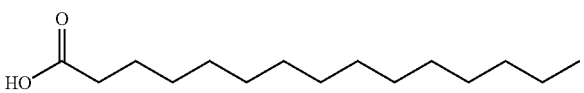
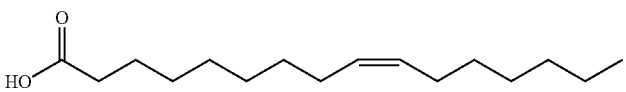
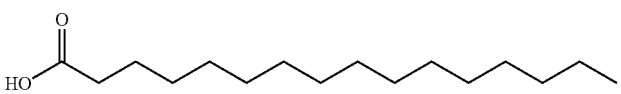
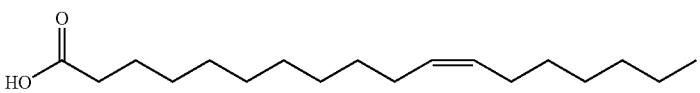
Name	Structure	MW	Percentage, %
Ethyl dodecanoate		228.2	1.82 ± 0.03
Ethyl tridecanoate		242.2	0.16 ± 0.01
Ethyl tetradecanoate		256.2	12.88 ± 0.16
Ethyl pentadecanoate		270.3	0.62 ± 0.02

TABLE 8-continued

Percentage of FAEE and FA in sample #23-30

Name	Structure	MW	Percentage, %
Ethyl cis-9-hexadecenoate		282.3	24.12 ± 0.20
Ethyl hexadecanoate		284.3	9.04 ± 0.11
Ethyl heptadecanoate		298.3	0.11 ± 0.01
Ethyl cis-11-octadecenoate		310.3	23.09 ± 0.33
Ethyl octadecanoate		312.3	0.19 ± 0.03
Dodecanoic acid		200.2	0.94 ± 0.02
Tetradecanoic acid		228.2	2.63 ± 0.03
Pentadecanoic acid		242.2	0.10 ± 0.01
cis-9-hexadecenoic acid		254.2	1.97 ± 0.01
Hexadecanoic acid		256.2	1.01 ± 0.01
cis-11-octadecenoic acid		282.3	2.00 ± 0.02

*Percentage is w/w %.

Surprisingly, sample #23-30 contained odd-numbered FA and FAEE.

3. Quantitative Elemental Analysis of Sample #23-30

Heavy metals are known to poison the catalysts used in catalytic cracking. To measure the levels of heavy metals in sample #23-30, sample #23-30 was sent to Galbraith Laboratories, Inc., for quantitative elemental analysis of arsenic, calcium, carbon, chlorine, cobalt, copper, hydrogen, iron, Karl Fisher water, lead, manganese, magnesium, mercury, molybdenum, nitrogen, potassium, sodium, sulfur, zinc, oxygen, and phosphorus. Preparatory and analytical methods are described below. Results are shown in Table 9. All amounts in Table 9 were below the level of quantitation (LOQ) except for carbon (73.38%), chlorine (91 ppm), hydrogen (12.1%), Karl Fisher water (0.998%), mercury (0.057 ppm), oxygen (14.53%), and phosphorus (343 ppm). Therefore, sample #23-30 did not contain high levels of the heavy metals of concern.

Method G-52, Rev 6: Microwave Digestion of Samples for Metals Analysis

An appropriate amount of sample was weighed into a microwave vessel to the nearest 0.001 g. The appropriate reagents were then added to the microwave vessel. If a visible reaction was observed the reaction was allowed to cease before capping the vessel. The vessel was then sealed and placed in the microwave according to the manufacturer's directions. The temperature of each vessel reached a minimum of 180±10° C. in 5 minutes. It remained at a minimum of 180±10° C. for 10 minutes. At the end of the microwave program the vessels were allowed to cool for a minimum of 5

minutes before removal. The vessels were then uncapped and transferred to volumetric flasks for analysis by the proper technique.

Method G-55, Rev 3: Parr Oxygen Bomb Combustion for the Determination of Halogens

Samples were weighed into a combustion cup, and mineral oil was added as a combustion aid. For chlorine (Cl) and bromine (Br) measurements, 1% hydrogen peroxide solution was added into the bomb. For sulfur (S) measurements, a 0.01 N sodium hydroxide solution was added. The sample and cup were sealed into a Parr oxygen combustion bomb along with a suitable absorbing solution. The bomb was purged with oxygen, then pressurized to 25-30 atm of oxygen pressure, and ignited. Afterwards, the contents of the bomb were well mixed and transferred to a beaker for subsequent analysis.

Method G-30B, Rev 7: Wet Ash Digestion of Inorganic and Organic Compounds for Metals Analysis

The sample was charred using H_2SO_4. If analyzing for metals that form insoluble sulfates, $HClO_4$ and HNO_3 were used to char the organic material. After charring the sample, HNO_3 was added and the sample was refluxed to solubilize the metals present. If the solution became cloudy, HCl was added to aid complete digestion. HF can be used if silicon was present in the sample but only if silicon was not an analyte of interest. All HF used was restricted to Teflon vessels. The clear digestate was quantitatively transferred to a Class A volumetric flask and brought to final volume. The sample was then analyzed.

Method ME-4A Rev 2: Determination of Anions Suppressed by Ion Chromatography

Instrument	Dionex Model DX500
Chromatograph Column	Dionex IonPac AS9-SC 4 × 250 mm
Eluent 2.4 mM Na_2CO_3	1.8 mM $NaHCO_3$
Preparation	Aqueous samples may be analyzed as is. Water-soluble samples are typically transferred by weight to a known volume. Other solid materials that are not water-soluble may be extracted to determine extractable quantities of various anions or combusted to determine total quantities of an element such as Cl or Br.
Calibration	Standards to bracket sample concentration. 0.2 mg/L-4.0 mg/L
Sample Intro	Auto injection (Hitachi Model AS7200)
Determination	Conductivity detection/linear regression
Quantitation Limit	Typically 0.2 mg/L in solution.
Interferences	Anions with similar retention times; overlapping peaks from major constituent anions.

Method S-300 Rev 7: Determination of Water by Coulometric Titration (Karl Fischer)

This method combined coulometry with the Karl Fischer titration. The sample was mixed with an amine-methanol mixture containing predominantly iodide ion (I—) and sulfur dioxide. The iodine produced at the anode through the electrolysis was allowed to react with water. In such cases, iodine was produced in direct proportion to the quantity of electricity according to Faraday's Law. Also, because 1 mole of water stoichiometrically reacts with 1 mole of iodine, 1 mg of water was equivalent to 10.71 coulombs of electricity. Utilizing this principle, the Moisture Meter determined the amount of water directly from the number of coulombs required for the electrolysis. This procedure included both direct introduction and a vaporizer pre-treatment technique.

Preparation	Weigh to obtain 100 µg to 3 mg H2O; Protect samples from atmospheric moisture during weighing and transfer.
Instrument	Mitsubishi Moisture Meter MCl Model CA-06 (Inst. #569) Mitsubishi Moisture Vaporizer, Model CA/VA-06 (Inst. #568)
Control	Sodium tartrate monohydrate (15.66%); Frequency: every 10 samples, one each day minimum, 95-105% recovery
Sample Intro	A. Entry port, Direct transfer; capillary, syringe, or scoop B. Furnace, tin capsules (Water Vaporizer VA-06); Temperature varies, 200° C. is default value used for standards. Most samples analyzed at 160° C. Other temperatures upon request.
Determination	Coulometric titration of Karl Fischer reagent via automatic titrator
Quantitation Limit	100 µg H_2O

Precision & Accuracy	RSD	RE	INSTR#
Sodium Tartrate	1.35%	−0.54%	569
Monohydrate	1.34%	−2.13%	568

Equations	$(2I^- - 2e^- \rightarrow I_2)$; $(I_2 + SO_2 + 3C_5H_5N + H_2O \rightarrow 2C_5H_5N\,HI + C_5H_5N\,SO_3)$ µg H_2O/spl wt (g) = ppm H_2O µgH_2O × 0.1/spl wt (mg) = % H_2)
Interferences	(direct transfer only) free alkali; oxidizing, reducing agent; mercaptans

Method E16-2, Rev 9 (Trace E16-2A): Sulfur Determination Using the LECO SC-432DR

The SC-432DR Sulfur Analyzer is a non-dispersive infrared, digitally controlled instrument designed to measure sulfur content in a variety of organic and inorganic materials. The sample was combusted at 1350±50° C. in an atmosphere of pure oxygen. The sulfur was oxidized to sulfur dioxide and quantitated by infrared absorption. The SC-432DR was equipped with two detectors, a high-range and a low-range infrared cell.

Instrument	LECO SC-432DR Sulfur Analyzer		
Sample Intro	Weigh sample to nearest 0.01 mg. Weigh samples directly into sample boat tared on electronic balance. Weight automatically transferred to SC432 database. Cover sample with LECO Com-Cat combustion accelerator as called for by sample type.		
Calibration	Three conditioners of 5-10 mg cystine. Seven calibration standards of 30-175 mg NIST SRM 8415 Whole Egg Powder (0.512% S). Internal calibration using a quadratic regressed curve.		
Control	NIST SRM 1549 Milk Powder (0.351%); others to match sample type. Frequency: one for every ten samples.		
Determination	Combustion in O_2 atmosphere at 1350° C. Determination of resulting SO_2 by infrared detector.		
Quantitation Limit	0.08 mg S		
Calculations	Internal		
	RSD (%)	Mean Recovery (%)	
Precision & Accuracy (milk powder)	2.60	97.97	

Method ME-2, Rev 14: Carbon, Hydrogen, and Nitrogen Determination

This instrument burns sample in pure oxygen at 950° C. under static conditions to produce combustion products of CO_2, H_2O, and N_2. The PE-240 automatically analyzes these products in a self-integrating, steady state thermal conductivity analyzer. Tungstic anhydride may be added to aid combustion. An extended combustion time (e.g., burn hard mode) may be employed for difficult to combust samples.

Instrument	PerkinElmer 240 Elemental Analyzer (Instrument # 409, 410)					
Sample intro	Weigh 1.0-2.5 mg into Al capsule; crimp (see GLI Procedure G-6) for liquids; washed with solvent prior to weighing upon request					
Decomposition	Combustion at ≥950° C., reduction at ≥675° C. = CO_2, H_2O, N_2					
Calibration	Cyclohexanone-2,4-dinitropheylhydrazone (1-2.5 mg)					
Control	s-1409, 2-1410: Cyclohexanone-2,4-dinitropheylhydrazone (51.79% C, 5.07% H, 20.14% N)					
Determination	CO_2, H_2O, N_2 by thermal conductivity analyzer					
Quantitation	0.5% C, 0.5% H, 0.5% N					
	Instrument #409			Instrument #410		
Precision & accuracy	C	H	N	C	H	N
RSD %	0.28	1026	0.39	0.35	1.12	0.41
Mean recovery (%)	99.94	101.25	99.86	100.13	100.40	100.04
Interferences	Metals and some halogens cause incomplete combustion. Combustion aids and/or an extended combustion time can be used to alleviate this problem.					
Calculations	Instrument calculates & prints w/w results for % C, % H, and % N. For samples crimped in an aluminum capsule, the % N is corrected with a factor; (μV/μg sample/K) × 100 = % Element, where K = calibration = μV/μg of C, or H, or N					

Method ME-70, Rev 4: Inductively Coupled Plasma Atomic Emission Spectrometry

This method describes multi-elemental determinations by ICP-AES using simultaneous optical systems and axial or radial viewing of the plasma. The instrument measures characteristic emission spectra by optical spectrometry. Samples were nebulized and the resulting aerosol was transported to the plasma torch. Element-specific emission spectra were produced by radio-frequency inductively coupled plasma. The spectra were dispersed by a grating spectrometer, and the intensities of the emission lines were monitored by photosensitive devices. Background correction was required for trace element determination. Background was measured adjacent to analyte lines on samples during analysis. The position selected for the background-intensity measurement, on either or both sides of the analytical line, was determined by the complexity of the spectrum adjacent to the analyte line. In one mode of analysis, the position used should be as free as possible from spectral interference and should reflect the

same change in background intensity as occurs at the analyte wavelength measured. Background correction is not required in cases of line broadening where a background correction measurement would actually degrade the analytical result.

Instrument	ICP-OES Optima 5300, 3300DV and 4300DV, or equivalent
Decomposition	Prior to analysis, samples must be acidified or digested using appropriate Sample Preparation Methods.
Calibration	0.01 ppm-60 ppm plus matrix specific calibrations
Sample Intro	Peristaltic pump, cross flow nebulizer, gemcone nebulizer, scott ryton spray chamber and quartz cylonic spray chamber
Determination	Atomic emission by radio frequency inductively coupled plasma of element-specific emission spectra through a grating spectrometer monitored by photosensitive devices.
Quantitation Limit	Element and calibration specific ranging from 0.01-2 ppm
Precision & Accuracy	±10% RSD
Interferences	Spectral, chemical, physical, memory
Calculations	wt % = (fc × v/10 × D)/spl ppm = (fc × v × D)/SPL Where fc = final concentration in µg/mL; v = sample volume in mL; D = dilution factor; spl = sample mass in mg; SPL = sample mass in g

Method E80-2, Rev 4: Determination of Mercury Aautomated Cold Vapor Technique)

This procedure is based on EPA SW846 Method 7471A. Cold Vapor Atomic Absorption is based on the general theory of atomic absorption, which holds that free atoms of the analyte absorb energy from a lamp source that is proportional to the concentration of analyte. By using a lamp containing the metal to be measured, the exact wavelength needed for absorption was produced and interferences were greatly reduced. Cold Vapor Atomic Absorption uses this principle, and the mercury atoms were liberated by reducing mercury ions with Tin (II) Chloride ($SnCl_2$). Nitrogen gas carried the atoms through an optical cell, with the Hg lamp on one end and the detector on the other end. Because the cold vapor method was employed, instead of a flame method, undigested organic compounds were an interference concern, because of their wide band of absorption wavelengths.

Instrument	PerkinElmer FIMS 400 Automated Mercury Analyzer or equivalent	
Decomposition	Variable, usually microwave digestion or permanganate hot water bath digestion	
Calibration	0.1-5.0 µg/L	
Sample Introduction	Autosampler, peristaltic pump	
Determination	Primary wavelength 253.7 nm, using a solid state detector	
Detection Limit	Varies with preparation method and sample matrix	
Precision & Accuracy	For microwave digestion:	For MnO_4^- digestion:
RE	−2.47%	4.90%
RSD	7.48%	5.20%
Interferences	Undigested organic compounds	
Calculations	$\text{ppb Hg} = \frac{\text{µg/L in solution} \times \text{volume (mL)} \times \text{dilution factor}}{\text{sample weight (g)}}$	

TABLE 9

Quantitative elemental analysis of sample #23-30

Element	Preparation Method	Analytical Method	Result
Arsenic	G-52	ME-70	<25 ppm
Calcium	G-30B	ME-70	<119 ppm
Carbon	N/A	ME-2	73.38%
Chlorine	G-55	ME-4A	91 ppm
Cobalt	G-30B	ME-70	<23 ppm
Copper	G-30B	ME-70	<23 ppm
Hydrogen	N/A	ME-2	12.1%
Iron	G-30B	ME-70	<136 ppm
Karl Fisher water	N/A	S-300	0.998%
Lead	G-52	ME-70	<25 ppm
Manganese	G-30B	ME-70	<23 ppm
Magnesium	G-30B	ME-70	<23 ppm
Mercury	G-52	E80-2	0.057 ppm
Molybdenum	G-30B	ME-70	<23 ppm
Nitrogen	N/A	ME-2	<0.5%
Potassium	G-30B	ME-70	<103 ppm
Sodium	G-30B	ME-70	<140 ppm
Sulfur	N/A	E16-2A	<0.140%
Zinc	G-30B	ME-70	<23 ppm
Oxygen	N/A	Subtraction*	14.53%
Phosphorus	G-30B	ME-70	343 ppm

Results presented as "<" are below LOQ.

*Oxygen content was determined by subtracting the observed results for all other elements from 100%.

Example 5

Production and Release of Fatty Alcohol from Production Host

acr1 (encoding acyl-CoA reductase) was expressed in *E. coli* cultured with glucose as the sole carbon and energy source. The *E. coli* produced small amounts of fatty alcohols such as dodecanol ($C_{12:0}$—OH), tetradecanol ($C_{14:0}$—OH), and hexadecanol ($C_{16:0}$—OH). In other samples, FadD (acyl-CoA synthase) was expressed together with acr1 in *E. coli*. A five-fold increase in fatty alcohol production was observed.

In other samples, acr1, fadD, and accABCD (acetyl-CoA carboxylase), in a plasmid carrying accABCD constructed as described in EXAMPLE 1, were expressed along with various individual thioesterases (TEs) in wild-type *E. coli* C41 (DE3) and an *E. coli* C41 (DE3 ΔfadE, a strain lacking acyl-

CoA dehydrogenase). This resulted in further increases in fatty alcohol production and modulation of the profiles of fatty alcohols (see FIG. **6**). For example, over-expression expression of *E. coli* (pETDuet-1-'TesA) in this system achieved about a 60-fold increase in $C_{12:0}$—OH, $C_{14:0}$—OH and $C_{16:0}$—OH, with $C_{14:0}$—OH being the major fatty alcohol. A very similar result was obtained when the ChFatB3 enzyme (FatB3 from *Cuphea hookeriana* in pMAL-c2X-TEcu) was expressed. When the UcFatB1 enzyme (FatB1 from *Umbellularia californicain* in pMAL-c2X-TEuc) was expressed, fatty alcohol production increased about 20-fold and $C_{12:0}$—OH was the predominant fatty alcohol.

Expression of ChFatB3 and UcFatB 1 also led to the production of significant amounts of the unsaturated fatty alcohols $C_{16:1}$—OH and $C_{14:1}$—OH, respectively. Fatty alcohols were also found in the supernatant of samples generated from the expression of 'tesA. At 37° C., about equal amounts of fatty alcohols were found in the supernatant and in the cell pellet. Whereas at 25° C., about 25% of the fatty alcohols was found in the supernatant. See FIG. **7**.

Example 6

Production of Fatty Alcohol Using a Variety of Acyl-CoA Reductases

This example describes fatty alcohol production using a variety of acyl-CoA reductases. Fatty alcohols can be the final product. Alternatively, the production host cells can be engineered to additionally express/overexpress ester synthases to produce fatty esters.

Each of four genes encoding fatty acyl-CoA reductases (Table 10) from various sources were codon-optimized for *E. coli* expression and synthesized by Codon Devices, Inc. (Cambridge, Mass.). Each of the synthesized genes was cloned as an NdeI-AvrII fragment into pCDFDuet-1-fadD vector (described in Example 2). Each of the plasmids carrying these acyl-CoA reductase genes with the *E. coli* fadD gene was transformed into *E. coli* strain C41 (DE) strain (purchased from Over-expression).

The recombinant strains were cultured in 3 mL of an LB broth (supplemented with 100 mg/L spectinomycin) at 37° C. overnight. 0.3 mL of the overnight culture was transferred to 30 mL of a fresh M9 medium (containing 100 mg/L spectinomycin) and cultured at 25° C. When the cultures reached OD_{600} of 0.5, 1 mM IPTG was added. Each culture was fed 0.1% of one of three fatty acids dissolved in H_2O at pH 7.0. The three fatty acids fed were sodium dodecanoate, sodium myristate, or sodium palmitate. A culture without the addition of fatty acid was also included as a control. After induction, the cultures were allowed to grow at the same temperature for an additional 40 hours at 25° C.

The quantification of fatty alcohol yield at the end of fermentation was performed using GC-MS as described above in EXAMPLE 3 and/or EXAMPLE 4. The resulting fatty alcohol produced from the corresponding fatty acid is shown in Table 11. The results indicated that three acyl-CoA reductases—Acr1, AcrM, and BmFAR—were able to convert all three fatty acids into corresponding fatty alcohols. The results also indicated that hFAR and JjFAR had activity when myristate and palmitate were the substrates. However, there was little or no activity when dodecanoate was the substrate. mFAR1 and mFAR2 only demonstrated low activity with myristate and demonstrated no activity with the other two fatty acids.

TABLE 10

Acyl-CoA reductases

Acyl-CoA reductase	Protein ID Accession number	Protein sources
mFAR1	AAH07178	*Mus musculus*
mFAR2	AAH55759	*Mus musculus*
JjFAR	AAD38039	*Simmondsia chinensis*
BmFAR	BAC79425	*Bombyx mori*
Acr1	AAC45217	*Acinetobacter baylyi* ADP1
AcrM	BAB85476	*Acinetobacter* sp. M1
hFAR	AAT42129	*Homo sapiens*

TABLE 11

Fatty alcohol production

		Peak Area[c]			
E. coli C41(DE3)	Acyl-CoA reductase genes	Dodecanoate/ dodecanol[b]	Myristate/ tetradecanol[b]	Palmitate/ hexadecanol[b]	No fatty acid feeding[a]/ hexadecanol
	mFAR1	7,400	85,700	8,465	70,900
	mFAR2	2,900	14,100	32,500	25,800
	JiFAR	5,200	8,500	53,112	33,800
	BmFAR	35,800	409,000	407,000	48,770
	acr1	202,000	495,000	1,123,700	58,515
	acrM	42,500	189,000	112,448	36,854
	hFAR1	5,050	59,500	109,400	94,400
vector control		4,000	1,483	32,700	27,500
media control		10,700	1,500	25,700	25,000

Note:
[a]Only hexadecanol was quantified in this case.
[b]Fatty acid fed/fatty alcohol produced.
[c]The area peak of fatty alcohol produced.

Example 7

Medium Chain Fatty Esters

Alcohol acetyl transferases (AATs, EC 2.3.1.84), which is responsible for acyl acetate production in various plants, can be used to produce medium chain length fatty esters, such as octyl octanoate, decyl octanoate, decyl decanoate, and the like. Fatty esters, synthesized from medium chain alcohol (such as C_6 and C_8) and medium chain acyl-CoA or fatty acids

(such as C_6 and C_8) have relatively low melting points. For example, hexyl hexanoate has a melting point of about −55° C. and octyl octanoate has a melting point of about −18° C. to about −17° C. The low melting points of these compounds make them suitable for use as biofuels.

In this example, an SAAT gene encoding a thioesterase was co-expressed in a production host *E. coli* C41(DE3, ΔfadE) (as described in International Application No. PCT/US08/058788, the disclosures of which is incorporated herein by reference) with fadD from *E. coli* and acr1 (alcohol reductase from *A. baylyi* ADP1). Octanoic acid was provided in the fermentation broth. This resulted in the production of octyl octanoate. Similarly, when the ester synthase gene from *A. baylyi* ADP1 was expressed in the production host instead of the SAAT gene, octyl octanoate was produced.

A recombinant SAAT gene was synthesized by DNA 2.0 (Menlo Park, Calif. 94025). The synthesized DNA sequence was based on the published gene sequence (GenBank Accession No. AF193789), but modified to eliminate the NcoI site. The synthesized SAAT gene (as a BamHI-HindIII fragment) was cloned in pRSET B (Invitrogen, Carlsbad, Calif.), linearized with BamHI and HindIII. The resulting plasmid, pHZ1.63A was cotransformed into an *E. coli* production host with pAS004.114B, which carries a fadD gene from *E. coli* and acr1 gene from *A. baylyi* ADP1. The transformants were cultured in 3 mL of an M9 medium containing 2% glucose. After IPTG induction and the addition of 0.02% octanoic acid, the culture was allowed to grow at 25° C. for 40 hours. 3 mL of acetyl acetate was then added to the whole culture and mixed several times using a mixer. The acetyl acetate phase was analyzed by GC/MS.

Surprisingly, no acyl acetate was observed in the acetyl acetate extract. However, octyl octanoate was observed. However, the control strain without the SAAT gene (C41(DE3, ΔfadE)/pRSET B+pAS004.114B) did not produce octyl octanoate. Furthermore, the strain (C41(DE3, ΔfadE)/pHZ1.43 B+pAS004.114B) in which the ester synthase gene from *A. baylyi* ADP1 was carried by pHZ1.43 produced octyl octanoate (see FIGS. **8**A-D).

The finding that SAAT activity produces octyl octanoate makes it possible to produce medium chain fatty esters, such as octyl octanoate and octyl decanoate, which have low melting points and are suitable for use as biofuels and for replacing triglyceride based biodiesel.

Example 8

Production of Fatty Esters in *E. coli* Strain LS9001

Fatty esters were produced by engineering an *E. coli* production host to express a fatty alcohol forming acyl-CoA reductase, thioesterase, and an ester synthase. Thus, the production host produced both the A and the B side of the ester and the structure of both sides was influenced by the expression of the thioesterase gene.

The LS9001 strain was transformed with plamids carrying an ester synthase gene from *A. baylyi* ADP1 (plasmid pHZ1.43), a thioesterase gene from *Cuphea hookeriana* (plasmid pMAL-c2X-Tech), and a fadD gene from *E. coli* (plasmid pCDFDuet-1-fad).

Plasmid pHZ1.43 carrying the ester synthase (WSadpl, GenBank Accession No. AA017391, EC 2.3.175) was constructed as follows. First the gene for WSadp1 was amplified with the following primers using genomic DNA sequence from *A. baylyi* ADP1 as template:

```
                                                    (SEQ ID NO: 35)
WSadp1_NdeI,  5'-TCATATGCGCCCATTACATCCG-3';
and

                                                    (SEQ ID NO: 36)
WSadp1_Avr,   5'-TCCTAGGAGGGCTAATTTAGCCCTTTAGTT-3'.
```

Then, the PCR product was digested with NdeI and AvrII and cloned into pCOLADuet-1 to give pHZ 1.43. The plasmid carrying wSadpl was then co-transformed into *E. coli* strain LS9001 with both pETDuet-1'TesA and pCDFDuet-1-fadD-acr1, and transformants were selected on LB plates supplemented with 50 mg/L of kanamycin, 50 mg/L of carbenicillin and 100 mg/L of spectinomycin.

Three transformants were inoculated in 3 mL of LBKCS (LB broth supplement with 50 mg/L kanamycin, 50 mg/L carbenicillin, 100 mg/L spectinomycin, and 10 g/L glucose) and incubated at 37° C. in a shaker (shaking at 250 rpm). When the cultures reached an OD_{600} of about 0.5, 1.5 mL of each culture was transferred into 250 mL flasks containing 50 mL LBKCS. The flasks were then incubated in a shaker (250 rpm) at 37° C. until the culture reached an OD_{600} of about 0.5 to about 1.0. IPTG was then added to a final concentration of 1 mM. The induced cultures were incubated at 37° C. in a shaker (250 rpm) for another 40-48 hours.

The cultures were then transferred into 50 mL conical tubes and the cells were centrifuged at 3,500×g for about 10 minutes. Each of the cell pellets was then mixed with 5 mL ethyl acetate. The ethyl acetate extracts were analyzed with GC/MS. The titer of fatty esters (including $C_{16}C_{16}$, $C_{14:1}C_{16}$, $C_{18:1}C_{18:1}$, C_2C_{14}, C_2C_{16}, $C_2C_{16:1}$, $C_{16}C_{16:1}$ and $C_2C_{18:1}$) was about 10 mg/L. When an *E. coli* strain only carrying empty vectors was cultured under the same conditions and following the same protocol, only 0.2 mg/L fatty esters was found in the ethyl acetate extract.

Example 9

Production and Release of Fatty-Ethyl Ester from Production Host

The LS9001 strain was transformed with plasmids carrying an ester synthase gene from *A. baylyi* (plasmid pHZ1.43), a thioesterase gene from *Cuphea hookeriana* (plasmid pMAL-c2X-TEcu) and a fadD gene from *E. coli* (plasmid pCDFDuet-1-fadD).

This recombinant strain was cultured at 25° C. in 3 mL of an M9 medium containing 50 mg/L kanamycin, 100 mg/L carbenicillin, and 100 mg/L spectinomycin. After IPTG induction, the medium was adjusted to a final concentration of 1% ethanol and 2% glucose.

The culture was allowed to grow for 40 hours after IPTG induction. The cells were separated from the spent medium by centrifugation at 3,500×g for 10 minutes. The cell pellet was re-suspended with 3 mL of the M9 medium. The cell suspension and the spent medium were then extracted with 1 volume of ethyl acetate. The resulting ethyl acetate phases from the cell suspension and the supernatant were subjected to GC-MS analysis.

The C_{16} ethyl ester was the most prominent ester species for this thioesterase and 20% of the fatty ester produced was released from the cell. See FIG. **9**. A control *E. coli* strain C41(DE3, ΔfadE) containing pCOLADuet-1 (empty vector for the ester synthase gene), pMAL-c2X-TEuc (containing fatB from *U. california*) and pCDFDuet-1-fadD (fadD gene from *E. coli*) failed to produce detectable amounts of fatty

acid ethyl esters. The fatty acid esters were quantified using commercial palmitic acid ethyl ester as the reference.

Fatty esters were also made using the methods described herein except that methanol or isopropanol was added to the fermentation broth. The expected fatty esters were produced.

Example 8

The Influence of Various Thioesterases on the Composition of Fatty-Ethyl Esters Produced in Recombinant *E. coli* Strains

The thioesterases FatB3 (*C. hookeriana*), 'TesA (*E. coli*), and FatB (*U. california*) were expressed simultaneously with ester synthase (from *A. baylyi*). A plasmid, pHZ1.61, which comprises a pCDFDuet-1 (Novagen, Madison, Wis.) backbone with the fadD gene, was constructed by replacing the NotI-AvrII fragment (carrying the acr1 gene) with the NotI-AvrII fragment from pHZ1.43 such that fadD and the ADP1 ester synthase were in one plasmid and each of the coding sequences was under the control of a separate T7 promoter. The construction of pHZ1.61 made it possible to use a two-plasmid system instead of the three-plasmid system. pHZ1.61 was then co-transformed into *E. coli* C41(DE3, ΔfadE) with one of the plasmids, each carrying a different thioesterase gene as described herein.

The total fatty acid ethyl esters (in both the supernatant and intracellular fatty acid ethyl fluid) produced by these transformants were evaluated using the technique described herein. The titers and the composition of fatty acid ethyl esters are summarized in Table 12.

TABLE 12

Titers (mg/L) and composition of fatty acid ethyl esters by recombinant *E. coli* C41(DE3, ΔfadE)/pHZ1.61 and plasmids carrying various thioesterase genes.

Thioesterases	C_2C_{10}	$C_2C_{12:1}$	C_2C_{12}	$C_2C_{14:1}$	C_2C_{14}	$C_2C_{16:1}$	C_2C_{16}	$C_2C_{18:1}$	Total
'TesA	0.0	0.0	6.5	0.0	17.5	6.9	21.6	18.1	70.5
ChFatB3	0.0	0.0	0.0	0.0	10.8	12.5	11.7	13.8	48.8
ucFatB	6.4	8.5	25.3	14.7	0.0	4.5	3.7	6.7	69.8
pMAL	0.0	0.0	0.0	0.0	5.6	0.0	12.8	7.6	26.0

Note:
'TesA, pETDuet-1-'TesA;
ChFatB3, pMAL-c2X-TEcu;
ucFatB, pMAL-c2X-TEuc;
pMAL, pMAL-c2X, the empty vector for thioesterase genes used in the study.

Example 9

Use of Various Ester Synthases to Produce Biofuel

Four genes encoding ester synthases were synthesized based on corresponding polynucleotide sequences reported in NCBI GenBank with minor modifications. These modifications include the removal of internal NcoI, NdeI, HindIII, and AvrII restriction sites without introducing other changes to the corresponding amino acid sequence. The four genes of interest were each synthesized with an NdeI site on the 5' end and an AvrII at the 3' end. The sequences were then cloned into the NdeI and AvrII site of pCOLADuet-1 (Novagene) to produce pHZ1.97-376, pHZ1.97-377, pHZ1.97-atfA1 and pHZ1.97-atfA2. The plasmids carrying each of the four genes of interest along with the respective GenBank Accession numbers and the GenPeptide Accessions numbers are listed in Table 13 below.

TABLE 13

Ester synthases

Plasmids	ID	DNA sequence original sources	GenBank Accession No.	GenPeptide accession No.
pHZ1.97-376	FES376(376)	*Marinobacter aquaeolei* VT8	CP000514.1	ABM17275
pHZ1.97-377	FES377(377)	*Marinobacter aquaeolei* VT8	CP000514.1	ABM20141
pHZ1.97-atfA1	FESA1(AtfA1)	*Alcanivorax borkumensis* SK2	NC_008260.1	YP_694462
pHZ1.97-atfA2	FESA2(AtfA2)	*Alcanivorax borkumensis* SK2	NC_008260.1	YP_693524

Each of the four plasmids was transformed into *E. coli* C41 (DE3, ΔfadEΔfabR)/pETDuet-1-'TesA+pCDFDuet-1-fadD. Three transformants from each transformation were selected for fermentation studies to determine their abilities to synthesize fatty acid ethyl esters. The fermentation step was performed as described in EXAMPLE 6, but at two different temperatures, 25° C. or 37° C. Strain C41 (DE3, ΔfadEΔfabR)/pETDuet-1-'TesA+pCDFDuet-1-fadD+pHZ1.43 (expressing ADP1 ester synthase) was used as a positive control and C41 (DE3, ΔfadEΔfabR)/pETDuet-1-'TesA+pCDFDuet-1-fadD as a negative control.

The expression of each of the four ester synthase genes in the *E. coli* strain with attenuated fadE and fabR activity and overexpressing 'tesA and fadD enabled each strain to produce about 250 mg/L of FAEE at 25° C. This was the same amount produced by the positive control that expressed ADP1 ester synthase. In contrast, the negative control strain produced less than 50 mg/L FAEE under the same conditions at 25° C. (see, FIG. **10**). The fatty acyl composition of FAEE produced from these four ester synthases was similar to that from ADP1 ester synthases (see, FIG. **11**)

Results from fermentations performed at 37° C. indicated that strains carrying pHZ1.97_aftA2 and strains carrying pHZ1.97_376 produced more FAEE than the positive control carrying pHZ1.43 (see, FIG. **12**). The strains carrying pHZ1.97_aftA2 and the strains carrying pHZ1.97_376 also produced large amount of free fatty acid (see, FIG. **13**). Whereas the strain carrying pHZ.143 did not accumulate free fatty acid. The results demonstrated that these four ester synthases were capable of accepting ethanol and a broad range of acyl-CoA as substrates.

Example 12

Use of Eukaryotic Ester Synthase to Produce Biofuel

This example describes the cloning and expression of an ester synthase from *Saccharomyces cerevisiae*. Plasmids were generated using standard molecular biology techniques.

TABLE 14

Plasmids with eeb1

Given Name	Vector Backbone	Construction
pGL10.59	pCOLADuet-1 (Novagen)	eeb1* gene inserted between BamHI and HindIII sites (KanR)
pGL10.104	pMAL c2x (NEB)	eeb1* gene inserted between BamHI and HindIII sites (AmpR)
pMAL-c2X-TEuc	pMAL c2x (NEB)	See Table 7 above
pCDFDuet-1-acr1	pCDFDuet-1 (Novagen)	See Table 7 above

*The *Saccharomyces cerevisiae* gene eeb1 (GenBank Accession number YPL095C) was PCR-amplifed from *S. cerevisiae* genomic DNA sequence using primers that introduced the 5' BamHI and 3' HindIII sites.

An *E. coli* C41 (DE3 ΔfadE) production host was used to express the various plasmids. The *E. coli* cells were cultured in an M9 minimal medium (containing 6 g/L Na_2HPO_4, 3 g/L KH_2PO_4, 0.5 g/L NaCl, 1 g/L NH_4Cl, 1 mg/L thiamine (vit. B1), 1 mM $MgSO_4$, 0.1 mM $CaCl_2$, 0.4% (w/v) or 2% (w/v) glucose). All fatty acid stock solutions were prepared by dissolving the fatty acid sodium or potassium salt in distilled deinoized water at pH 7.0. Octanoic acid stock was purchased from Sigma, St. Louis, Mo.

Fermentations were performed using the C41 (DE3 ΔfadE) strain containing plasmids pCDFDuet-1-acr1, pMAL-c2X-TEuc (ucFatB), and pGL10.59 (eebl). The control strain was C41 (DE3 ΔfadE) strain carrying pCDFDuet-1-acr1, pMAL-c2X-TEuc, and the empty pCOLADuet-1 vector. Each of the three colonies from each transformation were used to inoculate an M9+0.4% glucose starter culture supplemented with carbenicillin (100 μg/mL), spectinomycin (100 μg/mL), and kanamycin (50 μg/mL). The cultures were allowed to grow at 37° C. overnight. Production cultures were established by making a 1:100 dilution of starter culture to inoculate 3 mL M9 media+0.4% glucose. The production cultures were allowed to grow at 37° C. until OD_{600}=0.6 before being induced with 1 mM IPTG, fed 1% ethanol, and cultured for an additional 40 hours at 25° C. Whole cell cultures were extracted with an equal volume of ethyl acetate by vortexing vigorously for 30 seconds. The organic phase was taken and examined on the GC/MS using the method alkane_1_splitless_ctc.m for FAEE detection, which is described above in EXAMPLE 4, part 2, "Quantification of FA and FAEE in sample #23-30."

No FAEE peaks were detected in the samples. In order to determine whether eebl was correctly expressed, IPTG-induced and uninduced cultures were analyzed by SDS-PAGE. No band corresponding to the size of Eeb1 (about 52 kDa) was detected. This suggested that, for this particular plasmid system, Eeb1 was not well-expressed.

Additional expression experiments were performed using a different expression vector. The gene was cloned into the vector pMALc2x, which expressed the target protein as a maltose binding protein (MBP) fusion. SDS-PAGE analysis of whole-cell lysates revealed that cultures induced with 1 mM IPTG yielded an appropriately-sized band corresponding to the Eeb1-MBP fusion (about 92 kDa). The band was not present in uninduced cells. This experiment was described in detail in International Application No. PCT/US08/058788, the disclosures therein is incorporated by reference in the entirety.

Eeb1 enzymatic activity was assessed using the C41 (DE3 ΔfadE) *E. coli* strain carrying plasmids pCDFDuet-1-acr1 and pGL10.104 (eebl). A C41 (DE3 ΔfadE) with pCDFDuet-1-acr1 and pMALc2x served as the control strain. Three colonies were picked from each transformation and each was used to inoculate an M9+0.4% glucose overnight starter culture supplemented with carbenicillin (100 μg/mL) and spectinomycin (100 μg/mL). A 1:100 dilution of the starter culture was used to inoculate 10 mL of an M9+0.4% glucose production cultures. The production cultures were allowed to grow at 37° C. until OD_{600}=0.4-0.5 before inducing with 1 mM IPTG. The cultures were each fed about 1% ethanol, octanoic acid (to about 0.01% or about 0.02% of the final volume), and/or decanoic acid (to about 0.02% of the final volume). Fermentations were allowed to continue for 24 hours at 25° C. Extractions were carried out by adding 1/10 volume of 12 M HCl and an equal volume of ethyl acetate to the culture and vortexing for 30 seconds. Samples were analyzed by GC/MS as described above.

GC/MS data revealed a peak corresponding to the octanoic acid ethyl ester can be detected for cells expressing eebl and fed octanoic acid and ethanol. The vector control strain also showed a C_2C_8 peak, albeit a smaller peak than that of the eebl-expressing cells.

Cells that were fed 0.02% decanoic acid did not grow well; therefore, the following studies were conducted using 0.01% or 0.005% decanoic acid. To test the ability of Eeb1 to utilize alcohols other than ethanol in synthesizing fatty acid esters, fermentations were carried out using the same strain: C41 (DE3 ΔfadE) with pCDFDuet-1-acr1 and pGL10.104. Cells were cultured as previously described. At induction, the cells

were fed 0.02% octanoic acid along with 1% methanol, ethanol, propanol, or isopropanol. Cells were also fed 0.01% or 0.005% decanoic acid and 1% ethanol. Fermentations were allowed to continue post-induction for 24 hours at 25° C. To prepare for analysis by GC/MS, cultures were centrifuged to separate the pellet and the supernatant. The pellet was resuspended in an equal volume of a fresh M9+0.4% glucose medium. Both the resuspended pellets and supernatant samples were extracted as described above and analyzed by GC/MS.

All of the supernatant samples contained large amounts of fatty acid but no detectable fatty acid esters. Similarly, the vector control pellet samples contained no fatty acid ester peaks, as determined using GC/MS. However, cells fed a C_{10} fatty acid showed peaks that were identified as representing decanoic acid.

The pellet samples derived from the cells expressing Eeb1 and fed a C_8 fatty acid and propanol or ethanol showed small peaks corresponding to propyl or ethyl esters. No peak was detected from the cells that were fed methanol or isopropanol. Cultures fed 0.01% or 0.005% of a C_{10} fatty acid and ethanol also produced a C_2C_{10} FAEE, but the FAEE was found in the pellet samples.

The results indicated that Eeb1 was capable of synthesizing FAEEs using octanoic or decanoic acids, and was also able to use methanol to generate the octanoic methyl ester. However, these compounds were highly volatile and as such the GC/MS data might not have accurately reflected the true titers. To more accurately measure product formation a hexadecane overlay was used to facilitate the capture of more volatile FAEEs.

Eeb1 activity with regard to fatty acid substrates was assessed using strain C41 (DE3 ΔfadE) with pCDFDuet-1-acr1 and pGL10.104, which was fed different chain-length fatty acids. Cells were cultured as described above, but were induced at OD_{600}=0.8-0.9 so as to promote better cell growth post-induction. At this point, cells were fed 1% ethanol and 0.02% of a C_8 fatty acid or 0.01% of a combination of the following fatty acids: C_{10}, C_{12}, C_{14}, and C_{16}. Cultures that were fed C_8 or C_{10} fatty acids were overlaid with 20% total volume of hexadecane. Fermentations were carried out for an additional 24 hours at 25° C. post induction. For product analysis, whole cultures (without separating the supernatant from the pellet) were extracted as described herein, with 1/10 volume of HCl and an equal volume (to the volume of the culture) of ethyl acetate. Hexadecane-treated samples were injected directly into the GC/MS using the program hex_1_splitless_ctc.m, which is described above in EXAMPLE 4, part 2, "Quantification of FA and FAEE in sample #23-30."

None of the vector controls had any detectable FAEE peaks. For the C_8- and C_{10}-fed cells, large C_2C_8 and C_2C_{10} peaks were detected in the hexadecane samples, but not in the ethyl acetate samples. This demonstrated that hexadecane was able to successfully trap the volatile FAEEs. For the rest of the ethyl acetate samples, small peaks were detected for C_2C_{12} and C_2C_{14} FAEEs, but no C_2C_{16} FAEE was detected. Thus, Eeb1 generated ethyl esters using fatty acids with chain lengths from C_8 to C_{14}. Eeb1 favored C_8 and C_{10} over the longer-chain fatty acids.

Example 13

Genomic Integration of Recombinant Sequences to Make a Host Strain that Over-Expresses *E. coli* FabA and/or FabB Genes

It is known that the product of the fabR gene acts as a repressor of the expression of the fabA and fabB genes. It is also known that FadR works as an activator of the same genes. The FabR and predicted consensus binding sequences were previously published by Zhang et al., J. Biol. Chem. 277: 15558-15565, 2002. The consensus binding sequences and their locations relative to the fabA and fabB genes of *E. coli* is shown in FIG. **14**.

A fabR knockout strain of *E. coli* was created. Primers TrmA_R_NotI and FabR_FOP were used to amplify about 1,000 by upstream of fabR, and primers SthA_F_Bam and FabR_ROP were used to amplify about 1000 by downstream of fabR. Overlap PCR was applied to create a construct for in-frame deletion of the complete fabR gene. The fabR deletion construct was cloned into a temperature-sensitive plasmid pKOV3, which contained SacB for counterselection. A chromosomal deletion of fabR was made according to the method described in Link et al., J. Bact., 179:6228-6237, 1997.

TABLE 15

fabR knock-out primers

Primer Name	Primer Sequence (5' to 3')
TrmA_R_Not	ATAGTTTAGCGGCCGCAAATCGAGCTGGATCAGGATTA (SEQ ID NO: 37)
FabR_FOP	AGGATTCAGACATCGTGATGTAATGAAACAAGCAAATCA AGATAGA (SEQ ID NO: 38)
SthA_F_Bam	CGCGGATCCGAATCACTACGCCACTGTTCC (SEQ ID NO: 39)
FabR_ROP	TTGATTTGCTTGTTTCATTACATCACGATGTCTGAATCC TTG (SEQ ID NO: 40)

Example 14

Production Host Construction

Table 16 identifies the homologs of certain genes described herein, which are known to be expressed in microorganisms that produce biodiesels, fatty alcohols, and hydrocarbons. To increase fatty acid production and, therefore, hydrocarbon production in production hosts such as those identified in Table 16, heterologous genes can be expressed, such as those from *E. coli*.

One of ordinary skill in the art will appreciate that genes that are endogenous to the microorganisms provided in Table 16 can also be expressed, over-expressed, or attenuated using the methods described herein. Moreover, genes that are described in Table 16 can be expressed, overexpressed, or attenuated in production hosts that endogenously produce hydrocarbons to allow for the production of specific hydrocarbons with defined carbon chain length, saturation points, and branch points.

TABLE 16

Hydrocarbon production hosts

Organism	Gene Name	Accession No./SEQ ID/Loci	EC No.
Desulfovibrio desulfuricans G20	accA	YP_388034	6.4.1.2
Desulfovibrio desulfuricans G22	accC	YP_388573/YP_388033	6.3.4.14, 6.4.1.2
Desulfovibrio desulfuricans G23	accD	YP_388034	6.4.1.2
Desulfovibrio desulfuricans G28	fabH	YP_388920	2.3.1.180
Desulfovibrio desulfuricans G29	fabD	YP_388786	2.3.1.39
Desulfovibrio desulfuricans G30	fabG	YP_388921	1.1.1.100
Desulfovibrio desulfuricans G31	acpP	YP_388922/YP_389150	3.1.26.3, 1.6.5.3, 1.6.99.3
Desulfovibrio desulfuricans G32	fabF	YP_388923	2.3.1.179
Desulfovibrio desulfuricans G33	gpsA	YP_389667	1.1.1.94
Desulfovibrio desulfuricans G34	ldhA	YP_388173/YP_390177	1.1.1.27, 1.1.1.28
Erwinia (*micrococcus*) *amylovora*	accA	942060-943016	6.4.1.2
Erwinia (*micrococcus*) *amylovora*	accB	3440869-3441336	6.4.1.2
Erwinia (*micrococcus*) *amylovora*	accC	3441351-3442697	6.3.4.14, 6.4.1.2
Erwinia (*micrococcus*) *amylovora*	accD	2517571-2516696	6.4.1.2
Erwinia (*micrococcus*) *amylovora*	fadE	1003232-1000791	1.3.99.—
Erwinia (*micrococcus*) *amylovora*	plsB(D311E)	333843-331423	2.3.1.15
Erwinia (*micrococcus*) *amylovora*	aceE	840558-843218	1.2.4.1
Erwinia (*micrococcus*) *amylovora*	aceF	843248-844828	2.3.1.12
Erwinia (*micrococcus*) *amylovora*	fabH	1579839-1580789	2.3.1.180
Erwinia (*micrococcus*) *amylovora*	fabD	1580826-1581749	2.3.1.39
Erwinia (*micrococcus*) *amylovora*	fabG	CAA74944	1.1.1.100
Erwinia (*micrococcus*) *amylovora*	acpP	1582658-1582891	3.1.26.3, 1.6.5.3, 1.6.99.3
Erwinia (*micrococcus*) *amylovora*	fabF	1582983-1584221	2.3.1.179
Erwinia (*micrococcus*) *amylovora*	gpsA	124800-125810	1.1.1.94
Erwinia (*micrococcus*) *amylovora*	ldhA	1956806-1957789	1.1.1.27, 1.1.1.28
Kineococcus radiotolerans SRS30216	accA	ZP_00618306	6.4.1.2
Kineococcus radiotolerans SRS30216	accB	ZP_00618387	6.4.1.2
Kineococcus radiotolerans SRS30216	accC	ZP_00618040/ ZP_00618387	6.3.4.14, 6.4.1.2
Kineococcus radiotolerans SRS30216	accD	ZP_00618306	6.4.1.2
Kineococcus radiotolerans SRS30216	fadE	ZP_00617773	1.3.99.—
Kineococcus radiotolerans SRS30216	plsB(D311E)	ZP_00617279	2.3.1.15
Kineococcus radiotolerans SRS30216	aceE	ZP_00617600	1.2.4.1
Kineococcus radiotolerans SRS30216	aceF	ZP_00619307	2.3.1.12
Kineococcus radiotolerans SRS30216	fabH	ZP_00618003	2.3.1.180
Kineococcus radiotolerans SRS30216	fabD	ZP_00617602	2.3.1.39
Kineococcus radiotolerans SRS30216	fabG	ZP_00615651	1.1.1.100

TABLE 16-continued

Hydrocarbon production hosts

Organism	Gene Name	Accession No./SEQ ID/Loci	EC No.
Kineococcus radiotolerans SRS30216	acpP	ZP_00617604	3.1.26.3, 1.6.5.3, 1.6.99.3
Kineococcus radiotolerans SRS30216	fabF	ZP_00617605	2.3.1.179
Kineococcus radiotolerans SRS30216	gpsA	ZP_00618825	1.1.1.94
Kineococcus radiotolerans SRS30216	ldhA	ZP_00618879	1.1.1.28
Rhodospirillum rubrum	accA	YP_425310	6.4.1.2
Rhodospirillum rubrum	accB	YP_427521	6.4.1.2
Rhodospirillum rubrum	accC	YP_427522/YP_425144/YP_427028/ YP_426209/ YP_427404	6.3.4.14, 6.4.1.2
Rhodospirillum rubrum	accD	YP_428511	6.4.1.2
Rhodospirillum rubrum	fadE	YP_427035	1.3.99.—
Rhodospirillum rubrum	aceE	YP_427492	1.2.4.1
Rhodospirillum rubrum	aceF	YP_426966	2.3.1.12
Rhodospirillum rubrum	fabH	YP_426754	2.3.1.180
Rhodospirillum rubrum	fabD	YP_425507	2.3.1.39
Rhodospirillum rubrum	fabG	YP_425508/YP_425365	1.1.1.100
Rhodospirillum rubrum	acpP	YP_425509	3.1.26.3, 1.6.5.3, 1.6.99.3
Rhodospirillum rubrum	fabF	YP_425510/YP_425510/ YP_425285	2.3.1.179
Rhodospirillum rubrum	gpsA	YP_428652	1.1.1.94 1.1.1.27
Rhodospirillum rubrum	ldhA	YP_426902/YP_428871	1.1.1.28
Vibrio furnissii	accA	1, 16	6.4.1.2
Vibrio furnissii	accB	2, 17	6.4.1.2
Vibrio furnissii	accC	3, 18	6.3.4.14, 6.4.1.2
Vibrio furnissii	accD	4, 19	6.4.1.2
Vibrio furnissii	fadE	5, 20	1.3.99.—
Vibrio furnissii	plsB(D311E)	6, 21	2.3.1.15
Vibrio furnissii	aceE	7, 22	1.2.4.1
Vibrio furnissii	aceF	8, 23	2.3.1.12
Vibrio furnissii	fabH	9, 24	2.3.1.180
Vibrio furnissii	fabD	10, 25	2.3.1.39
Vibrio furnissii	fabG	11, 26	1.1.1.100
Vibrio furnissii	acpP	12, 27	3.1.26.3, 1.6.5.3, 1.6.99.3
Vibrio furnissii	fabF	13, 28	2.3.1.179
Vibrio furnissii	gpsA	14, 29	1.1.1.94
Vibrio furnissii	ldhA	15, 30	1.1.1.27, 1.1.1.28
Stenotrophomonas maltophilia R551-3	accA	ZP_01643799	6.4.1.2
Stenotrophomonas maltophilia R551-3	accB	ZP_01644036	6.4.1.2
Stenotrophomonas maltophilia R551-3	accC	ZP_01644037	6.3.4.14, 6.4.1.2
Stenotrophomonas maltophilia R551-3	accD	ZP_01644801	6.4.1.2
Stenotrophomonas maltophilia R551-3	fadE	ZP_01645823	1.3.99.—
Stenotrophomonas maltophilia R551-3	plsB(D311E)	ZP_01644152	2.3.1.15
Stenotrophomonas maltophilia R551-3	aceE	ZP_01644724	1.2.4.1
Stenotrophomonas maltophilia R551-3	aceF	ZP_01645795	2.3.1.12

TABLE 16-continued

Hydrocarbon production hosts

Organism	Gene Name	Accession No./SEQ ID/Loci	EC No.
Stenotrophomonas maltophilia R551-3	fabH	ZP_01643247	2.3.1.180
Stenotrophomonas maltophilia R551-3	fabD	ZP_01643535	2.3.1.39
Stenotrophomonas maltophilia R551-3	fabG	ZP_01643062	1.1.1.100
Stenotrophomonas maltophilia R551-3	acpP	ZP_01643063	3.1.26.3 1.6.5.3, 1.6.99.3
Stenotrophomonas maltophilia R551-3	fabF	ZP_01643064	2.3.1.179
Stenotrophomonas maltophilia R551-3	gpsA	ZP_01643216	1.1.1.94
Stenotrophomonas maltophilia R551-3	ldhA	ZP_01645395	1.1.1.28
Synechocystis sp. PCC6803	accA	NP_442942	6.4.1.2
Synechocystis sp. PCC6803	accB	NP_442182	6.4.1.2
Synechocystis sp. PCC6803	accC	NP_442228	6.3.4.14, 6.4.1.2
Synechocystis sp. PCC6803	accD	NP_442022	6.4.1.2
Synechocystis sp. PCC6803	fabD	NP_440589	2.3.1.39
Synechocystis sp. PCC6803	fabH	NP_441338	2.3.1.180
Synechocystis sp. PCC6803	fabF	NP_440631	2.3.1.179
Synechocystis sp. PCC6803	fabG	NP_440934	1.1.1.100, 3.1.26.3
Synechocystis sp. PCC6803	fabZ	NP_441227	4.2.1.60
Synechocystis sp. PCC6803	fabI	NP_440356	1.3.1.9
Synechocystis sp. PCC6803	acp	NP_440632	
Synechocystis sp. PCC6803	fadD	NP_440344	6.2.1.3
Synechococcus elongates PCC7942	accA	YP_400612	6.4.1.2
Synechococcus elongates PCC7942	accB	YP_401581	6.4.1.2
Synechococcus elongates PCC7942	accC	YP_400396	6.3.4.14, 6.4.1.2
Synechococcus elongates PCC7942	accD	YP_400973	6.4.1.2
Synechococcus elongates PCC7942	fabD	YP_400473	2.3.1.39
Synechococcus elongates PCC7942	fabH	YP_400472	2.3.1.180
Synechococcus elongates PCC7942	fabF	YP_399556	2.3.1.179
Synechococcus elongates PCC7942	fabG	YP_399703	1.1.1.100, 3.1.26.3
Synechococcus elongates PCC7942	fabZ	YP_399947	4.2.1.60
Synechococcus elongates PCC7942	fabI	YP_399145	1.3.1.9
Synechococcus elongates PCC7942	acp	YP_399555	
Synechococcus elongates PCC7942	fadD	YP_399935	6.2.1.3

The Accession Numbers of Table 16 are from GenBank, Release 159.0 as of Apr. 15, 2007, EC Numbers of Table 16 are from KEGG, Release 42.0 as of April 2007 (plus daily updates up to and including May 9, 2007), results for *Erwinia amylovora* strain Ea273 were obtained from the Sanger sequencing center, completed shotgun sequence as of May 9, 2007, positions for *Erwinia* represent locations on the Sanger psuedo-chromosome, sequences from *Vibrio furnisii* M1 are from the VFM1 pseudo-chromosome, v2 build, as of Sep. 28, 2006, and include the entire gene, and may also include flanking sequence.

Example 15

Additional Exemplary Production Strains

Table 17 provides additional exemplary production strains. Two example biosynthetic pathways are described for producing fatty acids, fatty alcohols, and wax esters. For example, Table 17 provides examples 1 and 2 that produce fatty acids. The production host strain used to produce fatty acids in example 1 is a production host cell that is engineered to have the desired synthetic enzymatic activities. Each "x"

marks the genes correlated to the activities, for example, acetyl-CoA carboxylase, thio-esterase, and acyl-CoA synthase activity. Production host cells can be selected from bacteria, yeast, and fungi. As provided in Table 17, additional production hosts can be created using the indicated exogenous genes.

TABLE 17

Combination of genes useful for making genetically engineered production strains

			II. Fatty acids		III. Fatty alcohols		IV. wax/fatty esters	
Peptide	Sources of genes	Genes	example 1	example 2	example 1	example 2	example 1	example 2
acetyl-CoA carboxylase	*E. coli*	accABCD	X	X	X	X	X	X
thio-esterase	*E.coli*	'TesA	X		X		X	X
	Cinnamomum camphora	ccFatB						
	Umbellularia californica	umFatB		X		X		
	Cuphea hookeriana	chFatB2						
	Cuphea hookeriana	chFatB3						
	Cuphea hookerian	chFatA						
	Arabidopsis thaliana	AtFatA1						
	Arabidopsis thaliana	AtFatB1 [M141T]						
acyl-CoA synthase	*E. coli*	fadD	X	X	X	X	X	X
acyl-CoA reductase	*Bombyx mori*	bFAR						
	Acinetobacter baylyi ADP1	acr1			X		X	
	Simmondsia chinesis	jjFAR				X		X
	Triticum aestivum	TTA1						
	Mus musculus	mFAR1						
	Mus musculus	mFAR2						
	Acinetpbacter sp M1	acrM1						
	Homo sapiens	hFAR						
Ester synthase/ alcohol acyl-transferase	*Fundibacter jadensis* DSM 12178	WST9						
	Acinetobacter sp. HO1-N	WSHN					X	
	Acinetobacter baylyl ADP1	WSadp1						X
	Mus musculus	mWS						
	Homo sapiens	hWS						
	Fragaria x *ananassa*	SAAT						
	Malus x *domestica*	MpAAT						
	Simmondsia chinensis	JjWS (AAD38041)						
Decarbonylase	*Arabidopsis thaliana*	cer1						
	Oryzasativa	cer1						
Transport protein	*Acinetobacter* sp. HO1-N	unknown					X	X
	Arabidopsis thaliana	Cer5						

Example 16

Use of Additional Acyl-CoA Synthases to Over Produce Acyl-CoA

Homologs to *E. coli* fadD can be expressed in *E. coli* by synthesizing codon-optimized genes based on a desired sequence from *M. tuberculosis* HR7Rv (NP_217021, FadDD35), *B. subtilis* (NP_388908, YhfL), *Saccharomyces cerevisiae* (NP_012257, Faa3p) or *P. aeruginosa* PAO1 (NP_251989). The synthetic genes can be designed to include NcoI- and HindII-compatible overhangs. The acyl-CoA synthases can then be cloned into a NcoI/HindIII digested pTrcHis2 vector (Invitrogen Corp., Carlsbad, Calif.) as described above and expressed in *E. coli* strain MG1655 ΔfadE. The expression in *E. coli* may lead to an increased production of acyl-CoA.

Fatty acid derivatives such as an FAEE can also be produced by co-transformation of the *E. coli* strain MG1655 ΔfadE with various acyl-CoA synthases in the pTrcHis2 vector with a compatible plasmid derived from pCL1920, which contains the thioester gene from *Cuphea hookeriana* with or without an ester synthase from *A. baylyi*. The resulting production host will produce FAEE when cultured in a medium containing ethanol as described above.

Example 17

Use of Additional Acyl-CoA Synthases to Overproduce Acyl-CoA

DNA sequences or protein sequences of many *E. coli* FadD homologs are known. However the biochemical properties of only a few have been described. See, e.g., Knoll et al., J. Biol. Chem. 269(23):16348-56, 1994; Shockey et al., Plant Physiol. 132: 1065-1076, 2003. Furthermore, their capacity to be expressed in an active form at sufficiently high levels for commercial purposes is unknown. To explore the possibility of using heterologous acyl-CoA synthases for esters production, several acyl-CoA synthase genes were cloned and expressed as follows. Although this example describes transforming the production host with separate plasmids for the thioesterase, ester synthase, and acyl-CoA synthase genes, these genes may alternatively be incorporated in a single plasmid to transform the production host.

1. Construction of pOP-80 Plasmid

To over-express the genes, a low-copy plasmid based on the commercial vector pCL1920 (Lerner and Inouye, NAR 18: 4631, 1990) carrying a strong transcriptional promoter was constructed by digesting pCL1920 with restriction enzymes AflII and SfoI (New England BioLabs Inc. Ipswich, Mass.). Three DNA sequence fragments were produced by this digestion. The 3737 by fragment was gel-purified using a gel-purification kit (Qiagen, Inc. Valencia, Calif.). In parallel, a fragment containing the trc-promoter and lacI region from the commercial plasmid pTrcHis2 (Invitrogen, Carlsbad, Calif.) was amplified by PCR using primers LF302: 5'-ATATGACGTCGGCATCCGCTTACAGACA-3' (SEQ ID NO:41); and LF303: 5'-AATTCTTAAGTCAGGAGAGCGTTCACCGACAA-3' (SEQ ID NO:42). These two primers also introduced recognition sites for the restriction enzymes ZraI (gacgtc) and AflII (cttaag), respectively, at the end of the PCR products. After amplification, the PCR products were purified using a PCR-purification kit (Qiagen, Inc. Valencia, Calif.) and digested with ZraI and AflII following the conditions recommended by the manufacturer (New England BioLabs Inc., Ipswich, Mass.). After digestion, the PCR product was gel-purified and ligated with the 3737 by DNA sequence fragment derived from pCL1920.

After transformation with the ligation mixture in TOP10 chemically competent cells (Invitrogen, Carlsbad, Calif.), transformants were selected on Luria agar plates containing 100 μg/mL spectinomycin. Many colonies were visible after overnight incubation at 37° C. Plasmids present in these colonies were purified, analyzed with restriction enzymes, and then sequenced. One plasmid produced in this way was retained, named pOP-80, and used for further experiments. A map of pOP-80 is shown in FIG. **16**.

The DNA sequences of relevant regions of plasmid pOP-80 were verified. It was found in the junctions where the 2 fragments were ligated that 3 to 4 bases at each end were missing. This was probably caused by an exonuclease activity contaminating one of the restriction enzymes. It was likely that these small deletions did not affect any relevant plasmid function. The resulting plasmid was used for all expression experiments described in this example. The full sequence of the plasmid is disclosed as SEQ ID NO:1 in FIG. **17**.

2. Cloning of fadD35 from *Mycobacterium tuberculosis* HR7Rv

An *E. coli* codon-optimized gene was synthesized by DNA 2.0 Inc. (Menlo Park, Calif.), using the protein sequence of the fadD35 gene deposited at NCBI with the GenBank Accession No. NP_217021 as a starting point. The synthetic gene contained a unique NcoI site at the 5'-end and a unique EcoRI site at the 3'-end. The synthetic gene was provided by DNA 2.0 Inc. cloned in plasmid pJ201:16084. The fad35 gene was released from this plasmid by digesting with NcoI and EcoRI. The sequence of this fragment is shown in SEQ ID NO:2 in FIG. **18**. The resulting DNA sequence fragment is disclosed in SEQ ID NO:2 was ligated with pOP-80, which was previously digested with NcoI and EcoRI. The ligation mixture was transformed into TOP10 chemically competent cells (Invitrogen, Carlsbad, Calif.), which were then plated on Luria agar plates containing 100 μg/mL spectinomycin and incubated at 37° C. overnight. Colonies that appeared the next day were screened, and a strain containing the correct plasmid was identified. The plasmid was named pDS9.

3. Cloning of FadD1 from *Pseudomonas aeruginosa* PAO1

An *E. coli* codon-optimized gene was synthesized by DNA 2.0 Inc. (Menlo Park, Calif.) using the protein sequence of the fadD1 gene deposited at NCBI with the GenBank Accession No. NP_251989 as a starting point. The synthetic gene contained a unique BspHI site at the 5'-end and a unique EcoRI site at the 3'-end. The synthetic gene was provided by DNA 2.0, Inc. and cloned in plasmid pJ201:16083. The fadD1 gene was released from this plasmid by digesting with BspHI and EcoRI. The sequence of this fragment is shown in SEQ ID NO:3 in FIG. **19**. The resulting DNA sequence fragment of SEQ ID NO:3 was ligated with pOP-80, which was previously digested with NcoI and EcoRI. The ligation mixture was transformed into TOP10 chemically competent cells (Invitrogen, Carlsbad, Calif.), which were then plated on Luria agar plates containing 100 μg/mL spectinomycin and incubated at 37° C. overnight. Colonies that appeared the next day were screened. A strain containing the correct plasmid was identified. The plasmid was named pDS8.

4. Cloning of YhfL from *Bacillus subtilis*

The yhfL gene was amplified by PCR using *Bacillus subtilis* 1168 chromosomal DNA sequence as a template, and two primers designed based on the DNA sequence deposited at NCBI with GenBank Accession No. NC_000964. The sequences of the 2 primers were:

```
BsyhfLBspHIF:
5'-CATCATGAATCTTGTTTC-3'          (SEQ ID NO: 4)
(FIG. 20)

BsyhfLEcoR:
5'-CGGAATTCTTATTGGGGCAAAATATC-3'  (SEQ ID NO: 5)
(FIG. 21)
```

These two primers introduced a BspIII recognition site at the 5'-end and an EcoRI recognition site at the 3'-end. The PCR product was cloned directly into pCR-Blunt II-TOPO vector using the Zero Blunt TOPO PCR cloning kit (Invitrogen, Carlsbad, Calif.). A plasmid carrying the yhfL gene was named pDS1. To subclone yhfL, plasmid pDS1 was digested with BspHI and EcoRI. The resulting DNA sequence fragment SEQ ID NO:6 (FIG. **22**) was gel-purified and cloned into pOP-80, which was previously digested with NcoI and EcoRI. The plasmid carrying the *B. subtilis* yhfL gene cloned into pOP-80 was named pDS4.

5. Cloning of Faa3p from *Saccharomyces cerevisiae* (NP_012257)

The faa3p gene was amplified by PCR using commercial *Saccharomyces cerevisiae* chromosomal DNA sequence ATCC 204508D (American Type Culture Collection, Manassas, Va.) as a template, and two primers that were designed based on the DNA sequence deposited at NCBI with the GenBank Accession No. NC_001141 as a template. The sequences of the two primers were:

```
Scfaa3pPciF:
5'-CGACATGTCCGAACAACAC-3'          (SEQ ID NO: 7)
(FIG. 23)

Scfaa3pPciI:
5'-GCAAGCTTCTAAGAATTTTCTTTG-3'     (SEQ ID NO: 8)
(FIG. 24)
```

These two primers introduced a PciI recognition site at the 5'-end and a HindIII recognition site at the 3'-end.

The PCR product was cloned directly into pCR-Blunt II-TOPO vector using the Zero Blunt TOPO PCR cloning kit (Invitrogen, Carlsbad, Calif.). A plasmid carrying the faa3p gene was named pDS2. To subclone faa3p, plasmid pDS2 was digested with PciI and HindIII. The DNA sequence fragment (SEQ ID NO:9) (FIG. **25**) was gel-purified and cloned into pOP-80, which was previously digested with NcoI and HindIII. The plasmid carrying the *S. cerevisiae* faa3p gene cloned into pOP-80 was named pDS5.

6. Cloning of ZP_01644857 from *Stenotrophomonas maltophilia* R551-3

The structural gene sequence for the protein ZP_01644857 is available at NCBI as part of the locus NZ_AAVZ01000044. The gene was amplified by PCR using *Stenotrophomonas maltophilia* R551-3 chromosomal DNA sequence as template, and two primers designed based on the deposited DNA sequence. The sequences of the two primers were:

```
Smprk59BspF:
5'-AGTCATGAGTCTGGATCG-3'           (SEQ ID NO: 10)
(FIG. 26)

Smprk59HindR:
5'-GGAAGCTTACGGGGCGGGCG-3'         (SEQ ID NO: 11)
(FIG. 27)
```

These two primers introduced a BspHI recognition site at the 5'-end and a HindIII recognition site at the 3'-end.

The PCR product was cloned directly into pCR-Blunt II-TOPO vector using the Zero Blunt TOPO PCR cloning kit (Invitrogen, Carlsbad, Calif.). A plasmid carrying the gene encoding the protein ZP_01644857 was named pDS3. To facilitate further subcloning of the gene, an internal BspHI site was removed by site directed mutagenesis using the primer PrkBsp:5'-GCGAACGGCCTGGTCTTTAT-GAAGTTCGGTGG-3'(SEQ ID NO:12) (FIG. **28**) and the QuikChange Multi Site-Directed mutagenesis kit (Stratagene, La Jolla, Calif.). After the proper mutation was corroborated by DNA sequencing, the resulting plasmid was digested with BspHI and HindIII, and was named pDS6. The DNA sequence fragment was gel-purified and cloned into pOP-80 previously digested with NcoI and HindIII. The plasmid carrying the gene encoding the protein ZP_01644857 cloned into pOP-80 was named pDS7. The protein sequence of ZP_01644857 is disclosed in FIG. **29** (SEQ ID NO:13).

7. Construction of Strains to Produce Fatty Esters.

An *E. coli* BL21(DE3) strain was first transformed with plasmid pETDuet-1-'TesA (described in EXAMPLE 2) carrying the *E. coli* 'tesA gene, and plasmid pHZ1.97 (described in EXAMPLE 9) carrying the atfA2 ester synthetase gene, respectively. Both genes were under the control of a T7 promoter inducible by IPTG. Two independent transformants carrying both plasmids were transformed with each of the recombinant plasmids carrying the heterologous fadD genes, and selected on Luria agar plates containing 100 μg/mL carbenicillin, 50 μg/mL kanamycin, and 100 μg/mL spectinomycin. Three independent colonies carrying the three plasmids were evaluated for fatty-ester production.

8. Analysis of Fatty Esters Produced Using ZP_01644857 from *Stenotrophomonas maltophilia* R551-3

To evaluate the use of the protein ZP_01644857 from *Stenotrophomonas maltophilia* R551-3 in a production host to produce fatty esters, an *E. coli* BL21(DE3) strain was transformed with plasmid pETDuet-1-'TesA (described in EXAMPLE 2) carrying the *E. coli* 'tesA gene, plasmid pHZ1.97 (described in EXAMPLE 9) carrying the atfA2 ester synthetase gene, and plasmid pDS7 carrying the gene encoding the protein ZP_01644857 (described above in the instant example). This production host was fermented to produce fatty esters as described in EXAMPLE 4. As a control, a second *E. coli* strain BL21(DE3)ΔfadE containing plasmids pETDuet-1-'TesA, pHZ1.97, and pCL1920 was used as a production host to produce fatty esters.

Table 18 below indicates the fatty ester yields from these production hosts.

TABLE 18

Fatty ester yields from a production host that produced ZP_01644857

	Ester type:								
	$C_2C_{12:1}$ mg/L	$C_2C_{12:0}$ mg/L	$C_2C_{14:1}$ mg/L	$C_2C_{14:0}$ mg/L	$C_2C_{16:1}$ mg/L	$C_2C_{16:0}$ mg/L	$C_2C_{18:1}$ mg/L	$C_2C_{18:0}$ mg/L	Total mg/L[c]
Control[a]	0.0	0.0	0.0	1.78	9.80	5.65	33.7	0.00	50.93
fadD ZP_01644857[b]	1.49	3.57	3.68	33.22	52.77	43.09	91.11	10.08	239.01

[a]Control: strain BL21(DE3) D fadE, containing plasmids pETDuet-1-'TesA, pHZ1.97 and pCL1920.
[b]Strain BL21(DE3) D fadE, containing plasmids pETDuet-1-'TesA, pHZ1.97 and pDS7.
[c]These values represent the average of 3 cultures.

Example 18

Down-Regulation of Beta-Oxidation

This example describes the creation of an *E. coli* strain MG1655 ΔfadE ΔydiO.

Fatty acid degradation can be eliminated or attenuated by attenuating any of the β-oxidation enzymatic reactions described herein (see, FIG. **2**). For example, the *E. coli* strain MG1655 ΔfadE can be further engineered using primers to amplify up-stream of ydiO and additional primers to amplify downstream of ydiO. Overlap PCR can then be used to create a construct for in-frame deletion of the complete ydiO gene. The ydiO deletion construct is then cloned into a temperature sensitive plasmid pKOV3, which contains a sacB gene for counter-selection. A chromosomal deletion of ydiO is then made according to the method of Link et al., J. Bact. 179: 6228-6237, 1997. The resulting strain will not be capable of degrading fatty acids and fatty acyl-CoAs. Additional methods of generating a double knockout of fadE and ydiO are described, for example, in Campbell et al., Mol. Microbiol. 47:793-805, 2003.

It is also possible to avoid fatty acid degradation by selecting or employing a production host that does not contain the β-oxidation pathway. For example, several species of *Streptococcus* have been sequenced and no β-oxidation genes have been found.

Example 19

Identification of Additional Ester Synthases

This example provides additional ester synthases and methods of using such synthases for the production of fatty esters.

Using bioinformatics, additional ester synthases were identified. These ester synthases contain motifs that differ from other known motifs, such as the motifs found in ADP1. The differences in the motifs are noted in Table 19, below.

TABLE 19

Comparison of ester synthases motifs

ADP1-motifs	HHAXVDGV	NDVVLA	GALRXYL	PLXAMVP	ISNVPGP	REPLYXNGA
Hypothetical protein BCG_3544c [*Mycobacterium bovis* BCG str. Pasteur 1173P2] gi/121639399	HHSLIDGY	NDVALA	GGLRRFL	SLIVVLP	VSNVPGP	EDVLYLRGS
Protein of unknown function UPF0089 [*Mycobacterium gilvum* PYR-GCK] gi/145221651	HHALVDGY	NDVALA	GGLRKFL	SLIAFLP	VSNVPGP	REPLYFNGS
Protein of unknown function UPF0089 [*Mycobacterium vanbaalenii* PYR-1] gi/120406715	HHALVDGY	NDVALA	GGLRKFL	SLIAFLP	VSNVPGP	REPLYFNGS

The identified sequences can be cloned using standard molecular biology techniques. These sequences can be expressed using the vectors described herein and used to make various fatty esters. The motifs can also be used to identify other ester synthases.

Example 20

Product Characterization

To characterize and quantify the fatty alcohols and fatty esters, gas chromatography (GC) coupled with electron impact mass spectra (MS) detection was used. Fatty alcohol samples were first derivatized with an excess of N-trimethylsilyl (TMS) imidazole to increase detection sensitivity. Fatty esters did not require derivatization. Fatty alcohol-TMS derivatives and fatty esters were dissolved in an appropriate volatile solvent, such as, for example, ethyl acetate.

The samples were analyzed on a 30 m DP-5 capillary column using the following method. After a 1 μl splitless injection onto the GC/MS column, the oven was held at 100° C. for 3 minutes. The temperature was incrementally raised to 320° C. at a rate of 20° C./minute. The oven was held at 320° C. for an additional 5 minutes. The flow rate of the carrier gas helium was 1.3 mL/minute. The MS quadrapole scanned from 50 to 550 m/z. Retention times and fragmentation patterns of product peaks were compared with authentic references to confirm peak identity.

For example, hexadeconic acid ethyl ester eluted at 10.18 minutes (FIGS. **15**A-B). The parent ion of 284 mass units was readily observed. More abundant were the daughter ions produced during mass fragmentation. The most prevalent daughter ion was of 80 mass units. The derivatized fatty alcohol hexadecanol-TMS eluted at 10.29 minutes and the parent ion of 313 were observed. The most prevalent ion was the M-14 ion of 299 mass units.

Quantification was carried out by injecting various concentrations of the appropriate authentic references using the GC/MS method as described herein. This information was used to generate a standard curve with response (total integrated ion count) versus concentration.

Example 21

Identification and Reclassification of a Microorganism Bellowing to the Genus *Jeotgalicoccus* that is an α-Olefin Producer

Micrococcus candicans ATCC 8456 was previously reported to synthesize aliphatic hydrocarbons with carbon chain lengths ranging from C_{18} to C_{20} (Morrison et al., J. Bacteriol. 108:353-358, 1971). To identify the hydrocarbons produced by this strain, ATCC 8456 cells were cultured in 15 mL TSBYE medium (3% Tryptic Soy Broth+0.5% Yeast Extract), for 40-48 hours at 30° C. Cells from 5 mL of culture were pelleted, resuspended in 1 mL methanol, sonicated for 30 minutes, and extracted with 4 mL hexane. After solvent evaporation, samples were resuspended in 0.1 mL hexane and analyzed by GC-MS. The hydrocarbons were identified to be the following α-olefins: 15-methyl-1-heptadecene (a-C_{18}), 16-methyl-1-heptadecene (i-C_{18}), 1-nonadecene (n-C_{19}), 17-methyl-1-nonadecene (a-C_{20}) and 18-methyl-1-nonadecene (i-C_{20}) (see FIG. **34** (i=iso, a=anteiso, n=straight chain) and FIG. **36**).

Based upon the following analyses, it was determined that ATCC 8456 was previously misidentified as belonging to the genus *Micrococci*. The phylogenetic classification of ATCC 8456 was reassessed by amplifying and sequencing the partial 16s rRNA gene using primers Eubac27 and 1492R (see DeLong et al., PNAS 89:5685, 1992). The 16s rRNA sequence of ATCC8456 was analyzed using the classifier program of the Ribosomal Database Project II (http://rdp.cme.msu.edu/index.jsp). Based upon this analysis, the strain was identified as belonging to the genus *Jeotgalicoccus*. The genus *Jeotgalicoccus* has been previously described (Jung-Hoon et al., Int. J. Syst. Evol. Microbiol. 53:595-602, 2003).

Additional analysis using the G+C content of ATCC 8456 was conducted. *Jeotgalicoccus* is a low G+C Gram-positive bacteria related to the genus *Staphylococcus* (see FIG. **37**). *Micrococci*, on the other hand, are high G+C Gram-positive bacteria. The ends of several clones from a cosmid library of ATCC 8456 genomic DNA were sequenced. Based upon a DNA sequence of about 4,000 bp, the G+C content was determined to be about 36%. Nucleotide sequence searches against a non-redundant protein database revealed that all sequences with a match to a database entry were similar to proteins from low G+C Gram-positive bacteria, such as species belonging to the genus *Staphylococcus* or *Bacillus*, but not species belonging to the genus *Micrococcus*.

Next, an analysis of the entire genome of ATCC 8456 was conducted. Based on a DNA sequence of about 2.1 MB, the G+C content of the entire genome was determined to be about 36.7%. In contrast, bacteria of the genus *Micrococcus* are known to have high G+C genomes, e.g., the genome of *Micrococcus luteus* NCTC 2665 has a G+C content of 72.9% (GenBank Accession No. ABLQ01000001-68). Based upon the G+C content analysis, it was determined that the ATCC 8456 microorganism does not belong to the genus *Micrococcus*.

Additional *Jeotgalicoccus* strains were also examined to determine if they produced α-olefins. The following strains of *Jeotgalicoccus* were examined: *Jeotgalicoccus halotolerans* DSMZ 17274, *Jeotgalicoccus psychrophiles* DSMZ 19085, and *Jeotgalicoccus pinnipedalis* DSMZ 17030. Each strain was cultured in 15 mL TSBYE medium (3% Tryptic Soy Broth+0.5% Yeast Extract) and the hydrocarbons were isolated and analyzed by GC-MS as described above. All three strains produced α-olefins similar to the ones produced by ATCC 8456 (FIGS. **34**B, **34**C and **34**D depict GC-MS traces for hydrocarbons produced by *Jeotgalicoccus halotolerans* DSMZ 17274 cells, *Jeotgalicoccus pinnipedalis* DSMZ 17030 cells, and *Jeotgalicoccus psychrophiles* DSMZ 19085 cells, respectively). These data indicate that the ability to produce α-olefins is widespread among the genus *Jeotgalicoccus*.

Example 22

Production of Increased Levels of Olefins and α-Olefins Not Normally Produced by ATCC 8456 Cells Using Fatty Acide Feeding

The fatty acids eicosanoic acid (straight-chain C_{20} fatty acid), 16-methyl octadecanoic acid and 17-methyl octadecanoic acid (branched-chain C_{19} fatty acids) were identified as components of ATCC 8456's lipids. These fatty acids were deduced to be the direct precursors, after decarboxylation, for 1-nonadecene, 15-methyl-1-heptadecene and 16-methyl-1-heptadecene biosynthesis, respectively. In order to improve α-olefin production and to produce olefins not normally produced by ATCC 8456 cells, fatty acid feeding experiments were carried out as described below.

ATCC 8456 cells were cultured in 15 mL of a TSBYE medium (containing 3% Tryptic Soy Broth+0.5% Yeast Extract). Fatty acids were added to the culture medium at a final concentration of 0.5 g/L (0.05%). After growth for 40-48 hrs at 30° C., cells from 5 mL of culture were pelleted, resuspended in 1 mL methanol, sonicated for 30 minutes and extracted with 4 mL hexane. After solvent evaporation, samples were resuspended in 0.1 mL hexane and analyzed by GC-MS.

When cultures were fed eicosanoic acid, an increase in 1-nonadecene production of about 18-fold was observed (see FIG. **38**A; black traces depict without and gray traces depict with fatty acid feeding). When cultures were fed stearic acid or palmitic acid, an increase in the production of the α-olefins 1-pentadecene and 1-heptadecene, respectively, was observed (see FIG. **38**B). These olefins are not normally produced by ATCC 8456 cells. This indicated that fatty acids were the direct precursors for α-olefins and that *Jeotgalicoccus* bacteria can be used to enzymatically convert fatty acids into α-olefins in vivo.

Alternatively, resting *Jeotgalicoccus* cells can be fed with various fatty acids to achieve similar results.

Example 23

In Vitro Synthesis of α-Olefins Using Cell Extracts and Partially Purified Proteins

A cell free extract of ATCC 8456 was used to convert free fatty acids into α-olefins. The cell free extract was generated using the following procedure: ATCC 8456 cells were cultured in a TSBYE medium (containing 3% Tryptic Soy Broth+0.5% Yeast Extract) at 30° C. for 24 hrs with shaking. The cells were then pelleted from the culture by centrifugation at 3,700 rpm for 20 minutes. The cell pellet was then resuspended in 50 mM Tris buffer pH 7.5 with 0.1 M NaCl and 2.0 mM dithiothreitol to a concentration of 0.1 g/mL cells. To this cell slurry, 200 units/mL of lysostaphin (Sigma) was added on ice. The cell lysis reaction continued for 30 minutes. The cells were then sonicated at 12 W on ice for three cycles of 1.5 seconds of sonication followed by 1.5 seconds of rest. Sonication lasted for a total of 9 seconds. This procedure was repeated 5 times with a 1-minute interval between sonication cycles. The lysed cells were then subjected to centrifugation at 12,000 rpm for 10 minutes to pellet the cell debris. The supernatant (cell free extract) was removed and used for the conversion of free fatty acids to α-olefins.

After obtaining the cell free extract, the free fatty acids stearic acid and eicosanoic acid were converted to α-olefins using the cell free extract as described below. First, a 5% stock solution of sodium or potassium stearate was made in 1% Tergitol solution (Sigma, St. Louis, Mo.). Next, 6 μl of the stock solution was added to 1 mL of the cell free extract at room temperature to obtain a final concentration of 1 mM free fatty acid salt. The reaction was conducted at room temperature for 3 hrs. The α-olefins were recovered by adding 200 μl of ethyl acetate to the mixture, vortexing briefly, centrifuging briefly, and then removing the organic phase. The α-olefins were identified and/or detected by GC/MS.

FIG. **39** shows the GC/MS trace for the resulting products. In sample 1, no stearic acid was added to the cell free extract. In sample 2, the cell free extract was replaced with 50 mM Tris pH 7.5 buffer with 0.1 M sodium chloride to which stearic acid was added. In sample, stearic acid was added to the cell free extract. The peak at 7.62 minute had the same retention time and the same mass spectra as 1-heptadecene (Sigma). When eicosanoic acid was added under similar conditions, 1-nonadecene was formed.

Boiling the cell free extract eliminated the production of α-olefins upon the addition of free fatty acids. This data strongly suggested that the ATCC 8456 catalyst was protein based.

The ATCC 8456 cell free extract did not require additional co-factors to produce α-olefins. When the cell free extract was supplemented with several co-factors in 1 mM concentrations, no increase in α-olefin synthesis was observed. The co-factors examined were NAD+, NADP+, NADH, NADPH, $FADH_2$, SAM, ATP, and CoA. In addition, Mg^{2+} was examined, but at a 10 mM concentration. The co-factor requirement was also tested by dialyzing the cell free extract with a 10 kDa cut-off membrane for 1.5 hrs in a volume that was 200-fold greater than the cell extract volume using a dialysis buffer: 50 mM Tris, pH 7.5 with 0.1 M sodium chloride. No decrease in α-olefin synthesis was observed after dialysis. Additionally, no decrease in α-olefin synthesis was observed when 10 mM EDTA pH 7.5 was added to the reaction mixture.

The ATCC 8456 cell free extract was further enriched by carrying out an ammonium sulfate precipitation. First, enough ammonium sulfate was added to the cell free extract to bring the concentration of ammonium sulfate to 50% (wt/vol) saturation. The mixture was stirred gently on ice for 60 minutes and then centrifuged at 13,000 rpm for 30 minutes. The supernatant was recovered and additional ammonium sulfate was added to bring the ammonium sulfate concentration to 65% (wt/vol). The mixture was allowed to mix on ice for 60 minutes and was centrifuged again for 30 minutes. The supernatant was discarded. The pellet was then resuspended in 50 mM Tris buffer pH 7.5 with 0.1 M sodium chloride. This mixture was then dialyzed in the aforementioned buffer to remove the ammonium sulfate. The cell free extract treated with ammonium sulfate had the same α-olefin synthesizing activity as the cell free extract.

Example 24

Purification and Identification of a Protein that Converts Fatty Acids into α-Olefins

To isolate the protein necessary for α-olefin production from ATCC 8456 cells, the following protein purification procedure was carried out. First, 6 L of ATCC 8456 cells were cultured in a TSBYE medium at 30° C. for 24 hours with shaking. The cells were pelleted by centrifugation at 3,700 rpm for 20 minutes at 4° C., and the supernatant was discarded. The cell pellet was resuspended in a solution of 100 mL of 50 mM Tris pH 8.0, 0.1 M NaCl, 2.0 mM DTT, and bacterial protease inhibitors. The cell slurry was then passed through a French press one time at a pressure of 30,000 psi. Next, the cell slurry was sonicated as described in Example 3 to shear the DNA. The cell free extract was centrifuged at 10,000 rpm for 60 minutes at 4° C. The supernatant was then removed and ammonium sulfate was added to a final concentration of 50% (wt/vol). The mixture was gently stirred at 4° C. for 60 minutes and then centrifuged at 10,000 rpm for 30 minutes. The supernatant was then removed and additional ammonium sulfate was added to 65% (wt/vol) saturation. The mixture was stirred again for 60 minutes at 4° C. and centrifuged at 10,000 rpm for 30 min. The supernatant was discarded. The remaining pellet was resuspended in 50 mL of 50 mM Tris pH 8.0 and 2.0 mM DTT.

The mixture was passed through a 5 mL HiTrap SP column (GE Healthcare) at 3 mL/min and 4° C. The following buffers were used as an elution gradient: buffer A contained 50 mM Tris pH 8.0 and 2.0 mM DTT; buffer B contained 50 mM Tris pH 8.0, 1.0 M NaCl, and 2.0 mM DTT. After the column was loaded with the mixture, the column was washed with 40% buffer B. Next a 20-minute gradient of 40% buffer B to 100% buffer B at 3.0 mL/min was carried out. 5 mL fractions were collected during the elution gradient. Each fraction was tested for activity as described in Example 3. Fractions containing α-olefin production activity typically eluted between 600 and

750 mM NaCl concentration. Fractions containing activity were then pooled and dialyzed into buffer A.

The dialyzed protein fraction was then loaded onto a 1 mL ResourceQ (GE Healthcare) column at 4 mL/min at 4° C. Buffer B used with the HiTrap SP column was also used for the ResourceQ column. A 7-minute elution gradient between 0% buffer B and 25% buffer B was run at 4 mL/min. 1.5 mL fractions were collected and assayed for activity. Active fractions eluted between 150 and 200 mM NaCl concentrations. Fractions containing activity were then pooled and concentrated with a Millipore Amicon protein concentrator (4 mL and 10 kDa exclusion size) to about 50 μL. The approximate protein concentration was determined with a Bradford assay (Bio-Rad). Final protein concentrations ranged from about 5 mg/mL to about 10 mg/mL. 30 μL of protein was then loaded onto a SDS PAGE gel (Invitrogen) along with an appropriate protein molecular weight marker. The gel was stained with Simple Safe Coomassie stain (Invitrogen). FIG. **40** depicts a representative gel. Two intense protein bands at 50 kDa and 20 kDa were observed.

To determine the identity of the protein bands, the bands were excised from the gel, digested with trypsin, and analyzed using LC/MS/MS. The LC/MS/MS data was analyzed using the program Mascot (Mann et al., Anal. Chem. 66:4390-4399, 1994). The ATCC 8456 genome was sequenced. The genomic data was used to interpret the LC/MS/MS data and to determine the identity of the protein bands. The 50 kDa band had a strong match with ORF880. The Mascot score assigned to this match was 919, a high score. Furthermore, ORF880 has a predicted molecular weight of 48,367 Da. The nucleotide and amino acid sequences of orf880 are presented in FIGS. **41**A and **41**B, respectively.

Example 25

Heterologous Expression of *Jeotgalicoccus* ATCC 8456 ORF880 in *E. coli*

Jeotgalicoccus ATCC 8456 Orf880 was identified as one of the two major proteins in a highly purified enzyme fraction that catalyzed the conversion of free fatty acids to α-olefins. The genomic DNA encoding ATCC 8456_orf880 was cloned into pCDF-Duet1 under the control of the T7 promoter, and *E. coli* was transformed with various vectors, as described below. The *E. coli* cells were cultured and the hydrocarbons produced by the cells were analyzed as described in Example 23. When 0.05% stearic acid was fed to cultures of *E. coli* transformed with the 8456_orf880-containing vector, the expression of 8456_orf880 led to the formation of 1-heptadecene in *E. coli* (see FIG. **42**, which depicts GC/MS traces of α-olefins from *E. coli* either without (black) or with (gray) 8456_orf880 expression). In contrast, adding 0.05% stearic acid to cultures of *E. coli* transformed with a vector control (not containing ATCC_orf880) did not result in the production of 1-heptadecene. This demonstrated that 8456_orf1080 synthesized α-olefins from free fatty acids in an *E. coli* heterologous host. This result indicates that α-olefin biosynthesis can be performed in heterologous organisms. Additionally, when *E. coli* cells expressing 8456_orf880 protein were fed with 0.05% palmitic acid or 0.05% eicosanoic acid, the production of 1-pentadecene or 1-nonadecene, respectively, was observed.

Example 26

In Vitro Synthesis of α-Olefins Using ORF880 Heterologously Expressed in and Purified from *E. coli*

The genomic DNA encoding ATCC8456_orf880 was cloned into the NdeI and XhoI sites of vector pET15b (Novagen) under the control of a T7 promoter for expression in and purification from *E. coli*. This plasmid expressed an N-terminal His-tagged version of 8456_orf880.

An *E. coli* BL21 strain (DE3) (Invitrogen) was transformed with pET15b-ORF 880 using routine chemical transformation techniques. Protein expression was carried out by first inoculating a colony of the *E. coli* strain in 5 mL of LB media supplemented with 100 mg/L carbenecillin and shaken overnight at 37° C. to produce a starter culture. This starter culture was used to inoculate 1 L of an LB medium supplemented with 100 mg/L carbenecillin. The culture was shaken at 37° C. until it reached an OD_{600} value of 0.6. The culture was placed on ice for 10 minutes before IPTG was added to a final concentration of 250 μM. The culture was then shaken at 18° C. for about 18 hours. The culture was then centrifuged at 3,700 rpm for 20 minutes at 4° C. The pellet was resuspended in 30 mL of buffer containing 100 mM sodium phosphate buffer at pH 7.2, supplemented with Bacterial ProteaseArrest (GBiosciences). The cells were sonicated at 12 W on ice for 9 seconds with 1.5 seconds of sonication followed by 1.5 seconds of rest. This procedure was repeated 5 times with 1 minute intervals between each sonication cycle. The cell free extract was centrifuged at 10,000 rpm for 30 minutes at 4° C. 5 mL of Ni-NTA (Qiagen) was added to the supernatant and the mixture was gently stirred at 4° C. The slurry was passed through a column to remove the resin from the lysate. The resin was then washed with 30 mL of buffer containing 100 mM sodium phosphate buffer at pH 7.2, and 30 mM imidazole. Finally, the protein was eluted with 15 mL of 100 mM sodium phosphate buffer at pH 7.2 plus 250 mM imidazole. The protein solution was dialyzed with 200 volumes of 100 mM sodium phosphate buffer at pH 7.2. Protein concentration was determined using the Bradford assay (Bio-Rad). 125 μg/mL of protein was obtained.

To assay the in vitro fatty acid substrate specificity of ORF880, potassium salts of the following fatty acids were prepared: tetradecanoic acid, hexadecanoic acid, octadecanoic acid, eicosanoic acid, and behenic acid (Sigma). The fatty acid solutions were made with 2% ethanol and 2% Tergitol solution (Sigma, St. Louis, Mo.) to a final concentration of 20 mM.

The kinetics of the decarboxylation reaction and production was determined. A 200 μl reaction mixture was prepared containing the following reactants: 1.25 μM of ORF880, 200 μM of potassium octadecanoate, 200 μl dithiothreitol, and 100 mM sodium phosphate buffer at pH 7.2. The reaction mixture was incubated at room temperature and time points were taken in duplicate between 5 minute and 120 minute. The reaction was quenched and extracted by adding 100 μl of ethyl acetate containing 1-octadecene at 5 mg/L as an internal reference. Samples were analyzed using GC/MS using the alkane 1 splitless method, using the following parameters: run time: 20 min; column: HP-5-MS Part No. 190915-433E (length of 30 meters; I.D.: 0.25 mm narrowbore; film: 0.25 μM); sample: standard ethyl acetate extraction; inject: 1 μl Agilent 6850 inlet; inlet: 300° C. splitless; carrier gas: helium; flow: 1.3 mL/min; oven temp: 100° C. hold 5 min, 320 at 20° C./min, 320 hold 5 min; det: Agilent 5975B VL MSD; det. temp: 300° C.; scan: 50-500 M/Z. Calibration

curves were generated using 1-heptadecene dissolved in ethyl acetate. Based upon this analysis, the product production was determined to be linear from 5 minute to 60 minute.

To assay the reaction rates of different fatty acid substrates, the following 200 μl reaction mixtures were prepared: 1.0 μM ORF 880 enzyme, 200 μM of a test fatty acid salt, 200 μL dithiothreitol, and 100 mM sodium phosphate buffer at pH 7.2. The reactions were carried out at room temperature and time points were taken in triplicates at 20 minute and 47 minute using the extraction and analysis procedures as described above. Reference curves were generated using available chemical standards. In some instances, the chemical standards were not available. Under those circumstances, for example, cis-9-heneicosene was used as a reference for 1-heneicosene, and 9-tricosene was used as a reference for 1-tricosene. Activities were calculated by taking the difference between the average α-olefin concentrations for each substrate at 47 minute and 20 minute and then dividing the difference by 27 minute. The results are summarized in Table 20.

TABLE 20

Activity of ORF880 with different fatty acid substrates

Substrate	Activity (nM alkene produced/min)
tetradecanoic acid	22.9
hexadecanoic acid	181.9
octadecanoic acid	77.2
eicosanoic acid	19.7
behenic acid	30.6

These results demonstrate that heterologously expressed ORF880 was able to convert fatty acid substrates to olefins in vitro. These data also show that ORF880 had greater activity when hexadecanoic acid was the fatty acid substrate.

Example 27

Production of α-Olefins from Glucose by Heterologous Expression of Jeotgalicoccus ATCC 8456 ORF880 in *E. coli* MG1655 ΔFadD

1. Construction of FadD Deletion Strain

The fadD gene of *E. coli* MG1655 was deleted using the lambda red system (Datsenko et al., Proc. Natl. Acad. Sci. USA. 97: 6640-6645, 2000) as follows:

The chloramphenicol acetyltransferase gene from pKD3 was amplified using the primers

```
fad1:
                                                (SEQ ID NO: 43)
5'-TAACCGGCGTCTGACGACTGACTTAACGCTCAGGCTTTATTGTCCAC

TTTGTGTAGGCTGGAGCTGCTTCG-3';
and

fad2:
                                                (SEQ ID NO: 44)
5'-CATTTGGGGTTGCGATGACGACGAACACGCATTTTAGAGGTGAAGAA

TTGCATATGAATATCCTCCTTTAGTTCC-3'.
```

This PCR product was electroporated into *E. coli* MG1655 (pKD46). The cells were plated on L-chloramphenicol (30 μg/mL) (L-Cm) and cultured overnight at 37° C. Individual colonies were selected and plated onto another L-Cm plate and cultured at 42° C. These colonies were then patched to L-Cm and L-carbenicillin (100 mg/mL) (L-Cb) plates and cultured at 37° C. overnight. Colonies that were Cm^R and Cb^S were evaluated further by PCR to ensure the PCR product inserted at the correct site. PCR verification was performed on colony lysates of these bacteria using primers fadF: 5'-CGTCCGTGGTAATCATTTGG-3' (SEQ ID NO:45); and fadR: 5'-TCGCAACCTTTTCGTTGG-3' (SEQ ID NO:46). Expected size of the ΔfadD::Cm deletion was about 1200 by (FIG. **10**). The chloramphenicol resistance gene was eliminated using a FLP helper plasmid as described in Datsenko et al. Proc. Natl. Acad. Sci. USA. 97: 6640-6645, 2000. PCR verification of the deletion was performed with primers fadF and fadR. The MG1655 ΔfadD strain was unable to grow on M9+oleate agar plates (oleate as carbon source). It was also unable to grow in M9+oleate liquid media.

2. Expression of *Jeotgalicoccus* ATCC 8456 orf880 in *E. coli* MG1655 ΔfadD

The genomic DNA encoding ATCC 8456_orf880, which was codon-optimized for expression in *E. coli*, was cloned into vector OP80 (pCL1920 derivative) under the control of a P_{trc} promoter, and *E. coli* MG1655 ΔfadD was transformed with the resulting vector. The *E. coli* cells were cultured at 37° C. in an M9 mineral medium supplemented with 20 μg/mL uracil and 100 μg/mL spectinomycin. Glucose (1%, w/v) was the only source of carbon and energy. When the culture reached an OD_{600} of 0.8 to 1.0, IPTG (1 mM) was added and the temperature was shifted to 25° C. After growth for an additional 18 to 24 hours at 25° C., cells from 10 mL of culture were pelleted, resuspended in 1 mL methanol, sonicated for 30 minutes, and extracted with 4 mL hexane. After solvent evaporation, samples were resuspended in 0.1 mL hexane and analyzed by GC-MS. In contrast to the vector-only control, *E. coli* cells transformed with the orf880-bearing vector produced the α-olefins 1-pentadecene and heptadecadiene. This result indicates that expression of ORF880 confers the ability to biosynthesize α-olefins to *E. coli* when cultured on glucose, and that the direct precursors are the most abundant fatty acids in *E. coli*, namely hexadecanoic acid and vaccenic acid (11-cis-octadecenoic acid).

Example 28

Identification of Carboxylic Acid Reductase (CAR) Homologs

The carboxylic acid reductase (CAR) from *Nocardia* sp. strain NRRL 5646 can reduce carboxylic acids into corresponding aldehydes without separate activating enzymes, such as acyl-CoA synthases (Li et al., J. Bacteriol. 179:3482-3487, 1997; He et al., Appl. Environ. Microbiol. 70:1874-1881, 2004)). A BLAST search using the NRRL 5646 CAR amino acid sequence (Genpept Accession No. AAR91681) as the query sequence identified about 20 homologous sequences. Three homologs, listed in Table 21, were evaluated for their ability to convert fatty acids into fatty aldehydes in vivo when expressed in *E. coli*. At the nucleotide sequence level, carA, carB, and fadD9 (demonstrated 62.6%, 49.4%, and 60.5% homology, respectively, to the car gene (AY495697) of *Nocardia* sp. NRRL 5646. At the amino acid level, CARA, CARB, and FadD9 demonstrated 62.4%, 59.1% and 60.7% identity, respectively, to CAR of *Nocardia* sp. NRRL 5646.

TABLE 21

CAR-like Protein and the corresponding coding sequences.

Genpept Accession	Locus_tag	Annotation in GenBank	Gene name
NP_217106	Rv 2590	Probable fatty-acid-CoA ligase (FadD9)	fadD9
ABK75684	MSMEG 2956	NAD dependent epimerase/dehydratase family protein	carA
YP_889972.1	MSMEG 5739	NAD dependent epimerase/dehydratase family protein	carB

Example 29

Expression of CAR Homologs in *E. coli*

1. Plasmid Construction

Three *E. coli* expression plasmids were constructed to express the genes encoding the CAR homologs listed in Table 22, below. First, fadD9 was amplified from genomic DNA of *Mycobacterium tuberculosis* H37Rv (obtained from The University of British Columbia, and Vancouver, BC Canada) using the primers fadD9F and FadDR (see Table 22). The PCR product was first cloned into PCR-blunt (Invitrogen) and then released as an NdeI-AvrII fragment. The NdeI-AvrII fragment was then cloned between the NdeI and AvrII sites of pACYCDuet-1 (Novogen) to generate pACYCDuet-1-fadD9.

The carA and carB genes were amplified from the genomic DNA of *Mycobacterium smegmatis* MC2 155 (obtained from the ATCC (ATCC 23037D-5)) using primers CARMCaF and CARMCaR or CARMCbF and CARMCbR, respectively (see, Table 22). Each PCR product was first cloned into PCR-blunt and then released as an NdeI-AvrII fragment. Each of the two fragments was then subcloned between the NdeI and AvrII sites of pACYCDuet-1 (Novogen) to generate pACYCDUET-carA and pACYCDUET-carB.

TABLE 22

Primers used to amplify genes encoding CAR homologs

fadD9F	CAT ATGTCGATCAACGATCAGCGACTGAC (SEQ ID NO: 47)
fadD9R	CCTAGG TCACAGCAGCCCGAGCAGTC (SEQ ID NO: 48)
CARMCaF	CAT ATGACGATCGAAACGCG (SEQ ID NO: 49)
CARMCaR	CCTAGG TTACAGCAATCCGAGCATCT (SEQ ID NO: 50)
CARMCbF	CAT ATGACCAGCGATGTTCAC (SEQ ID NO: 51)
CARMCbR	CCTAGG TCAGATCAGACCGAACTCACG (SEQ ID NO:52)

2. Evaluation of Fatty Aldehyde Production

Plasmids encoding the CAR homologs (pACYCDUET-fadD9, pACYCDUET-carA, and pACYCDUET-carB) were separately co-transformed into the *E. coli* strain C41 (DE3, ΔfadE) (described in PCT/US08/058788) together with pET-Duet-1-'TesA (described in PCT/US08/058788, the disclosures of which is incorporated by reference herein).

The *E. coli* transformants were cultured in 3 mL of an LB medium supplemented with carbenicillin (100 mg/L) and chloramphenicol (34 mg/L) at 37° C. After overnight growth, 15 μl of culture was transferred into 2 mL of a fresh LB medium supplemented with carbenicillin and chloramphenicol. After 3.5 hours of growth, 2 mL of culture were transferred into a 125 mL flask containing 20 mL of an M9 medium with 2% glucose and with carbenicillin and chloramphenicol. When the OD_{600} of the culture reached 0.9, 1 mM of IPTG was added to each flask. After 20 hours of growth at 37° C., 20 mL of ethyl acetate (with 1% of acetic acid, v/v) was added to each flask to extract the organic compounds produced during the fermentation. The crude ethyl acetate extract was directly analyzed with GC/MS as described below. The co-expression of the leaderless 'TesA and any of the three car genes in *E. coli* resulted in detectable fatty aldehyde production. In one fermentation, LS9001/pACYC-DUET carB+pETDuet-1-'TesA produced an average of 120 mg/L of fatty aldehydes. The retention times were 6.959 minutes for dodecanal, 8.247 minutes for 7-tetradecenal, 8.37 minutes for tetradecanal, 9.433 minutes for 9-hexadecenal, 9.545 minutes for hexadecanal, and 10.945 minutes for 11-octadecenal. The presence of large amounts of fatty aldehydes is consistent with CAR being an aldehyde-generating, fatty acid reductase (AFAR). This mechanism is different from the alcohol-generating fatty acyl-CoA reductases (FAR), for example, JjFAR, and fatty acyl-CoA reductases, such as Acr1.

3. Substrate Preferences of the CAR Homologs

Distinct substrate preferences were observed among the three CAR homologs evaluated. FadD9 exhibited a strong preference for C_{12} fatty acids relative to other fatty acids with carbon chain lengths greater than 12. Both CarA and CarB demonstrated wider substrate ranges than FadD9.

4. Quantification and Identification of Fatty Aldehydes

A GC-MS experiment was performed using an Agilent 5975B MSD system equipped with a 30 m×0.25 mm (0.10 μm film) DB-5 column. The column temperature was 3-minute isothermal at 100° C. The column was programmed to rise from 100° C. to 320° C. at a rate of 20° C./min. When the final temperature was reached, the column remained isothermal for 5 minutes at 320° C. The injection volume was 1 μL. The carrier gas, helium, was released at 1.3 mL/min. The mass spectrometer was equipped with an electron impact ionization source. The ionization source temperature was set at 300° C.

Prior to quantification, various aldehydes were identified using two methods. First, the GC retention time of each compound was compared to the retention time of a known standard, such as laurylaldehyde (dodecanal). Second, identification of each compound was confirmed by matching the compound's mass spectrum to a standard's mass spectrum in the mass spectra library.

Example 30

Production of Fatty Alcohol by Heterologous Expression of Car Homologs in *E. coli* MG1655 (DE3, ΔFadD)

1. Construction of FadD Deletion Strain

The fadD gene of *E. coli* MG1655 was deleted using the lambda red system (Datsenko et al., PNAS (USA). 97: 6640-6645, 2000) as follows: The chloramphenicol acetyltransferase gene from pKD3 was amplified with primers fad1: 5'-TAACCGGCGTCTGACGACTGACT-TAACGCTCAGGCTTTATTGTC-

CACTTTGTGTAGGCTG GAGCTGCTTCG-3'(SEQ ID NO:43); and fad2: 5'-CATTTGGGGTTGCGATGACGAC-GAACACGCATTTTAGAGGTGAAGAATTG-CATATGAAT ATCCTCCTTTAGTTCC-3'(SEQ ID NO:44). This PCR product was electroporated into *E. coli* MG1655 (pKD46). The cells were plated on L-chloramphenicol (30 μg/mL) (L-Cm) and cultured overnight at 37° C. Individual colonies were selected and plated onto another L-Cm plate and cultured at 42° C. These colonies were then patched to L-Cm and L-carbenicillin (100 mg/mL) (L-Cb) plates and cultured at 37° C. overnight. Colonies that were Cm^R and Cb^S were evaluated further by PCR to ensure the PCR product inserted at the correct site. PCR verification was performed on colony lysates of these bacteria using primers fadF: 5'-CGTCCGTGGTAATCATTTGG-3'(SEQ ID NO:45); and fadR: 5'-TCGCAACCTTTTCGTTGG-3'(SEQ ID NO:46). Expected size of the ΔfadD::Cm deletion was about 1200 bp. The chloramphenicol resistance gene was eliminated using a FLP helper plasmid as described in Datsenko et al., Proc. Natl. Acad. Sci. USA, 97:6640-6645, 2000. PCR verification of the deletion was performed using primers fadF and fadR. The MG1655 ΔfadD strain was unable to grow on M9+oleate agar plates (using oleate as carbon source). It was also unable to grow in M9+oleate liquid media. The growth defect was complemented by an *E. coli* fadD gene supplied in trans (in pCL1920-Ptrc).

2. Construction of MG1655(DE3, ΔfadD) Strain

To generate a T7-responsive strain, the λDE3 Lysogenization Kit (Novagen) was utilized, which is designed for site-specific integration of λDE3 prophage into an *E. coli* host chromosome, such that the lysogenized host can be used to express target genes cloned in T7 expression vectors. λDE3 is a recombinant phage carrying the cloned gene for T7 RNA polymerase under lacUV5 control. Briefly, the host strain was cultured in an LB medium supplemented with 0.2% maltose, 10 mM $MgSO_4$, and antibiotics at 37° C., to an OD_{600} of 0.5. Next, 10^8 pfu λDE3, 10^8 pfu Helper Phage, and 10^8 pfu Selection Phage were incubated with 10 μl host cells. The host/phage mixture was incubated at 37° C. for 20 minutes to allow the phage to be adsorbed into the host. Finally, the mixture was pipetted onto an LB plate supplemented with antibiotics. The mixture was spread evenly using plating beads, and the plates were inverted plates and incubated at 37° C. overnight.

λDE3 lysogen candidates were evaluated for their ability to support the growth of the T7 Tester Phage. T7 Tester Phage is a T7 phage deletion mutant that is completely defective unless active T7 RNA polymerase is provided by the host cell. The T7 Tester Phage makes very large plaques on authentic λDE3 lysogens in the presence of IPTG, while much smaller plaques are observed in the absence of inducer. The relative size of the plaques in the absence of IPTG is an indication of the basal level expression of T7 RNA polymerase in the lysogen, and can vary widely between different host cell backgrounds.

The following procedure was used to determine the presence of DE3 lysogeny. First, candidate colonies were cultured in LB media supplemented with 0.2% maltose, 10 mM $MgSO_4$, and antibiotics at 37° C., to an OD_{600} of 0.5. An aliquot of T7 Tester Phage was then diluted in 1× Phage Dilution Buffer to a titer of 2×10^3 pfu/mL. In duplicate tubes, 100 μl host cells were mixed with 100 μL diluted phage. The host/phage mixture was incubated at room temperature for 10 minutes to allow the phage to be adsorb into the host. Next, 3 mL of molten top agarose was added to each tube containing host and phage. The contents of one duplicate were plated onto an LB plate and the other duplicate onto an LB plate supplemented with 0.4 mM IPTG (isopropyl-b-thiogalactopyranoside) to evaluate induction of T7 RNA polymerase. Plates were allowed to sit undisturbed for 5 minutes until the top agarose hardened. The plates were then inverted at 30° C. overnight.

3. Construction of MG1655(DE3, ΔfadD, yjgB::kan) Strain

The yjgB knockout strain, MG1655(DE3, ΔfadD, yjgB::kan), was constructed using the following the protocol of the lambda red system (Datsenko et al., Proc. Natl. Acad. Sci. USA 97:6640-6645, 2000):

The kanamycin resistant gene from pKD13 was amplified with primers yjgBRn: 5'-GCGCCTCAGATCAGCGCTGC-GAATGATTTTCAAAAATCGGCTTTCAA-CACTGTAGGCTG GAGCTGCTTCG-3'SEQ ID NO:53); and yjgBFn: 5'-CTGCCATGCTCTACACTTCCCAAA-CAACACCAGAGAAGGACCAAAAAATGAT-TCCGGGG ATCCGTCGACC-3'(SEQ ID NO:54). The PCR product was then electroporated into *E. coli* MG1655 (DE3, ΔfadD)/pKD46. The cells were plated on kanamycin (50 μg/mL) (L-Kan) and cultured overnight at 37° C. Individual colonies were selected and plated onto another L-Kan plate and cultured at 42° C. These colonies were then patched to L-Kan and carbenicillin (100 mg/mL) (L-Cb) plates and cultured at 37° C. overnight. Colonies that were kan^R and Cb^S were evaluated further by PCR to ensure the PCR product was inserted at the correct site. PCR verification was performed on colony lysates of these bacteria using primers BF: 5'-GT-GCTGGCGATACGACAAAACA-3'(SEQ ID NO:55); and BR: 5'-CCCCGCCCTGCCATGCTCTACAC-3'(SEQ ID NO:56). The expected size of the yjgB::kan knockout was about 1450 bp.

4. Evaluation of FadD on Fatty Alcohol Production Using MG1655 (DE3, ΔfadD) Strain

In Example 2, a fadE deletion strain was used for fatty aldehyde and fatty alcohol production from 'TesA, CAR homologs, and endogenous alcohol dehydrogenase(s) in *E. coli*. To demonstrate that CAR homologs used fatty acids instead of acyl-CoA as a substrate, the gene encoding for acyl-CoA synthase in *E. coli* (fadD) was deleted so that the fatty acids produced were not activated with CoA. *E. coli* strain MG1655 (DE3, ΔfadD) was transformed with pET-Duet-1-'TesA and pACYCDuet-1-carB. The transformants were evaluated for fatty alcohol production using the methods described herein. These transformants produced about 360 mg/L of fatty alcohols (dodecanol, dodecenol, tetredecanol, tetredecenol, cetyl, hexadecenol, and octadecenol).

YjgB is an alcohol dehydrogenase. To confirm that YjgB was an alcohol dehydrogenase responsible for converting fatty aldehydes into their corresponding fatty alcohols, pET-Duet-1-'TesA and pACYCDuet-1-fadD9 were co-transformed into either MG1655(DE3, ΔfadD) or MG1655(DE3, ΔfadD, yjgB::kan). At the same time, MG1655(DE3, ΔfadD, yjgB::kan) was transformed with both pETDuet-1-'tesA-yjgB and pACYCDuet-1-fadD9.

The *E. coli* transformants were cultured in 3 mL of an LB medium supplemented with carbenicillin (100 mg/L) and chloramphenicol (34 mg/L) at 37° C. After overnight growth, 15 μL of culture was transferred into 2 mL of a fresh LB medium supplemented with carbenicillin and chloramphenicol. After 3.5 hrs of growth, 2 mL of culture was transferred into a 125 mL flask containing 20 mL of an M9 medium containing 2% glucose, carbenicillin, and chloramphenicol. When the OD_{600} of the culture reached 0.9, 1 mM of IPTG was added to each flask. After 20 hours of growth at 37° C., 20 mL of ethyl acetate (with 1% of acetic acid, v/v) was added to each flask to extract the fatty alcohols produced during the

fermentation. The crude ethyl acetate extract was directly analyzed using GC/MS as described herein.

The yjgB knockout strain resulted in significant accumulation of dodecanal and a lower fatty alcohol titer. The expression of yjgB from plasmid pETDuet-1-'tesA-yjgB in the yjgB knockout strain effectively removed the accumulation of dodecanal. The data indicated that YjgB was involved in converting dodecanal into dodecanol and that there may be other alcohol dehydrogenase(s) present in *E. coli* to convert other aldehydes into alcohols. Dodecanal accumulated in the yjgB knockout strain, but it was not observed in either the wild-type strain (MG1655(DE3, ΔfadD)) or the yjgB knockout strain with the yjgB expression plasmid.

Example 31

Generation of 'TesA Library

In this Example, methods are described for preparing a mutant library of 'TesA. A suitable expression vector such as pACYC-'TesA that encodes 'TesA, the truncated TesA lacking a signal peptide, enables production of the 'TesA protein in the host strain. The plasmid pACYC-'TesA includes the 'tesA sequence under the regulation of a trc promoter, a transcription terminator, a p15a origin of replication, an open reading frame encoding laclq, and the beta-lactamase antibiotic resistance gene.

The 'TesA protein amino acid sequence is provided in FIG. **57** (SEQ ID NO:31).

The QuikChange Mutagenesis kit (Stratagene) enables the facile construction of large numbers of mutants. Use of this kit to construct each 'TesA mutant starts with two complementary primers containing one or more mismatched bases required to change the encoded amino acid at the desired position. The primers are 25-45 nucleotides in length, with melting temperature ≥78° C. as calculated using the formula:

$$T_m = 81.5 + 0.41(\%\ GC) 675/N$$

where T_m is the melting temperature, % GC is the percent of residues in the primer that are guanosine or cytidine, and N is the number of nucleotides in the primer. For example, the primers:

(SEQ ID NO: 57)
CACGTTATTGATTCTGGGTAATAGCCTGAGCGCCGGGTATCG
and

(SEQ ID NO: 58)
CGATACCCGGCGCTCAGGCTATTACCCAGAATCAATAACGTG

were used to mutate the aspartic acid at residue 9 to asparagine, where the underlined bases indicate the codon that was changed.

The primers were used in a polymerase chain reaction with pACYC-'TesA as a template, using the following temperature cycling program: 1 minute at 95° C.; followed by 18 cycles of 50 seconds at 95° C., 50 seconds at 60° C., and 5 minutes at 68° C.; and 7 minutes at 68° C. The reaction products were then digested using the restriction enzyme DpnI, to selectively degrade the methylated template DNA. The remaining DNA was then transformed into *E. coli* for isolation of plasmid clones, which were then sequenced to verify that the desired substitutions have been obtained.

Example 32

Assays

In the following Examples, assays for determining protein content, free fatty acid levels, and hydrolysis of acyl-PNP and acyl-CoA substrates are described. Specific assays used herein are also set forth below.

1. Assay for Determination of Protein Content in Cell Lysates

Cell lysates of *E. coli* expression cultures producing 'TesA variants were prepared for characterization. To generate the expression cultures, seed cultures were grown overnight at 37° C. in an LB medium containing 1% (w/v) glucose and 100 μg/mL carbenicillin. The seed cultures were then diluted 1:100 into the same medium and grown for 3 hours at 37° C. with shaking (200 rpm). A 40 μL aliquot of each culture was then added to 360 μL of LS9-1 medium (described below) supplemented with 100 μg/mL carbenicillin and grown in a 96-well culture plate. After 3 additional hours of growth, isopropyl β-D-1-thiogalactopyranoside (IPTG, at 1 mM final concentration) and Bis-Tris Propane (pH 7.0, at 0.1 M final concentration) were added, and the cultures were allowed to grow overnight.

Cell pellets were harvested by centrifugation of the expression cultures (10 minutes at 3,500 rpm). The growth medium is discarded and the cell pellets stored at −80° C. To prepare soluble extracts, the frozen cell pellets are lysed in 50% BugBuster (EMD Biosciences, Cat. No. 70584-4) in 25 mM sodium phosphate, pH 7.0. Following 40 minutes of agitation, the cell lysates are clarified by centrifugation (10 minutes at 3,500 rpm). The concentration of protein in the supernatant of the cell lysate is then measured using the bicinchoninic acid (BCA) assay, according to the protocol provided by manufacturer (Thermo Scientific, Cat. No. 23225). The supernatant is then used in the assays described below.

Medium:

5x Salt Solution		1X final concentration
Na_2HPO_4	30 g	6 g/L
KH_2PO_4	15 g	3 g/L
NaCl	2.5 g	0.5 g/L
NH_4Cl	5 g	1 g/L
dH_2O	to 1 L	

stock solutions:	final concentration:
10 mg/mL Thiamine (Vitamin B1)	1 mg/L
1M $MgSO_4$	1 mM
1M $CaCl_2$	0.1 mM
20% glucose	2.00%
sterile water	20 mg/mL
uracil	20 μg/mL high pH
trace minerals 1000x	1x

For 1 L LS9-1 media with 1.0% glucose:

200 mL 5x Salt Solution
100 μL Thiamine (B1)
1 ml $MgSO_4$
100 μL $CaCl_2$
50 mL 20% Glucose
1 mL trace minerals
1 mL Uracil
Water to 1 L (premake it 750 mL)
TM solution (filter sterilized):

27 g/L $FeCl_3$—$6H_2O$
2 g/L $ZnCl_2$—$4H_2O$
2 g/L $CaCl_2$—$6H_2O$
2 g/L Na_2MoO_4—$2H_2O$
1.9 g/L $CuSO_4$—$5H_2O$
0.5 g/L H_3BO_3
100 mL/L concentrated HCl
q.s. w/ Milli-Q water

2. Free Fatty Acid Analysis

'TesA variants are produced in *E. coli* expression cultures, and the free fatty acids produced by the cultures were analyzed. To generate the expression cultures, seed cultures were first grown overnight at 37° C. in an LB medium containing 1% (w/v) glucose and 100 μg/mL carbenicillin, and then diluted 1:100 into the same medium and grown for 3 hours at 37° C. with shaking (200 rpm). 40 μL of each culture was then added to 360 μL of LS9-1 medium supplemented with 100 μg/mL carbenicillin, and grown in a 96-well culture plate. After 3 additional hours of growth, isopropyl β-D-1-thiogalactopyranoside (IPTG, at 1 mM final concentration) and Bis-Tris Propane (pH 7.0, at 0.1 M final concentration) were added, and the cultures were allowed to grow overnight.

The cultures were then acidified with 1 N HCl to a final pH of about 2.5 and then extracted with 600 μL ethyl acetate. Free fatty acids in the organic phase were derivatized with tetramethylammonium hydroxide (TMAH) to generate the respective methyl esters, which were then analyzed on a gas chromatograph equipped with a flame ionization detector.

3. Fatty Acyl-PNP Hydrolysis Assay

In this assay system, the reagent solutions used were:

1. 2% Triton X-100 in 50 mM sodium phosphate, pH 7.0

2. 10 mM acyl-para-nitrophenol (acyl-PNP) in acetone

To prepare an acyl-PNP working solution, 600 μL acyl-PNP stock was added to 9.4 mL phosphate buffer and mixed well.

The assay was performed by adding 40 μL of the acyl-PNP working solution to each well of a 96-well plate, followed by the rapid addition of 40 μL of clarified cell lysate. The solutions were mixed for 15 seconds, and the absorbance change was read at 405 nm in a microtiter plate reader at 25° C. The esterase activity was expressed as the ratio of $(\Delta A405/sec)_{mut}/(\Delta A405/sec)_{wt}$, wherein $(\Delta A405/sec)_{mut}$ was the change in absorbance at 405 nm per second in samples containing mutant 'TesA, and $(\Delta A405/sec)_{wt}$ was the change in absorbance at 405 nm per second in samples containing wildtype 'TesA.

4. Acyl-CoA Hydrolysis Assay

In this assay system, the reagent solutions used were:
10 mM acyl-coenzyme A (acyl-CoA) in 50 mM sodium phosphate, pH 7.0
50 mM sodium phosphate, pH 8.0, 50 mM monobromobimane (MBB) (Novagen, Cat. No. 596105) in acetonitrile. To prepare acyl-CoA working solution, 0.5 mL acyl-CoA stock and 0.5 mL MBB stock were added to 29 mL phosphate buffer followed by mixing.

The assay was performed by adding 60 μL of the acyl-CoA working solution to each well of a black 96-well plate, followed by the rapid addition of 40 μL of clarified cell lysate. After mixing for 15 seconds, the progress of the reaction was monitored by fluorescence (λ_{ex}=380 nm, λ_{em}=480 nm) in a microtiter plate reader at 25° C. The acyl-CoA thioesterase activity was expressed as the ratio of $(\Delta RFU/sec)_{mut}/(\Delta RFU/sec)_{wt}$, where $(\Delta RFU/sec)_{mut}$ was the change in relative fluorescence units per second in samples containing mutant 'TesA, and $(\Delta RFU/sec)_{wt}$ was the change in relative fluorescence units per second in samples containing wildtype 'TesA.

5. Applying the Z Score Methodology

A Z-score determination was conducted following the Z score methodology as follows.

The Z score for a sample is defined as the number of standard deviations the sample signal differs from the control population signal mean. The Z score has been used to rank the mutants according to properties of interest such as, for example, substrate chain length specificity, relative preference for ester over thioester bonds, relative preference for thioester bonds over ester bonds, and the proportion or percentage of ester produced. The Z score is measured using the following calculation:

$$Z = (\text{sample value} - \text{control average})/\text{Standard deviation of controls}$$

The positive control used to generate the mutant 'TseA library herein was wild type 'TesA.

In a normal distribution, about 2.1% of the data will comprise 2 or more standard deviations above the mean, and about 0.1% of the data will comprise 3 or more standard deviations above the mean. Therefore Z scores of 2 or greater, 3 or greater, −2 or less, −3 or less and so forth are used to define more and more stringent classes of data that are unlikely to occur by random chance.

Those variants that have a Z score greater than 3 were marked as having an improved performance in terms of preference for substrates of certain chain lengths and/or catalytic rate. Also, those variants that have a Z score greater than 3 were marked, under other circumstances, as providing an improved or enhanced proportional or percentage yield for fatty esters vs. free fatty acids. Additionally, those variants that have a Z score of −3 or less were marked, in yet other circumstances, as providing a reduced proportional or percentage yield for fatty esters vs. free fatty acids.

Substrate specificity numbers are defined as the kinetic slope of a given mutant for one substrate, divided by the total of the kinetic slopes for the three substrates studied in the PNP assay (C_{10}, C_{12}, C_{14}), where the kinetic slope is the observed initial rate for the hydrolysis of a given ester substrate.

For example, to calculate a substrate specificity number for C_{10}:

$$C_{10}\ \text{SubsSpec} = \text{Mutant Slope } C_{10}/(\text{Mutant Slope } C_{10} + C_{12} + C_{14})$$

Next a substrate specificity Z score was calculated. The Average and Standard Deviations of the substrate specificity numbers for the positive controls were first calculated (for each plate), and the following formula was applied:

$$\text{Mutant } C_{10}\ \text{SubSpec } Z\ \text{score} = (\text{Mutant SubSpec } C_{10} - \text{AvgSubSpec})/\text{SDSubSpec}$$

As another example, to calculate an ester specificity number:

$$\text{EsterSpec} = \text{Mutant Slope } C_{14}\text{-}PNP/\text{Mutant Slope } C_{14}\text{-CoA}$$

Next an ester specificity Z score was calculated. The Average and Standard Deviations of the ester specificity numbers for the positive controls were first calculated (for each plate), and the following formula was applied:

$$\text{Mutant Ester Specificity } Z\ \text{score} = (\text{Mutant EsterSpec} - \text{AvgEsterSpec})/\text{SDEsterSpec}$$

Those variants which have an Ester Specificity Z score greater than 3 were defined and marked as having a preference for ester over thioester, and/or as having improved activity (i.e., catalytic rate) with regard to ester over thioester. Those variants which have an Ester Specificity Z score less than −3 were marked as having a preference for thioester over ester.

Example 33

Free Fatty Acid Analysis of 'TesA Variants

In this Example, assay results identifying various properties of 'TesA variants are provided. The analysis was conducted using the methods described above in Example 32. In the tables of FIGS. **45** and **46**, the mutations are presented

using "Variant Codes," each of which provides the wildtype amino acid, followed by the position in the amino acid sequence, followed by the replacement amino acid (e.g., "S10A" indicates that the serine at position 10 in the amino acid sequence has been replaced by alanine in this particular variant). All amino acid position numbering in FIGS. **45** and **46** is according to the alignment of SEQ ID NO: 73 shown in FIG. **47**. All amino acid position numbering is according to SEQ ID NO: 73.

Example 34

Anaysis of 'TesA Variants

Assay results for 'TesA variants are provided in FIGS. **45** and **46**. The analysis was conducted using the methods described above in Example 32. As shown in FIG. **45**, activity levels on C_{10}, C_{12} and C_{14} substrates and substrate specificities were analyzed.

FIG. **45** depicts performance indices of certain 'TesA variants of the mutant 'TesA library, which demonstrated improved performance compared to the wildtype enzyme. FIG. **45**A-B depict performance indices of 'TesA mutants in terms of specificity for substrates of certain chain lengths.

FIG. **46**A depicts 'TesA mutants that provided increased or enhanced proportional or percentage yield of fatty esters vs. free fatty acids. FIG. **46**B depicts 'TesA mutants that provided reduced proportional or percentage yield of fatty esters vs. free fatty acids. Only mutants that had Z scores above 3 are illustrated in the table and other mutants having lesser activity are not included. Notwithstanding the presentation of data, it is submitted that a lower Z score may identify valuable mutants and the Z score cut-off of 3 provided in FIG. **45** is not intended to limit the scope of the invention.

The results are represented graphically along the entire length of the 'TesA molecule in FIGS. **57**A-C.

1. Fatty Acid Production Activity for 'TesA Variants

Assay results for fatty acid production activity in 'TesA variants are conducted using the methods described above in Example 32.

2. Fatty Acyl-PNP Assay of 'TesA Variants

Assay results for fatty acyl-PNP activity of 'TesA variants are provided in FIG. **45**. The analysis was conducted using the methods described above in Example 32.

3. Acyl-CoA Analysis of 'TesA Variants

Assay results for acyl-CoA activity of 'TesA variants are provided in FIG. **45**. The analysis was conducted using the methods described above in Example 32.

4. Preference for Thioester (Acyl-CoA) Over Ester (Acyl-PNP)

Assay results for acyl-CoA activity and acyl-PNP activity of 'TesA variants are conducted using the methods described above in Example 32.

5. Preference for Ester (Acyl-CoA) Over Thioester (Acyl-CoA)

Assay results for acyl-CoA activity and acyl-PNP activity of 'TesA variants are conducted using the methods described above in Example 32.

Example 35

Direct Production of Fatty Esters in the Absence of Ester Synthase

In this example, the ability of 'TesA to catalyze the transesterification of a fatty acyl-CoA into the corresponding fatty ester in the presence of an alcohol in vitro is demonstrated. *E. coli* 'TesA enzyme was recombinantly expressed and purified to homogeneity as an N-terminal 6× His-tagged protein. In particular, the 'TesA gene encoding thioesterase I enzyme from *E. coli* (SEQ ID NO:31 of FIG. **57**) was inserted into a pET 15-b vector (Novagen), which vector carried an N-terminal 6× His-tag, and transformed into BL21-DE3 cells for expression. Cells were cultured in LB media at 37° C., 200 rpm, until OD_{600} reached 1.0, induced with 0.5 mM IPTG (final), and then allowed to grow at 28° C. for an additional 5 hours. After harvesting at 6,000 rpm, the pellet was resuspended in 40 mL of 100 mM Tris-HCl, pH 7.4, sonicated and centrifuged at 10,000 rpm for 20 minutes. Clarified lysate was then applied to a His-bind column (Calbiochem) and the protein was purified as per the manufacturer's instruction. Eluted protein was then dialyzed into a buffer containing 25 mM sodium phosphate, pH 7.2, and 10% glycerol for storage and use. Thioesterase activity of the purified 'TesA enzyme was determined.

Catalysis of fatty acyl-CoA to fatty ester by 'TesA involves a nucleophilic attack by an alcohol on the carbonyl center subsequent to the exit of the coenzyme A moiety from the active site. The rate of spontaneous transesterification of palmitic acid by ethanol in the absence of 'TesA was analyzed to prove that ethanol can replace water as the nucleophile to form fatty esters instead of fatty acids.

Accordingly, a 4 mM (about 1 mg/mL) aliquot of palmitic acid (C_{16}—COOH) (Sigma) was incubated with varying amounts of ethanol for different time periods at room temperature. Samples were extracted with a 1:1 volumetric ratio of ethyl acetate and the extract was analyzed using GC-MS for the presence of ethyl palmitate. The results are compiled in Table 23 below, which indicated that spontaneous transesterification between ethanol and palmitic acid occurs at a conversion rate of less than 0.01 mole/mole of palmitic acid.

TABLE 23

% Ethanol (v/v)	C_2C_{16} formed*, mg/L	% conversion (g/g)	% conversion (mole/mole)
0	0	0	0
20	0.34	0.034	0.030
30	0.25	0.025	0.022
40	0.25	0.025	0.022
50	0.35	0.035	0.031

*Average of two data points.

The rate of in vitro transesterification catalyzed by 'TesA on palmitoyl-CoA substrate was analyzed. Reactions were carried out at room temperature for 1 hour in a buffer containing 100 μM of palmitoyl-CoA, 100 μM of Phosphate buffer pH 7.0 and 1 mM BSA, either in the presence or absence of 1.5 μM of purified 'TesA. Ethanol concentrations varied between 0-60% (v/v). 1:1 volumetric ratio of ethyl acetate was used for quenching and subsequent extraction. Formation of ethyl palmitate was monitored using GC-MS. Table 24 summarizes the results.

TABLE 24

Ethanol	Ethyl palmitate (mg/L)		Ethyl palmitate formed	% conversion	% conversion
% v/v	−'TesA	+'TesA	(mg/L)	(g/g of C16-CoA)	(mole/mole)
0	0	0	0	0	0
5	0	0	0	0	0

TABLE 24-continued

Ethanol	Ethyl palmitate (mg/L)		Ethyl palmitate formed	% conversion	% conversion
% v/v	−'TesA	+'TesA	(mg/L)	(g/g of C16-CoA)	(mole/mole)
10	0	4.12	4.12	4.12	14.57
20	0	6.64	6.64	6.64	23.49
40	0	1.88	1.88	1.88	6.65
60	0	1.74	1.74	1.74	6.15

The results indicate that 'TesA thioesterases efficiently catalyzes the transesterification of an acyl-CoA, palmitoyl-CoA, into ethyl palmitate in presence of ethanol. Maximum yield obtained was 23.5 mole/mole of palmitoyl-CoA. Given that yields for spontaneous conversion of palmitic acid to palmitic ester are extremely low compared to those in presence of 'TesA (i.e., indicating a >1,000-fold increase) the conversion occurs enzymatically. Based on our data, maximum transesterification yields occurred at 10-20% ethanol (v/v) levels. Higher alcohol concentrations affect enzyme stability and/or activity adversely and therefore result in lower ester yields.

From these results, a conclusion was reached that thioesterase can catalyze the direct esterification of an acyl-CoA substrate in the presence of alcohol. It will be possible to modify the ester product by changing the alcohol (e.g., by using methanol, propanol or butanol) and/or the alcohol concentration.

Example 36

In Vivo Production of Fatty Esters by Thioesterase

In this example, the ability of 'TesA to produce esters in vivo in the absence of heterologously expressed ester synthase was investigated. Ester formation in the absence of a heterologously expressed ester synthase was observed in the *E. coli* strain MG1655 (ΔfadE), which also carries an artificial operon containing 'tesA and fadD under the control of a trc promoter, along with a kanamycin marker gene. The operon was integrated into the chromosome, interrupting the native lacZ gene. This strain was tested in a shake flask fermentation using media comprising 6 g/L Na_2HPO_4, 3 g/L KH_2PO_4, 0.5 g/L NaCl, 1 g/L NH_4Cl, 1 mg/L thiamine, 1 mM $MgSO_4$, 0.1 mM CaCl, supplemented with extra NH_4Cl (an additional 1 g/L), Bis-Tris buffer (0.2 M), Triton X-100 (0.1% v/v), and trace minerals (27 mg/L $FeCl_3$-$6H_2O$, 2 mg/L $ZnCl_2$-$4H_2O$, 2 mg/L $CaCl_2$-$6H_2O$, 2 mg/L Na_2MoO_4-$2H_2O$, 1.9 mg/L $CuSO_4$-$5H_2O$, 0.5 mg/L H_3BO_3, 100 mL/L concentrated HCl).

An LB+antibiotics pre-seed culture was inoculated with a scraping from a glycerol stock or from a single colony. It was cultured for 6 to 8 hours until the OD_{600} reached >1.0. A fermentation medium plus 2% glucose (w/v)+antibiotics overnight seed culture was inoculated with the LB pre-seed culture to 4% (v/v). 15 mL fermentation media+3% glucose (w/v)+antibiotics production cultures were prepared in 125 mL baffled shake flasks. An appropriate amount of the overnight seed culture was used to inoculate the production culture such that the starting OD_{600} in the production culture flask was about 0.5. The flasks were allowed to grow until the OD_{600} therein reached 1.0, at which point the cultures were induced with 1 mM IPTG (final concentration) and fed methanol or ethanol (at 2% v/v). The fermentation runs were allowed to continue for the indicated amount of time post-induction. All culture steps were performed at 32° C. with shaking at 200 rpm.

Whole broth extractions were performed using a standard microextraction procedure. In brief, 500 μl of broth was transferred to a microcentrifuge tube, to which 100 μl of 1M HCl was added. The acidified cultures were extracted with 500 μl of ethyl acetate, vortexed for 5 minutes, and centrifuged at top speed for 1 minute. The organic layer was analyzed using GC-FID for both simultaneous fatty acid methyl ester (FAME) and free fatty acid (FFA) quantification and simultaneous fatty acid ethyl ester (FAEE) and FFA quantification.

In samples containing FAEE and FFA, the FFA were derivatized with Bis(trimethylsilyl)trifluoroacetamide before quantification.

The MG1655 (ΔfadE) pTrc-'TesA_fadD strain, which was cultured and fed 2% methanol at induction, produced 2 g/L total FAMEs by the 24 hour time point and 3.5 g/L total FAMEs by the end of the fermentation at 48 hours (FIG. **48**). Minimal amounts of FFAs were detected, about 100 mg/L in total. The cultures reached their highest density, OD_{600} about 11, after 24 hours and did not continue to grow in the following 24 hours. Specific productivity was calculated to be about 200 mg/L/OD at 24 hours, and about 300 mg/L/OD at 48 hours. These data indicated that, with the overexpression of 'tesA and fadD, even in the absence of a wax synthase, FAME production was observed.

To assess the ability of FadD or 'TesA to independently produce FAME, a second fermentation was carried out testing two different *E. coli* strains carrying plasmids with either fadD, 'tesA, or both fadD and 'tesA. The plasmids were all pACYC-based and expression was driven by a trc promoter. Three different MG1655 (ΔfadE) strains were tested, one with a fadD only plasmid, one with a 'tesA only plasmid, and one with 'tesA and fadD with 'tesA being located upstream of fadD. Two C41 (ΔfadE) were tested, both carrying 'tesA and fadD, but with the genes in different order relative to the promoter. These strains were cultured in the media described above and fed 2% methanol at induction and grown for an additional 25 hours post-induction. The strain expressing only fadD did not produce any FAMEs while the 'tesA strain produced only about 150 mg/L FAMEs (FIG. **49**). Having both 'TesA and fadD improves upon FAME production over 'TesA alone. The two C41 strains produced a further increase in FAME production, as observed in the strain carrying a plasmid in which fadD is upstream of 'tesA, over the strain expressing 'tesA and fadD in the opposite order. This suggested that higher FadD expression enhanced the ability of 'TesA to produce esters. Since 'TesA can cleave both acyl-ACPs and acyl-CoAs, it is likely that the production of acyl-CoAs by FadD is allowing for the FFAs generated by 'TesA to be recycled back to the thioesterase to either be converted back into FFAs by hydrolysis or taken all the way to FAMEs by alcoholysis. Examination of the FFA titers leads to the conclusion that only the strain expressing 'TesA produced significant amounts of FFA, while the strains expressing fadD produced very little FFA (FIG. **50**).

'TesA was tested for its ability to utilize ethanol for the direct formation of fatty acid ethyl ester (FAEE). The two MG1655 (ΔfadE) strains from the experiment described above, the fadD overexpression strain and the 'TesA overexpression strain, were tested. Also included in this experiment was the MG1655 (ΔfadE) with the integrated 'tesAjadD operon under the control of a trc promoter. All strains were cultured using the protocol described above. At induction, all strains were fed 2% (v/v) of methanol or 2% (v/v) of ethanol. In addition, the MG1655 (ΔfadE)+fadD strain was fed 0.05%

(w/v) of C14:0 fatty acid to ensure that sufficient free fatty acid substrate was available to FadD for catalyzing the potential alcoholysis reaction. The fermentations were allowed to continue for 24 hours.

Under these fermentation conditions, FadD alone was again unable to produce the requisite C_1C_{14}:0 FAME or the C_2C_{14}:0 FAEE, indicating that FadD was not sufficient for ester formation (FIG. **51**). However, 'TesA alone was able to produce FAEEs and as before, overexpression of 'tesA and fadD boosts overall production of FAEEs over having 'tesA alone. While overall FAEE titers were lower than FAME titers, this data demonstrate that 'TesA can also use ethanol in addition to methanol for the formation of fatty esters. Analysis of FFA formation under these fermentation conditions indicates that the strains behaved similarly with ethanol feeding as they did with methanol feeding (FIG. **52**).

The FFA present in the fadD samples was contributed almost entirely by the C_{14}:0 FFA fed during fermentation. The strain expressing 'tesA produced a large amount of FFA, while the strain expressing 'tesA and fadD showed very little accumulation of FFA. In the presence of 'TesA, only 14% conversion of FFA to FAME or a 2.3% of FFA to FAEE was observed. In the presence of 'TesA and FadD, nearly a 100% conversion of FFA to either FAME or FAEE was observed. These data suggest that 'TesA is necessary and sufficient for fatty acid alcohol ester formation, but the overexpression of FadD along with 'TesA is important for increased FAME and FAEE formation.

The previous results suggest that *E. coli* 'TesA can produce FAME and FAEE when fed the appropriate alcohols during fermentation. To determine whether this is a function unique to *E. coli* 'TesA, the ability of other heterologously expressed thioesterases to produce FAMEs was investigated. 'TesA homologs from *Photorhabdus luminescens* and *Vibrio harveyi* along with a TesB from *Photobacterium profundum* were overexpressed from pACYC-based plasmids in the strain MG1655 (ΔfadE) and tested alongside the *E. coli* 'TesA overexpression strain from the previous fermentations. Shake flask fermentations were carried out in fermentation media and allowed to continue for 24 hours post-induction. The results indicated that the two 'TesA homologs were also able to generate FAMEs (FIG. **53**). *P. luminescens* 'TesA produced FAME at a level comparable to *E. coli* 'TesA, while the *V. harveyi* 'TesA was able to produce much more FAME than *E. coli* 'TesA. When looking at the FFA titers, the *P. luminescens* 'TesA produced less FFA than *E. coli* 'TesA, but again, the *V. harveyi* 'TesA produced much larger FFA titers when compared to its *E. coli* counterpart (FIG. **54**). Interestingly, the *V. harveyi* 'TesA was highly active and was able to produce higher FAME and FFA titers than the control strain expressing *E. coli* 'TesA; moreover, its FFA to FAME conversion rate was over 30% to *E. coli* 'TesA's 14%. Additionally, despite producing lower total FAME titers, the strain expressing *P. luminescens* 'TesA showed that FAME constituted over 60% of the total FAME+FFA titer.

1. Ester Synthase Activity in Other 'TesA Homologs

The 'TesA homologs from *Escherichia coli, Pectobacterium atrosepticum, Photobacterium profundum, Photorhabdus luminescens, Pseudomonas putida*, and *Vibrio harveyi* were cloned into the expression vector pACYC under the control of a trc promoter. All sequences were cloned as truncated genes lacking a signal peptide sequence, in order to achieve cytoplasmic expression. DNA and amino acid sequences for the homologs are shown in Table 26. An alignment of the amino acid sequences is shown in Table 27.

The plasmids were transformed into *E. coli* MG1655 ΔfadE and cultured overnight at 37° C. on LB agar plates containing 100 μg/mL carbenicillin. Individual colonies were selected and cultured at 37° C. in an LB broth containing 1% (w/v) glucose and 100 μg/mL carbenicillin until OD_{600} reached a value of about 1.0. 200 μL of the culture was then diluted into 1.8 mL of an M9 medium containing 100 μg/mL carbenicillin. After growing the cultures for 3 hours at 37° C., IPTG (1 mM final concentration), as well as Bis-Tris Propane buffer (0.1 M, pH 7.0), and methanol (2% v/v) were added.

After 20 hours of growth at 37° C., 1 mL of culture was extracted by adding 100 μL 1 N HCl and 250 μL ethyl acetate. A C20 free fatty acid internal standard was included in the ethyl acetate solution.

The fatty acids and methyl esters were analyzed on a gas chromatograph Trace GC Ultra (Thermo Electron Corp) equipped with a flame ionization detector. The total amount of fatty acid (FFA) and fatty acyl methyl ester (FAME) produced varied among the homologs studied (see FIG. **59**).

E. coli 'TesA produced about 300 mg/L in total fatty products, while the *Pseudomonas putida* homolog generated nearly 4 times that amount. The proportion of FAME produced was also dependent on which 'TesA homolog was expressed. Whereas only 3% of total product generated by 'TesA from *Pseudomonas putida* was FAME, more than 25% of total product generated by *Vibrio harveyi* 'TesA was FAME. These results indicate that ester formation is catalyzed and influenced by 'TesA, rather than being a purely chemical process that is not affected by the enzyme. It follows that this activity is a function of the amino acid sequence of the enzyme and that it can be engineered to increase or decrease the propensity for ester production.

To determine whether FadD overexpression would increase FAME titers, the plasmids were then transformed into *E. coli* MG1655 ΔfadE carrying the fadD gene on the pCL1920 plasmid, under the control of a trc promoter. The transformed cells were cultured overnight at 37° C. on LB agar plates containing 100 μg/mL carbenicillin and 100 μg/mL spectinomycin. Individual colonies were selected and cultured at 37° C. in LB broth containing 1% (w/v) glucose, 100 μg/mL carbenicillin, and 100 μg/mL spectinomycin until OD_{600} reached a value of about 1.0. 200 μL of the culture was then diluted into 1.8 ml of an M9 medium containing 100 μg/mL carbenicillin and 100 μg/mL spectinomycin. After growing the cultures for 3 hours at 37° C., IPTG (1 mM final concentration), as well as Bis-Tris Propane buffer (0.1 M, pH 7.0) and methanol (2% v/v) were added.

After 20 hours of growth at 37° C., 1 ml of culture was extracted by adding 100 μL 1 N HCl and 250 μL ethyl acetate. A C_{20} free fatty acid internal standard was included in the ethyl acetate solution.

The fatty acids and methyl esters were analyzed on a gas chromatograph Trace GC Ultra (Thermo Electron Corp) equipped with a flame ionization detector. As observed previously with *E. coli* 'TesA, coexpression of FadD increased the proportion of FAME produced for all homologs tested (See FIG. **60**). Therefore, co-expression of an acyl-CoA synthase in conjunction with 'TesA homologs can be used to increase ester production. Interestingly, the total titer of FFA plus FAME produced by 'TesA from *P. putida* was much lower when FadD was co-expressed. This suggests that *P. putida* 'TesA may be more specific for acyl-ACP substrates than acyl-CoAs, and can be co-expressed with an ester synthase or other thioesterase with greater activity against acyl-CoAs to further increase ester production.

2. Enhanced Ester Synthesis by a 'TesA Mutant

As mentioned above, the studies of 'TesA homologs have indicated that ester synthase activity in 'TesA in an engineerable trait; that is, one can make changes in the amino acid

sequence of the enzyme to improve the production of esters. To this end, a mutant of *E. coli* 'TesA was constructed with enhanced ester synthase activity. Replacing Ser10, the nucleophilic serine residue in the active site of 'TesA, with cysteine to generate the S10C mutant yields an improved 'TesA enzyme that produces a higher proportion of FAME.

Plasmids encoding wildtype *E. coli* 'TesA, the S10C mutant, or no 'TesA were transformed into *E. coli* MG1655 ΔfadE and cultured overnight at 37° C. on LB agar plates containing 100 μg/mL carbenicillin. Individual colonies were selected and cultured overnight at 37° C. in an LB broth containing 1% (w/v) glucose and 100 μg/ml carbenicillin. The cultures were then diluted 1:100 in a fresh LB medium supplemented with 1% (w/v) glucose and 100 μg/mL carbenicillin, and cultured at 37° C. until OD_{600} reached a value of about 1.0. 200 μL of the culture was then diluted into 1.8 mL of an M9 medium containing 100 μg/mL carbenicillin. After growing the cultures for 3 hours at 37° C., IPTG (1 mM final concentration) was added, as well as Bis-Tris Propane buffer (0.1 M, pH 7.0) and methanol (2% v/v).

After 20 hours of growth at 37° C., 1 mL of culture was extracted by adding 100 μL 1 N HCl and 250 μL ethyl acetate. A C_{20} free fatty acid internal standard was included in the ethyl acetate solution.

The fatty acids and methyl esters were analyzed on a gas chromatograph Trace GC Ultra (Thermo Electron Corp) equipped with a flame ionization detector. The total amount of fatty acid (FFA) and fatty acyl methyl ester (FAME) was greater in cultures of wildtype *E. coli* 'TesA (316 mg/L) compared to the S10C mutant (136 mg/L), but the proportion of FAME in S10C (47%) was greater than that observed with wildtype 'TesA (9%). This demonstrates that the sequence of 'TesA can be modified to affect the proportion of esters produced (See FIG. **61**).

TABLE 26

Sequences of 'TesA homologs studied in Example 36

Species	DNA Sequence	Amino Acid Sequence
Escherichia coli	ATGGCGGACACGTTATTGA TTCTGGGTGATAGCCTGAG CGCCGGGTATCGAATGTCT GCCAGCGCGGCCTGGCCTG CCTTGTTGAATGATAAGTG GCAGAGTAAAACGTCGGTA GTTAATGCCAGCATCAGCG GCGACACCTCGCAACAAGG ACTGGCGCGCCTTCCGGCT CTGCTGAAACAGCATCAGC CGCGTTGGGTGCTGGTTGA ACTGGGCGGCAATGACGGT TTGCGTGGTTTTCAGCCAC AGCAAACCGAGCAAACGCT GCGCCAGATTTTGCAGGAT GTCAAAGCCGCCAACGCTG AACCATTGTTAATGCAAAT ACGTCTGCCTGCAAACTAT GGTCGCCGTTATAATGAAG CCTTTAGCGCCATTTACCC CAAACTCGCCAAAGAGTTT GATGTTCCGCTGCTGCCCT TTTTTATGGAAGAGGTCTA CCTCAAGCCACAATGGATG CAGGATGACGGTATTCATC CCAACCGCGACGCCCAGCC GTTTATTGCCGACTGGATG GCGAAGCAGTTGCAGCCTT TAGTAAATCATGACTCATA A (SEQ ID NO: 32)	MADTLLILGDSLSAGY RMSASAAWPALLNDKW QSKTSVVNASISGDTS QQGLARLPALLKQHQP RWVLVELGGNDGLRGF QPQQTEQTLRQILQDV KAANAEPLLMQIRLPA NYGRRYNEAFSAIYPK LAKEFDVPLLPFFMEE VYLKPQWMQDDGIHPN RDAQPFIADWMAKQLQ PLVNHDS (SEQ ID NO: 31)

TABLE 26-continued

Sequences of 'TesA homologs studied in Example 36

Species	DNA Sequence	Amino Acid Sequence
Pectobacterium atrosepticum	ATGGCTGATACATTATTAA TTCTGGGTGATAGCCTCAG TGCGGGCTACCAGATGCCG GCCGCTAACGCCTGGCCAA CGCTGCTGAACACGCAGTG GCAGACGCAGAAAAAGGGC ATCGCCGTGGTTAACGCCA GCATTAGCGGCGACACCAC CGCACAGGGGCTGGCGCGA CTTCCTGCCTTACTGAAAC AACATCAGCCGCGTTGGGT GTTGATTGAACTGGGCGGC AATGACGGGCTTCGGGGGT TTCCGGCACCCAATATCGA GCAGGATCTGGCGAAAATC ATTACGCTAGTCAAACAGG CTAACGCTAAGCCTCTGCT GATGCAGGTTCGTTTGCCA ACCAACTATGGCCGCCGCT ACACCGAGTCATTCAGCAA CATTTACCCCAAACTCGCG GAGCAGTTTGCGCTTCCTC TGCTGCCTTTCTTTATGGA GCAGGTGTATCTTAAACCG GAGTGGATCATGGAAGATG GCATCCATCCAACCCGTGA TGCCCAACCGTTTATCGCA GAATGGATGGCGAAGCAGC TGGAACCCTTAGTTAACCA TGAGTCTTAA (SEQ ID NO: 60)	MADTLLILGDSLSAGY QMPAANAWPTLLNTQW QTQKKGIAVVNASISG DTTAQGLARLPALLKQ HQPRWVLIELGGNDGL RGFPAPNIEQDLAKII TLVKQANAKPLLMQVR LPTNYGRRYTESFSNI YPKLAEQFALPLLPFF MEQVYLKPEWIMEDGI HPTRDAQPFIAEWMAK QLEPLVNHES (SEQ ID NO: 59)
Photobacterium profundum	ATGGGCAACACATTACTGG TTGTCGGTGATAGCTTGAG CGCGGGCTATCAAATGCGG GCAGAACAAAGCTGGCCGG TGTTACTGCAACCCGCATT AAAGCAACAAGGTCACGAA ATCACCGTTGTAAATGCCA GTATTTCAGGCGATACAAC AGGAAACGGCTTGGCTCGA TTGCCTACATTATTACAAC AACATAAACCAGCTTACGT CATAATTGAACTCGGGGCG AATGATGGCTTACGTGGTT TCCCTCAAGGTACTATACG TAACAATCTCAGCCAAATG ATCACTGAAATTCAAAATG CTGATGCCAAGCCAATGCT CGTGCAGATAAAAGTGCCG CCCAATTACGGCAAACGCT ACAGTGATATGTTCAGTTC TATTTACCCTCAACTCAGT AAAGAGTTAGCCACACCAC TGTTACCTTTCTTTTTAGA GCAGATCATTTTAAAACAA GAATGGATGATGAATGACG GTTTGCATCCTAAATCTGA TGCTCAGCCATGGATTGCC GAATATATGGCTGAGAATA TCGCGCCTTATTTATAA (SEQ ID NO: 62)	MAWGNTLLVVGDSLSA GYQMRAEQSWPVLLQP ALKQQGHEITVVNASI SGDTTGNGLARLPTLL QQHKPAYVIIELGAND GLRGFPQGTIRNNLSQ MITEIQNADAKPMLVQ IKVPPNYGKRYSDMFS SIYPQLSKELATPLLP FFLEQHLKQEWMMNDG LHPKSDAQPWIAEYMA ENIAPYL (SEQ ID NO: 61)
Photorhabdus luminescens	ATGGCTGATACCCTTCTGA TTCTCGGTGATAGCCTTAG TGCCGGTTACCATCTGCCT ATTGAGCAGTCATGGCCTG CTTTGATGGAAAAAAAGTG GCAAAAATCCGGCAATAAA ATCACGGTCATCAACGGCA GCATCAGCGGCAACACCGC CGCTCAGGGCCTTGAGCGG CTACCTGAATTACTTAAAC	MADTLLILGDSLSAGY HLPIEQSWPALMEKKW QKSGNKITVINGSISG NTAAQGLERLPELLKQ HKPRWVLIELGANDGL RGFPPQHTEQDLQQHT LVKQANIQPLLMQIRL PPNYGRRYTEMEQVAI KPEWVQQDGLHPNLAA QPFIADWMSDTLSAHL

TABLE 26-continued

Sequences of 'TesA homologs studied in Example 36

Species	DNA Sequence	Amino Acid Sequence
	AACATAAACCCCGTTGGGT	NYS
	ACTGATAGAGCTGGGTGCC	(SEQ ID NO: 63)
	AACGATGGATTACGCGGTT	
	TTCCTCCACAACACACCGA	
	ACAAGATCTACAACAGATC	
	ATTACTTTAGTGAAACATT	
	GATGCAGATCCGTCTACCA	
	CCAAACTATGGGCGCCGTT	
	ATACCGAGTCTTTTGCCAA	
	GATTTACCCCAAACTGGCA	
	GAATATAATCAAATTCCCC	
	TGCTCCCGTTTTATATGGA	
	GCAAGTCGCCATTAAACCG	
	GAGTGGGTGCAACAAGAAG	
	ATGGGTTACATCCTAATCT	
	GGCAGCCCAACCATTTATC	
	GCCGATTGGATGTCTGACA	
	CACTATCAGCACATCTTAA	
	TTATTCTTAA	
	(SEQ ID NO: 64)	
Pseudomonas putida	ATGGCAGGAACACTGCTGG	MAGTLLVVGDSISAGF
	TTGTTGGCGATAGTATCAG	GLDSRQGWVSLLQARL
	CGCCGGTTTTGGCCTGGAT	RDEGFDDKVVNASISG
	AGCCGTCAGGGCTGGGTGT	DTSAGGQARLPALLAA
	CTCTCTTGCAGGCCCGTCT	HKPSLVVLELGGNDGL
	CAGGGACGAAGGTTTTGAC	RGQPPAQLQQNLASMI
	GACAAAGTGGTCAATGCTT	ERSRQAGAKVLLLGMR
	CGATCAGTGGCGATACCAG	LPPNYGVRYTTAFAKV
	CGCAGGTGGCCAGGCGCGG	YEQLAADKQVPLVPFF
	CTGCCGGCGCTGCTTGCAG	LEGVGGVPELMQADGI
	CACATAAACCGAGCCTGGT	HPAQGAQQRLLENAWP
	GGTGCTGGAGCTGGGCGGC	AIKPLL
	AACGATGGCCTGCGCGGGC	(SEQ ID NO: 65)
	AGCCGCCTGCACAATTGCA	
	ACAAAATCTTGCCTCGATG	
	ATCGAGCGTTCGCGTCAGG	
	CAGGGGCCAAGGTGCTGCT	
	ATTGGGCATGCGCCTGCCG	
	CCCAATTATGGTGTGCGTT	
	ACACCACCGCCTTTGCCAA	
	GGTGTATGAACAGCTGGCA	

TABLE 26-continued

Sequences of 'TesA homologs studied in Example 36

Species	DNA Sequence	Amino Acid Sequence
	GCGGACAAACAGGTTCCCT	
	TGGTGCCGTTTTTCCTCGA	
	AGGGGTAGGGGGCGTACCT	
	GAACTGATGCAGGCTGATG	
	GCATCCATCCGGCCCAGGG	
	GGCTCAGCAGCGCCTGCTG	
	GAAAATGCCTGGCCAGCGA	
	TAAAACCCTTGCTGTGA	
	(SEQ ID NO: 66)	
Vibrio harveyi	ATGAGCGAAAAGCTACTTG	MSEKLLVLGDSLSAGY
	TTTTGGGCGACAGCCTGAG	QMPIEESWPSLLPGAL
	CGCTGGTTATCAAATGCCT	LEHGQDVKVVNGSISG
	ATAGAGGAGAGTTGGCCTA	DTTGNGLARLPSLLEQ
	GCTTACTCCCAGGCGCGTT	HTPDLVLIELGANDGL
	ATTAGAACATGGCCAAGAT	RGFPPKLITLNLSKMI
	GTAAAAGTTGTAAACGGTA	TMIKDSGADVVMMQIR
	GCATCTCTGGTGACACCAC	VPPNYGKRYSDMFYDI
	AGGCAATGGCCTTGCACGG	YPKLAEHQQVALMPFF
	TTACCTTCTCTCCTTGAGC	LEHVIIKPEWMMDDGL
	AACACACGCCCGATTTGGT	HPKPEAQPYIADFVAQ
	ACTGATTGAGCTTGGCGCT	ELVKHL
	AACGATGGCCTACGCGGTT	(SEQ ID NO: 67)
	TCCCACCTAAACTTATTAC	
	GTTAAACCTATCGAAAATG	
	ATTACCATGATCAAAGATT	
	CTGGTGCGGATGTCGTCAT	
	GATGCAAATCCGCGTCCCA	
	CCAAATTATGGTAAGCGTT	
	ACAGCGATATGTTCTACGA	
	CATCTACCCTAAACTGGCA	
	GAACATCAGCAAGTAGCGC	
	TAATGCCGTTCTTCTTAGA	
	GCATGTCATCATTAAACCA	
	GAATGGATGATGGACGATG	
	GCTTGCACCCAAAACCGGA	
	AGCTCAACCCTACATTGCT	
	GACTTTGTCGCTCAAGAAT	
	TGGTTAAACATCTCTAA	
	(SEQ ID NO: 68)	

TABLE 27

Alignment of 'TesA sequences

```
'TesA  --MADTLLILGDSLSAGYRMSASAAWPALLNDKWQSKT---SVVNASISGDTSQQGLARL   55
PatrA  --MADTLLILGDSLSAGYQMPAANAWPTLLNTQWQTQKKGIAVVNASISGDTTAQGLARL
PlumA  --MADTLLILGDSLSAGYHLPIEQSWPALMEKKWQKSGNKITVINGSISGNTAAQGLERL
PproA  MAWGNTLLVVGDSLSAGYQMRAEQSWPVLLQPALKQQGHEITVVNASISGDTTGNGLARL
VhA    --MSEKLLVLGDSLSAGYQMPIEESWPSLLPGALLEHGQDVKVVNGSISGDTTGNGLARL
PputA  --MAGTLLVVGDSISAGFGLDSRQGWVSLLQARLRDEGFDDKVVNASISGDTSAGGQARL

'TesA  PALLKQHQPRWVLVELGGNDGLRGFQPQQTEQTLRQILQDVKAANAEPLLMQIRLPANYG  115
PatrA  PALLKQHQPRWVLIELGGNDGLRGFPAPNTEQDLAKIITLVKQANAKPLLMQVRLPTNYG
PlumA  PELLKQHKPRWVLIELGANDGLRGFPPQHTEQDLQQIITLVKQANIQPLLMQIRLPPNYG
PproA  PTLLQQHKPAYVIIELGANDGLRGFPQGTIRNNLSQMITEIQNADAKPMLVQIKVPPNYG
VhA    PSLLEQHTPDLVLIELGANDGLRGFPPKLITLNLSKMITMIKDSGADVVMMQIRVPPNYG
PputA  PALLAAHKPSLVVLELGGNDGLRGQPPAQLQQNLASMIERSRQAGAKVLLLGMRLPPNYG

'TesA  RRYNEAFSAIYPKLAKEFDVPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKQL  175
PatrA  RRYTESFSNIYPKLAEQFALPLLPFFMEQVYLKPEWIMEDGIHPTRDAQPFIAEWMAKQL
PlumA  RRYTESFAKIYPKLAEYNQIPLLPFYMEQVAIKPEWVQQDGLHPNLAAQPFIADWMSDTL
PproA  KRYSDMFSSIYPQLSKELATPLLPFFLEQIILKQEWMMNDGLHPKSDAQPWIAEYMAENI
VhA    KRYSDMFYDIYPKLAEHQQVALMPFFLEHVIIKPEWMMDDGLHPKPEAQPYIADFVAQEL
PputA  VRYTTAFAKVYEQLAADKQVPLVPFFLEGVGGVPELMQADGIHPAQGAQQRLLENAWPAI

'TesA  QPLVNHDS                                                    183
PatrA  EPLVNHES
PlumA  SAHLNYS
PproA  APYL
```

TABLE 27-continued

Alignment of 'TesA sequences
VhA VKHL
PputA KPLL.

Example 37

Production of Fame in the Absence of a Wax Synthesis in Fermentors

This Example demonstrates that a process as described in Example 36, supra, can be scaled up to produce fatty acid esters at commercial scale in accordance with the present invention.

Cells from a frozen stock were revived in an LB broth for 4-8 hours and then cultured in a defined medium containing: 1.5 g/L of KH_2PO_4, 4.54 g/L of K_2HPO_4 trihydrate, 4 g/L of $(NH_4)_2SO_4$, 0.15 g/L of $MgSO_4$ heptahydrate, 20 g/L of glucose, 200 mM of Bis-Tris buffer (pH 7.2), 1.25, and 1.25 mL/L of a vitamin solution. The trace metals solution comprised 27 g/L of $FeCl_3.6H_2O$, 2 g/L of $ZnCl_2.4H_2O$, 2 g/L of $CaCl_2.6H_2O$, 2 g/L of $Na_2MoO_4.2H_2O$, 1.9 g/L of $CuSO_4.5H_2O$, 0.5 g/L of H_3BO_3, and 100 mL/L of concentrated HCl. The vitamin solution comprised 0.42 g/L of riboflavin, 5.4 g/L of pantothenic acid, 6 g/L of niacin, 1.4 g/L of pyridoxine, 0.06 g/L of biotin, and 0.04 g/L of folic acid.

100 mL of a culture grown overnight was used to inoculate 2 liters of the same medium, but with only 2 g/L of glucose, in a fermentor under tightly controlled temperature, pH, agitation, aeration and dissolved oxygen. The conditions in the fermentor were 32° C., pH 6.8, and a dissolved oxygen (DO) level equal to 30% of saturation. The pH was maintained by addition of NH_4OH, which also acted as a nitrogen source for cell growth. When the initial glucose became almost consumed, a feed containing 60% glucose, 3.9 g/L $MgSO_4$ heptahydrate and 10 mL/L of the trace minerals solution was supplied to the fermentor. The feed rate was set up to match the cell growth rate to avoid accumulation of glucose in the fermentor. By avoiding glucose accumulation, it was possible to reduce or eliminate the formation of byproducts such as acetate, formate and ethanol, which are otherwise commonly produced by *E. coli*. During the first 16-24 hours, the feed was supplied exponentially, allowing the cells to grow at a fixed growth rate. Once the feed rate reached a desired maximum (from 6 to 10 g glucose/L fermentor/h) it was maintained at that level for the remainder of the fermentation run. In the early phases of the growth, the production of FAME was induced by the addition of 1 mM IPTG and 25 mL/L of pure methanol. The fermentation was allowed to continue for a period of 3 days. Methanol was added several times during the run to replenish what had been consumed by the cells, but mostly what had been lost by evaporation in the off-gas. The additions were used to maintain the concentration of methanol in the fermentation broth at between 10 and 30 mL/L, so as to guarantee efficient production while avoiding inhibition of cell growth.

The progression of the fermentation was followed by measurements of OD600 (optical density at 600 nm), glucose consumption, and ester production.

Glucose consumption throughout the fermentation was analyzed by High Pressure Liquid Chromatography (HPLC). The HPLC analysis was performed according to methods commonly used for certain sugars and organic acids in the art, using, for example, the following conditions: Agilent HPLC 1200 Series with Refractive Index detector; Column: Aminex HPX-87H, 300 mm×7.8 mm; column temperature: 35° C.; mobile phase: 0.01 M H_2SO_4 (aqueous); flow rate: 0.6 mL/min; injection volume: 20 μl.

The production of fatty acid methyl and ethyl esters was analyzed by gas chromatography with a flame ionization detector (GC-FID). The samples from fermentation broth were extracted with ethyl acetate in a ratio of 1:1 vol/vol. After strong vortexing, the samples were centrifuged and the organic phase was analyzed by gas chromatography (GC). The analysis conditions were as follows:

Instrument: Trace GC Ultra, Thermo Electron Corporation with Flame ionization detector (FID) detector;

Column: DB-1 (1% diphenyl siloxane; 99% dimethyl siloxane) CO1 UFM 1/0.1/5 01 DET from Thermo Electron Corporation, phase pH 5, FT: 0.4 μm, length 5 m, id: 0.1 mm;

Inlet conditions: 250° C. splitless, 3.8 minute 1/25 split method used depending upon sample concentration with split flow of 75 mL/min;

Carrier gas, flow rate: Helium, 3.0 mL/min;

Block temperature: 330° C.;

Oven temperature: 0.5 minute hold at 50° C.; 100° C./minute to 330° C.; 0.5 minute hold at 330° C.;

Detector temperature: 300° C.;

Injection volume: 2 μL;

Run time/flow rate: 6.3 min/3.0 mL/min (splitless method), 3.8 min/1.5 mL/min (split 1/25 method), 3.04 min/1.2 mL/min (split 1/50 method).

This protocol was applied in fermentation runs of two different strains: ID1 (MG1655 ΔfadE::P_{TRC} tesA-fadD) and IDG5 (MG1655 ΔfadE ΔfhuA Δadh Δldh ΔpflB::P_{TRC} tesA, P_{T5L}fadD), neither of which contained the gene coding for an ester synthase. Cells were induced at 4 hours after inoculation by an IPTG addition, and methanol was fed to the fermentors to provide the alcohol for production of FAMEs. In separate experiments, the cultures were fed glucose at two different maximum feed rates: 6 and 10 g/L/h.

With both strains and at each glucose feed rate, the cultures indicated a preference for the production of FAME over free fatty acids, as shown in FIG. **62** and FIG. **63**. In 70-hour fermentations, ID1 produced about 19 g/L of FAME and less than 1 g/L FFA when fed at 6 g/L/h, and produced 28 g/L FAME and about 1 g/L FFA when fed at 10 g/L/h. IDG5 produced 20 g/L FAME and less than 1 g/L FFA at the lower glucose feed, and produced 25 g/L FAME and about 10 g/L FFA at the higher glucose feed.

Example 38

Identification of Naturally-Occuring Thioestereases for Altered Properties Based on Protein Engineering Results

E. coli 'TesA engineering experiments conducted herein are useful in identifying many amino acid residues, the mutations of which lead to altered properties. 'TesA is an enzyme that belongs to the SGNH family, a broad category of enzymes. It is likely that other homologs of 'TesA can also be used in the production of biodiesel using the pathways

described herein. This example identifies homologs of 'TesA with potentially altered properties as compared to 'TesA. The method is outlined below.

Homologs of 'TesA were identified using the strategy outlined below.

Scheme

E. coli TesA protein sequence

↓ BLAST using nr database, E-value cutoff 10, maximum hits 500, scoring matrix BLOSUM62 with all other default parameters using Discovery Studio Program (Accelrys, CA)

List of homologs

↓ -Remove sequences that do not contain active site residues corresponding to Ser10, Asp154, His157 of *E.coli* TesA
-Multiple sequence alignment with pairwise alignment-fast, scoring matrix-BLOSUM, Gap open penalty-10, gap extension penalty-0.05, with all other default parameters using Discovery Studio Program (Accelrys, CA)

-continued

Final list of homologs

↓ Identify homologs that contain substitutions corresponding to positions identified in TesA screen

Examples of homologs that contain substitutions identified in TesA screen

EQUIVALENTS

While specific examples of the subject inventions are explicitly disclosed herein, the above specification and examples herein are illustrative and not restrictive. Many variations of the inventions will become apparent to those skilled in the art upon review of this specification including the examples. The full scope of the inventions should be determined by reference to the examples, along with their full scope of equivalents, and the specification, along with such variations.

All publications, patents, patent applications, and other references cited in this application are herein incorporated by reference in their entirety as if each publication, patent, patent application or other reference were specifically and individually indicated to be incorporated by reference.

SEQUENCE LISTING

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<210> SEQ ID NO 1
<211> LENGTH: 5903
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide expression vector pOP-80

<400> SEQUENCE: 1

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<211> LENGTH: 1697
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

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<210> SEQ ID NO 4
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 4

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<211> LENGTH: 26
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 5

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<210> SEQ ID NO 6
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<212> TYPE: DNA
<213> ORGANISM: Bacillus subtilis

<400> SEQUENCE: 6

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<210> SEQ ID NO 7
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 7

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<210> SEQ ID NO 8
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 8

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<210> SEQ ID NO 9
<211> LENGTH: 1685
<212> TYPE: DNA
<213> ORGANISM: Saccharomyces cerevisiae

<400> SEQUENCE: 9

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<210> SEQ ID NO 10
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 10

agtcatgagt ctggatcg 18

<210> SEQ ID NO 11
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 11

ggaagcttac ggggcgggcg 20

<210> SEQ ID NO 12
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 12

gcgaacggcc tggtctttat gaagttcggt gg 32

<210> SEQ ID NO 13
<211> LENGTH: 1685
<212> TYPE: DNA
<213> ORGANISM: Stenotrophomonas maltophilia

<400> SEQUENCE: 13

tcatgagtct ggatcgtccc tggctgcaga gctatccgaa aggcgttccc gccgaaatcg 60

acgtcaacga attccattcg gtcgcctcgg tcttcgacgc ttccgtcgcg aaattccgcg 120

accgtcccgc ctactccagc ttcggcaagg tcctcaccta tggtgagacg gacgcgctgg 180

tcacccagtt cgccgcctac ctgctgggtg agctcaagct caagaagggt gaccgcgtcg 240

ccctgatgat gcccaactgc ctgcagtacc cggtggccac cttcggcgtg ctgcgcgccg 300

gcctgaccgt ggtcaacgtc aacccgctgt acaccgcgcg cgaactcaag caccagctgg 360

ttgatgccgg cgtcagcgcc ctggtggtgg tcgacaactt cggcgacacc gtcgaacagg 420

tcatcgccga tacaccggtc aagcacgtgg tcaccaccgg cctgggcgac ctgctcggcg 480

ccaagggcgc gatcgtcaac ttcgtgctga agtacatcaa gaagatggtg cccaactacc 540

acatcaaggg cgccgtccgc ttcaagcagg cgctcaagct gggcagccgc cacgcgcttc 600

cgccggtcga gatcgaccac gacgacattg ccttcctgca gtacaccggc gggaccaccg 660

gcgtggccaa gggtgcgatg ctgaccaacc gcaacctgat cgccaacatg cagcaggcgt 720

cagcgtggct gtccacctcc ggcatcgagc cgggcaagga agtgatcatc actgccctgc 780

cgctgtacca catcttcgca ttgaccgcga acggcctggt ctttatgaag ttcggtggct 840

gcaaccacct gatcaccaac ccacgcgaca tgaagggctt cgtaaaggag ctcaagggca 900

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cccgcttcac tgccatcacc ggcgtcaaca cgctgttcaa cggcctgctc aacaccccgg    960

gcttcgacga gatcgacttc tcttcggtca agttcaccct gggcggcggc atggcggtgc   1020

aacgtgccgt ggccgaacgc tggaagaagg tcaccggcgt gaccctggtc gaagcctatg   1080

gcctgaccga gacctcgccc gcggcctgca tcaatccgct caccctgccc gagtacaacg   1140

gtgccatcgg cctgccgatc ccgtctaccg atgcctgcat caaggacgac aacggcaaca   1200

tcctggcgct gggcgaagtg ggcgagctgt gcatcaaggg cccgcaggta atgaagggct   1260

actggcagcg tccggaagaa accgccaccg ccatcgatgc ggacggctgg ctgcacaccg   1320

gcgacatggc gaagatggac gaacagggct tcttctacat cgtcgaccgc aagaaggaca   1380

tgatcctggt gtccggcttc aacgtgtacc cgaatgaggt cgaagacgtc atcgcgatga   1440

tgccgggcgt gctggaagtc gccgccgtcg gtgtcccgga cgaaaagtcc ggcgaagtgg   1500

tcaaggtcgt gatcgtgaag aaggacccga acctgaccgc ggaaatggtc aaggaacatg   1560

cgcgggcaaa cctgaccggt tacaagcacc ccagaatcgt agaattccga aaggagctgc   1620

cgaagaccaa cgtcggcaag atcctccgtc gcgagctgcg tgatacgccc gccccgtaag   1680

aattc                                                              1685
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<210> SEQ ID NO 14
<211> LENGTH: 558
<212> TYPE: PRT
<213> ORGANISM: Stenotrophomonas maltophilia

<400> SEQUENCE: 14

```
Met Ser Leu Asp Arg Pro Trp Leu Gln Ser Tyr Pro Lys Gly Val Pro
1               5                   10                  15

Ala Glu Ile Asp Val Asn Glu Phe His Ser Val Ala Ser Val Phe Asp
            20                  25                  30

Ala Ser Val Ala Lys Phe Arg Asp Arg Pro Ala Tyr Ser Ser Phe Gly
        35                  40                  45

Lys Val Ile Thr Tyr Gly Glu Thr Asp Thr Leu Val Asn Gln Phe Ala
    50                  55                  60

Ala Tyr Leu Leu Gly Glu Leu Lys Leu Lys Lys Gly Asp Arg Val Ala
65                  70                  75                  80

Leu Met Met Pro Asn Cys Leu Gln Tyr Pro Val Ala Thr Phe Gly Val
                85                  90                  95

Leu Arg Ala Gly Leu Thr Val Val Asn Val Asn Pro Leu Tyr Thr Ala
            100                 105                 110

Arg Glu Leu Lys His Gln Leu Val Asp Ala Gly Val Ser Ala Leu Val
        115                 120                 125

Val Val Asp Asn Phe Gly Asp Thr Val Glu Gln Val Ile Ala Asp Thr
    130                 135                 140

Pro Val Lys His Val Ile Thr Thr Gly Leu Gly Asp Leu Leu Gly Ala
145                 150                 155                 160

Lys Gly Ala Ile Val Asn Phe Val Leu Lys Tyr Val Lys Lys Met Val
                165                 170                 175

Pro Asn Tyr His Ile Lys Gly Ala Val Arg Phe Lys Gln Ala Leu Lys
            180                 185                 190

Leu Gly Ser Arg His Thr Leu Pro Ala Val Glu Ile Asp His Asp Asp
        195                 200                 205

Ile Ala Phe Leu Gln Tyr Thr Gly Gly Thr Thr Gly Val Ala Lys Gly
    210                 215                 220

Ala Met Leu Thr Asn Arg Asn Leu Ile Ala Asn Met Gln Gln Ala Ser
```

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225                 230                 235                 240

Ala Trp Leu Ser Thr Ser Gly Ile Glu Pro Gly Lys Glu Val Ile Ile
                245                 250                 255

Thr Ala Leu Pro Leu Tyr His Ile Phe Ala Leu Thr Ala Asn Gly Leu
            260                 265                 270

Val Phe Met Lys Phe Gly Gly Cys Asn His Leu Ile Thr Asn Pro Arg
        275                 280                 285

Asp Met Lys Gly Phe Val Lys Glu Leu Lys Gly Thr Arg Phe Thr Ala
    290                 295                 300

Ile Thr Gly Val Asn Thr Leu Phe Asn Gly Leu Leu Asn Thr Pro Gly
305                 310                 315                 320

Phe Asp Glu Ile Asp Phe Ser Ser Val Lys Phe Thr Leu Gly Gly Gly
                325                 330                 335

Met Ala Val Gln Arg Ala Val Ala Glu Arg Trp Lys Lys Thr Thr Gly
            340                 345                 350

Val Thr Leu Val Glu Ala Tyr Gly Leu Thr Glu Thr Ser Pro Ala Ala
        355                 360                 365

Cys Ile Asn Pro Leu Thr Leu Pro Glu Tyr Asn Gly Ser Ile Gly Leu
    370                 375                 380

Pro Ile Pro Ser Thr Asp Ala Cys Ile Lys Asp Asp Asn Gly Asn Ile
385                 390                 395                 400

Leu Pro Leu Gly Glu Val Gly Glu Leu Cys Ile Lys Gly Pro Gln Val
                405                 410                 415

Met Lys Gly Tyr Trp Gln Arg Pro Glu Glu Thr Ala Thr Ala Ile Asp
            420                 425                 430

Ala Asp Gly Trp Leu His Thr Gly Asp Met Ala Arg Met Asp Glu Gln
        435                 440                 445

Gly Phe Phe Tyr Ile Val Asp Arg Lys Lys Asp Met Ile Leu Val Ser
    450                 455                 460

Gly Phe Asn Val Tyr Pro Asn Glu Val Glu Asp Val Ile Ala Met Met
465                 470                 475                 480

Pro Gly Val Leu Glu Val Ala Ala Val Gly Val Pro Asp Glu Lys Ser
                485                 490                 495

Gly Glu Val Val Lys Val Val Ile Val Lys Lys Asp Pro Asn Leu Thr
            500                 505                 510

Ala Glu Met Val Lys Glu His Ala Arg Ala Asn Leu Thr Gly Tyr Lys
        515                 520                 525

His Pro Arg Ile Val Glu Phe Arg Lys Glu Leu Pro Lys Thr Asn Val
    530                 535                 540

Gly Lys Ile Leu Arg Arg Glu Leu Arg Asp Thr Pro Ala Pro
545                 550                 555


<210> SEQ ID NO 15
<211> LENGTH: 3525
<212> TYPE: DNA
<213> ORGANISM: Nocardia iowensis

<400> SEQUENCE: 15

atggcagtgg attcaccgga tgagcggcta cagcgccgca ttgcacagtt gtttgcagaa     60

gatgagcagg tcaaggccgc acgtccgctc gaagcggtga gcgcggcggt gagcgcgccc    120

ggtatgcggc tggcgcagat cgccgccact gttatggcgg gttacgccga ccgcccggcc    180

gccgggcagc gtgcgttcga actgaacacc gacgacgcga cgggccgcac ctcgctgcgg    240

ttacttcccc gattcgagac catcacctat cgcgaactgt ggcagcgagt cggcgaggtt    300
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gccgcggcct ggcatcatga tcccgagaac cccttgcgcg caggtgattt cgtcgccctg 360

ctcggcttca ccagcatcga ctacgccacc ctcgacctgg ccgatatcca cctcggcgcg 420

gttaccgtgc cgttgcaggc cagcgcggcg gtgtcccagc tgatcgctat cctcaccgag 480

acttcgccgc ggctgctcgc ctcgaccccg gagcacctcg atgcggcggt cgagtgccta 540

ctcgcgggca ccacaccgga acgactggtg gtcttcgact accaccccga ggacgacgac 600

cagcgtgcgg ccttcgaatc cgcccgccgc cgccttgccg acgcgggcag cttggtgatc 660

gtcgaaacgc tcgatgccgt gcgtgcccgg ggccgcgact taccggccgc gccactgttc 720

gttcccgaca ccgacgacga cccgctggcc ctgctgatct acacctccgg cagcaccgga 780

acgccgaagg gcgcgatgta caccaatcgg ttggccgcca cgatgtggca ggggaactcg 840

atgctgcagg ggaactcgca acgggtcggg atcaatctca actacatgcc gatgagccac 900

atcgccggtc gcatatcgct gttcggcgtg ctcgctcgcg gtggcaccgc atacttcgcg 960

gccaagagcg acatgtcgac actgttcgaa gacatcggct tggtacgtcc caccgagatc 1020

ttcttcgtcc cgcgcgtgtg cgacatggtc ttccagcgct atcagagcga gctggaccgg 1080

cgctcggtgg cgggcgccga cctggacacg ctcgatcggg aagtgaaagc cgacctccgg 1140

cagaactacc tcggtgggcg cttcctggtg gcggtcgtcg gcagcgcgcc gctggccgcg 1200

gagatgaaga cgttcatgga gtccgtcctc gatctgccac tgcacgacgg gtacgggtcg 1260

accgaggcgg gcgcaagcgt gctgctcgac aaccagatcc agcggccgcc ggtgctcgat 1320

tacaagctcg tcgacgtgcc cgaactgggt tacttccgca ccgaccggcc gcatccgcgc 1380

ggtgagctgt tgttgaaggc ggagaccacg attccgggct actacaagcg gcccgaggtc 1440

accgcggaga tcttcgacga ggacggcttc tacaagaccg gcgatatcgt ggccgagctc 1500

gagcacgatc ggctggtcta tgtcgaccgt cgcaacaatg tgctcaaact gtcgcagggc 1560

gagttcgtga ccgtcgccca tctcgaggcc gtgttcgcca gcagcccgct gatccggcag 1620

atcttcatct acggcagcag cgaacgttcc tatctgctcg cggtgatcgt ccccaccgac 1680

gacgcgctgc gcggccgcga caccgccacc ttgaaatcgg cactggccga atcgattcag 1740

cgcatcgcca aggacgcgaa cctgcagccc tacgagattc cgcgcgattt cctgatcgag 1800

accgagccgt tcaccatcgc caacggactg ctctccggca tcgcgaagct gctgcgcccc 1860

aatctgaagg aacgctacgg cgctcagctg gagcagatgt acaccgatct cgcgacaggc 1920

caggccgatg agctgctcgc cctgcgccgc gaagccgccg acctgccggt gctcgaaacc 1980

gtcagccggg cagcgaaagc gatgctcggc gtcgcctccg ccgatatgcg tcccgacgcg 2040

cacttcaccg acctgggcgg cgattccctt tccgcgctgt cgttctcgaa cctgctgcac 2100

gagatcttcg gggtcgaggt gccggtgggt gtcgtcgtca gcccggcgaa cgagctgcgc 2160

gatctggcga attacattga ggcggaacgc aactcgggcg cgaagcgtcc caccttcacc 2220

tcggtgcacg gcggcggttc cgagatccgc gccgccgatc tgaccctcga caagttcatc 2280

gatgcccgca ccctggccgc cgccgacagc attccgcacg cgccggtgcc agcgcagacg 2340

gtgctgctga ccggcgcgaa cggctacctc ggccggttcc tgtgcctgga atggctggag 2400

cggctggaca agacgggtgg cacgctgatc tgcgtcgtgc gcggtagtga cgcggccgcg 2460

gcccgtaaac ggctggactc ggcgttcgac agcggcgatc ccggcctgct cgagcactac 2520

cagcaactgg ccgcacggac cctggaagtc ctcgccggtg atatcggcga cccgaatctc 2580

ggtctggacg acgcgacttg gcagcggttg gccgaaaccg tcgacctgat cgtccatccc 2640

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gccgcgttgg tcaaccacgt ccttccctac acccagctgt tcggccccaa tgtcgtcggc   2700

accgccgaaa tcgtccggtt ggcgatcacg gcgcggcgca agccggtcac ctacctgtcg   2760

accgtcggag tggccgacca ggtcgacccg gcggagtatc aggaggacag cgacgtccgc   2820

gagatgagcg cggtgcgcgt cgtgcgcgag agttacgcca acggctacgg caacagcaag   2880

tgggcggggg aggtcctgct gcgcgaagca cacgatctgt gtggcttgcc ggtcgcggtg   2940

ttccgttcgg acatgatcct ggcgcacagc cggtacgcgg gtcagctcaa cgtccaggac   3000

gtgttcaccc ggctgatcct cagcctggtc gccaccggca tcgcgccgta ctcgttctac   3060

cgaaccgacg cggacggcaa ccggcagcgg gcccactatg acggcttgcc ggcggacttc   3120

acggcggcgg cgatcaccgc gctcggcatc caagccaccg aaggcttccg gacctacgac   3180

gtgctcaatc cgtacgacga tggcatctcc ctcgatgaat tcgtcgactg gctcgtcgaa   3240

tccggccacc cgatccagcg catcaccgac tacagcgact ggttccaccg tttcgagacg   3300

gcgatccgcg cgctgccgga aaagcaacgc caggcctcgg tgctgccgtt gctggacgcc   3360

taccgcaacc cctgcccggc ggtccgcggc gcgatactcc cggccaagga gttccaagcg   3420

gcggtgcaaa cagccaaaat cggtccggaa caggacatcc cgcatttgtc cgcgccactg   3480

atcgataagt acgtcagcga tctggaactg cttcagctgc tctga                   3525
```

<210> SEQ ID NO 16
<211> LENGTH: 1174
<212> TYPE: PRT
<213> ORGANISM: Nocardia iowensis

<400> SEQUENCE: 16

```
Met Ala Val Asp Ser Pro Asp Glu Arg Leu Gln Arg Arg Ile Ala Gln
1               5                   10                  15

Leu Phe Ala Glu Asp Glu Gln Val Lys Ala Ala Arg Pro Leu Glu Ala
            20                  25                  30

Val Ser Ala Ala Val Ser Ala Pro Gly Met Arg Leu Ala Gln Ile Ala
        35                  40                  45

Ala Thr Val Met Ala Gly Tyr Ala Asp Arg Pro Ala Ala Gly Gln Arg
    50                  55                  60

Ala Phe Glu Leu Asn Thr Asp Asp Ala Thr Gly Arg Thr Ser Leu Arg
65                  70                  75                  80

Leu Leu Pro Arg Phe Glu Thr Ile Thr Tyr Arg Glu Leu Trp Gln Arg
                85                  90                  95

Val Gly Glu Val Ala Ala Ala Trp His His Asp Pro Glu Asn Pro Leu
            100                 105                 110

Arg Ala Gly Asp Phe Val Ala Leu Leu Gly Phe Thr Ser Ile Asp Tyr
        115                 120                 125

Ala Thr Leu Asp Leu Ala Asp Ile His Leu Gly Ala Val Thr Val Pro
    130                 135                 140

Leu Gln Ala Ser Ala Ala Val Ser Gln Leu Ile Ala Ile Leu Thr Glu
145                 150                 155                 160

Thr Ser Pro Arg Leu Leu Ala Ser Thr Pro Glu His Leu Asp Ala Ala
                165                 170                 175

Val Glu Cys Leu Leu Ala Gly Thr Thr Pro Glu Arg Leu Val Val Phe
            180                 185                 190

Asp Tyr His Pro Glu Asp Asp Asp Gln Arg Ala Ala Phe Glu Ser Ala
        195                 200                 205

Arg Arg Arg Leu Ala Asp Ala Gly Ser Leu Val Ile Val Glu Thr Leu
    210                 215                 220
```

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```
Asp Ala Val Arg Ala Arg Gly Arg Asp Leu Pro Ala Ala Pro Leu Phe
225                 230                 235                 240

Val Pro Asp Thr Asp Asp Asp Pro Leu Ala Leu Leu Ile Tyr Thr Ser
                245                 250                 255

Gly Ser Thr Gly Thr Pro Lys Gly Ala Met Tyr Thr Asn Arg Leu Ala
            260                 265                 270

Ala Thr Met Trp Gln Gly Asn Ser Met Leu Gln Gly Asn Ser Gln Arg
        275                 280                 285

Val Gly Ile Asn Leu Asn Tyr Met Pro Met Ser His Ile Ala Gly Arg
    290                 295                 300

Ile Ser Leu Phe Gly Val Leu Ala Arg Gly Gly Thr Ala Tyr Phe Ala
305                 310                 315                 320

Ala Lys Ser Asp Met Ser Thr Leu Phe Glu Asp Ile Gly Leu Val Arg
                325                 330                 335

Pro Thr Glu Ile Phe Phe Val Pro Arg Val Cys Asp Met Val Phe Gln
            340                 345                 350

Arg Tyr Gln Ser Glu Leu Asp Arg Arg Ser Val Ala Gly Ala Asp Leu
        355                 360                 365

Asp Thr Leu Asp Arg Glu Val Lys Ala Asp Leu Arg Gln Asn Tyr Leu
    370                 375                 380

Gly Gly Arg Phe Leu Val Ala Val Val Gly Ser Ala Pro Leu Ala Ala
385                 390                 395                 400

Glu Met Lys Thr Phe Met Glu Ser Val Leu Asp Leu Pro Leu His Asp
                405                 410                 415

Gly Tyr Gly Ser Thr Glu Ala Gly Ala Ser Val Leu Leu Asp Asn Gln
            420                 425                 430

Ile Gln Arg Pro Pro Val Leu Asp Tyr Lys Leu Val Asp Val Pro Glu
        435                 440                 445

Leu Gly Tyr Phe Arg Thr Asp Arg Pro His Pro Arg Gly Glu Leu Leu
    450                 455                 460

Leu Lys Ala Glu Thr Thr Ile Pro Gly Tyr Tyr Lys Arg Pro Glu Val
465                 470                 475                 480

Thr Ala Glu Ile Phe Asp Glu Asp Gly Phe Tyr Lys Thr Gly Asp Ile
                485                 490                 495

Val Ala Glu Leu Glu His Asp Arg Leu Val Tyr Val Asp Arg Arg Asn
            500                 505                 510

Asn Val Leu Lys Leu Ser Gln Gly Glu Phe Val Thr Val Ala His Leu
        515                 520                 525

Glu Ala Val Phe Ala Ser Ser Pro Leu Ile Arg Gln Ile Phe Ile Tyr
    530                 535                 540

Gly Ser Ser Glu Arg Ser Tyr Leu Leu Ala Val Ile Val Pro Thr Asp
545                 550                 555                 560

Asp Ala Leu Arg Gly Arg Asp Thr Ala Thr Leu Lys Ser Ala Leu Ala
                565                 570                 575

Glu Ser Ile Gln Arg Ile Ala Lys Asp Ala Asn Leu Gln Pro Tyr Glu
            580                 585                 590

Ile Pro Arg Asp Phe Leu Ile Glu Thr Glu Pro Phe Thr Ile Ala Asn
        595                 600                 605

Gly Leu Leu Ser Gly Ile Ala Lys Leu Leu Arg Pro Asn Leu Lys Glu
    610                 615                 620

Arg Tyr Gly Ala Gln Leu Glu Gln Met Tyr Thr Asp Leu Ala Thr Gly
625                 630                 635                 640
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Gln Ala Asp Glu Leu Leu Ala Leu Arg Arg Glu Ala Ala Asp Leu Pro
               645                 650                 655

Val Leu Glu Thr Val Ser Arg Ala Ala Lys Ala Met Leu Gly Val Ala
           660                 665                 670

Ser Ala Asp Met Arg Pro Asp Ala His Phe Thr Asp Leu Gly Gly Asp
       675                 680                 685

Ser Leu Ser Ala Leu Ser Phe Ser Asn Leu Leu His Glu Ile Phe Gly
   690                 695                 700

Val Glu Val Pro Val Gly Val Val Val Ser Pro Ala Asn Glu Leu Arg
705                 710                 715                 720

Asp Leu Ala Asn Tyr Ile Glu Ala Glu Arg Asn Ser Gly Ala Lys Arg
               725                 730                 735

Pro Thr Phe Thr Ser Val His Gly Gly Gly Ser Glu Ile Arg Ala Ala
           740                 745                 750

Asp Leu Thr Leu Asp Lys Phe Ile Asp Ala Arg Thr Leu Ala Ala Ala
       755                 760                 765

Asp Ser Ile Pro His Ala Pro Val Pro Ala Gln Thr Val Leu Leu Thr
   770                 775                 780

Gly Ala Asn Gly Tyr Leu Gly Arg Phe Leu Cys Leu Glu Trp Leu Glu
785                 790                 795                 800

Arg Leu Asp Lys Thr Gly Gly Thr Leu Ile Cys Val Val Arg Gly Ser
               805                 810                 815

Asp Ala Ala Ala Ala Arg Lys Arg Leu Asp Ser Ala Phe Asp Ser Gly
           820                 825                 830

Asp Pro Gly Leu Leu Glu His Tyr Gln Gln Leu Ala Ala Arg Thr Leu
       835                 840                 845

Glu Val Leu Ala Gly Asp Ile Gly Asp Pro Asn Leu Gly Leu Asp Asp
   850                 855                 860

Ala Thr Trp Gln Arg Leu Ala Glu Thr Val Asp Leu Ile Val His Pro
865                 870                 875                 880

Ala Ala Leu Val Asn His Val Leu Pro Tyr Thr Gln Leu Phe Gly Pro
               885                 890                 895

Asn Val Val Gly Thr Ala Glu Ile Val Arg Leu Ala Ile Thr Ala Arg
           900                 905                 910

Arg Lys Pro Val Thr Tyr Leu Ser Thr Val Gly Val Ala Asp Gln Val
       915                 920                 925

Asp Pro Ala Glu Tyr Gln Glu Asp Ser Asp Val Arg Glu Met Ser Ala
   930                 935                 940

Val Arg Val Val Arg Glu Ser Tyr Ala Asn Gly Tyr Gly Asn Ser Lys
945                 950                 955                 960

Trp Ala Gly Glu Val Leu Leu Arg Glu Ala His Asp Leu Cys Gly Leu
               965                 970                 975

Pro Val Ala Val Phe Arg Ser Asp Met Ile Leu Ala His Ser Arg Tyr
           980                 985                 990

Ala Gly Gln Leu Asn Val Gln Asp  Val Phe Thr Arg Leu  Ile Leu Ser
       995                 1000                1005

Leu Val  Ala Thr Gly Ile Ala  Pro Tyr Ser Phe Tyr  Arg Thr Asp
   1010                1015                1020

Ala Asp  Gly Asn Arg Gln Arg  Ala His Tyr Asp Gly  Leu Pro Ala
   1025                1030                1035

Asp Phe  Thr Ala Ala Ala Ile  Thr Ala Leu Gly Ile  Gln Ala Thr
   1040                1045                1050

Glu Gly  Phe Arg Thr Tyr Asp  Val Leu Asn Pro Tyr  Asp Asp Gly
```

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    1055                1060                1065

Ile Ser  Leu Asp Glu Phe Val  Asp Trp Leu Val Glu  Ser Gly His
    1070                1075                1080

Pro Ile  Gln Arg Ile Thr Asp  Tyr Ser Asp Trp Phe  His Arg Phe
    1085                1090                1095

Glu Thr  Ala Ile Arg Ala Leu  Pro Glu Lys Gln Arg  Gln Ala Ser
    1100                1105                1110

Val Leu  Pro Leu Leu Asp Ala  Tyr Arg Asn Pro Cys  Pro Ala Val
    1115                1120                1125

Arg Gly  Ala Ile Leu Pro Ala  Lys Glu Phe Gln Ala  Ala Val Gln
    1130                1135                1140

Thr Ala  Lys Ile Gly Pro Glu  Gln Asp Ile Pro His  Leu Ser Ala
    1145                1150                1155

Pro Leu  Ile Asp Lys Tyr Val  Ser Asp Leu Glu Leu  Leu Gln Leu
    1160                1165                1170

Leu


<210> SEQ ID NO 17
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Carboxylic acid
      reductase peptide motif
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (3)..(4)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Ser, Ala or Thr
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: Trp or Leu

<400> SEQUENCE: 17

Gly Tyr Xaa Xaa Xaa Lys Xaa
1               5


<210> SEQ ID NO 18
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Carboxylic acid
      reductase peptide motif
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(3)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Any naturally-occurring amino acid

<400> SEQUENCE: 18

Gly Xaa Xaa Gly Xaa Leu Gly
1               5


<210> SEQ ID NO 19
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
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<223> OTHER INFORMATION: Description of Unknown: Carboxylic acid reductase peptide motif
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Leu, Val or Ile
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (6)..(7)
<223> OTHER INFORMATION: Any naturally-occurring amino acid

<400> SEQUENCE: 19

Xaa Gly Gly Asp Ser Xaa Xaa Ala
1 5

<210> SEQ ID NO 20
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Carboxylic acid reductase peptide motif
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Leu, Ile, Val, Met, Phe or Tyr
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Any naturally-occurring amino acid except Glu
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: Any naturally-occurring amino acid except Val, Glu or Ser
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: Ser, Thr or Gly
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Ser, Thr, Ala or Gly
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: Ser or Thr
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Ser, Thr, Glu, Ile or Ala
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: Ser or Gly
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: Pro, Ala, Ser, Leu, Ile, Val or Met
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: Lys or Arg

<400> SEQUENCE: 20

Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> SEQ ID NO 21
<211> LENGTH: 21
<212> TYPE: PRT

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<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Carboxylic acid reductase peptide motif
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Ser or Thr
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: Thr or Asn
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: Phe or Trp
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: Phe or Tyr
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: Ala or Thr
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: Glu or Gln

<400> SEQUENCE: 21

Arg Thr Val Leu Leu Xaa Gly Ala Xaa Gly Xaa Leu Gly Arg Xaa Leu
1 5 10 15

Xaa Leu Xaa Trp Leu
20

<210> SEQ ID NO 22
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Carboxylic acid reductase peptide motif
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(3)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (5)..(6)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (11)..(12)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (16)..(16)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: Any naturally-occurring amino acid

<400> SEQUENCE: 22

Leu Xaa Xaa Gly Xaa Xaa Gly Xaa Leu Gly Xaa Xaa Leu Xaa Leu Xaa
1 5 10 15

Trp Leu Xaa Arg
20

<210> SEQ ID NO 23
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Carboxylic acid reductase peptide motif
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: Any naturally-occurring amino acid

<400> SEQUENCE: 23

Trp Ala Xaa Glu Val Leu Leu Arg
1 5

<210> SEQ ID NO 24
<211> LENGTH: 35
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Carboxylic acid reductase peptide motif
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(3)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (5)..(6)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (11)..(12)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: Leu or Ile
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (16)..(16)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: Trp or Leu
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (19)..(32)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (34)..(34)
<223> OTHER INFORMATION: Any naturally-occurring amino acid or absent

<400> SEQUENCE: 24

Leu Xaa Xaa Gly Xaa Xaa Gly Xaa Leu Gly Xaa Xaa Leu Xaa Xaa Xaa
1 5 10 15

Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Leu Xaa Arg

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35

<210> SEQ ID NO 25
<211> LENGTH: 1269
<212> TYPE: DNA
<213> ORGANISM: Jeotgalicoccus sp.
<220> FEATURE:
<223> OTHER INFORMATION: ATCC8456

<400> SEQUENCE: 25

atggcaacac ttaagaggga taagggctta gataatactt tgaaagtatt aaagcaaggt 60

tatctttaca caacaaatca gagaaatcgt ctaaacacat cagttttcca aactaaagca 120

ctcggtggta aaccattcgt agttgtgact ggtaaggaag gcgctgaaat gttctacaac 180

aatgatgttg ttcaacgtga aggcatgtta ccaaaacgta tcgttaatac gctttttggt 240

aaaggtgcaa tccatacggt agatggtaaa aaacacgtag acagaaaagc attgttcatg 300

agcttgatga ctgaaggtaa cttgaattat gtacgagaat taacgcgtac attatggcat 360

gcgaacacac aacgtatgga aagtatggat gaggtaaata tttaccgtga atctatcgta 420

ctacttacaa aagtaggaac acgttgggca ggcgttcaag caccacctga agatatcgaa 480

agaatcgcaa cagacatgga catcatgatc gattcattta gagcacttgg tggtgccttt 540

aaaggttaca aggcatcaaa agaagcacgt cgtcgtgttg aagattggtt agaagaacaa 600

attattgaga ctcgtaaagg gaatattcat ccaccagaag gtacagcact ttacgaattt 660

gcacattggg aagactactt aggtaaccca atggactcaa gaacttgtgc gattgactta 720

atgaacacat tccgcccatt aatcgcaatc aacagattcg tttcattcgg tttacacgcg 780

atgaacgaaa acccaatcac acgtgaaaaa attaaatcag aacctgacta tgcatataaa 840

ttcgctcaag aagttcgtcg ttactatcca ttcgttccat tccttccagg taaagcgaaa 900

gtagacatcg acttccaagg cgttacaatt cctgcaggtg taggtcttgc attagatgtt 960

tatggtacaa cgcatgatga atcactttgg gacgatccaa atgaattccg cccagaaaga 1020

ttcgaaactt gggacggatc accatttgac cttattccac aaggtggtgg agattactgg 1080

acaaatcacc gttgtgcagg tgaatggatc acagtaatca tcatggaaga aacaatgaaa 1140

tactttgcag aaaaaataac ttatgatgtt ccagaacaag atttagaagt ggacttaaac 1200

agtatcccag gatacgttaa gagtggcttt gtaatcaaaa atgttcgcga agttgtagac 1260

agaacataa 1269

<210> SEQ ID NO 26
<211> LENGTH: 422
<212> TYPE: PRT
<213> ORGANISM: Jeotgalicoccus sp.
<220> FEATURE:
<223> OTHER INFORMATION: ATCC8456

<400> SEQUENCE: 26

Met Ala Thr Leu Lys Arg Asp Lys Gly Leu Asp Asn Thr Leu Lys Val
1 5 10 15

Leu Lys Gln Gly Tyr Leu Tyr Thr Thr Asn Gln Arg Asn Arg Leu Asn
20 25 30

Thr Ser Val Phe Gln Thr Lys Ala Leu Gly Gly Lys Pro Phe Val Val
35 40 45

Val Thr Gly Lys Glu Gly Ala Glu Met Phe Tyr Asn Asn Asp Val Val
50 55 60

Gln Arg Glu Gly Met Leu Pro Lys Arg Ile Val Asn Thr Leu Phe Gly

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65                  70                  75                  80

Lys Gly Ala Ile His Thr Val Asp Gly Lys Lys His Val Asp Arg Lys
                85                  90                  95

Ala Leu Phe Met Ser Leu Met Thr Glu Gly Asn Leu Asn Tyr Val Arg
            100                 105                 110

Glu Leu Thr Arg Thr Leu Trp His Ala Asn Thr Gln Arg Met Glu Ser
        115                 120                 125

Met Asp Glu Val Asn Ile Tyr Arg Glu Ser Ile Val Leu Leu Thr Lys
    130                 135                 140

Val Gly Thr Arg Trp Ala Gly Val Gln Ala Pro Pro Glu Asp Ile Glu
145                 150                 155                 160

Arg Ile Ala Thr Asp Met Asp Ile Met Ile Asp Ser Phe Arg Ala Leu
                165                 170                 175

Gly Gly Ala Phe Lys Gly Tyr Lys Ala Ser Lys Glu Ala Arg Arg Arg
            180                 185                 190

Val Glu Asp Trp Leu Glu Glu Gln Ile Ile Glu Thr Arg Lys Gly Asn
        195                 200                 205

Ile His Pro Pro Glu Gly Thr Ala Leu Tyr Glu Phe Ala His Trp Glu
    210                 215                 220

Asp Tyr Leu Gly Asn Pro Met Asp Ser Arg Thr Cys Ala Ile Asp Leu
225                 230                 235                 240

Met Asn Thr Phe Arg Pro Leu Ile Ala Ile Asn Arg Phe Val Ser Phe
                245                 250                 255

Gly Leu His Ala Met Asn Glu Asn Pro Ile Thr Arg Glu Lys Ile Lys
            260                 265                 270

Ser Glu Pro Asp Tyr Ala Tyr Lys Phe Ala Gln Glu Val Arg Arg Tyr
        275                 280                 285

Tyr Pro Phe Val Pro Phe Leu Pro Gly Lys Ala Lys Val Asp Ile Asp
    290                 295                 300

Phe Gln Gly Val Thr Ile Pro Ala Gly Val Gly Leu Ala Leu Asp Val
305                 310                 315                 320

Tyr Gly Thr Thr His Asp Glu Ser Leu Trp Asp Asp Pro Asn Glu Phe
                325                 330                 335

Arg Pro Glu Arg Phe Glu Thr Trp Asp Gly Ser Pro Phe Asp Leu Ile
            340                 345                 350

Pro Gln Gly Gly Gly Asp Tyr Trp Thr Asn His Arg Cys Ala Gly Glu
        355                 360                 365

Trp Ile Thr Val Ile Ile Met Glu Glu Thr Met Lys Tyr Phe Ala Glu
    370                 375                 380

Lys Ile Thr Tyr Asp Val Pro Glu Gln Asp Leu Glu Val Asp Leu Asn
385                 390                 395                 400

Ser Ile Pro Gly Tyr Val Lys Ser Gly Phe Val Ile Lys Asn Val Arg
                405                 410                 415

Glu Val Val Asp Arg Thr
            420


<210> SEQ ID NO 27
<211> LENGTH: 1507
<212> TYPE: DNA
<213> ORGANISM: Jeotgalicoccus sp.
<220> FEATURE:
<223> OTHER INFORMATION: ATCC8456

<400> SEQUENCE: 27

ggttaccttg ttacgacttc accccaatta tcaatcccac ctttgacggc tacctccatt     60
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aaggttagtc caccggcttc aggtgttayc gactttcgtg gtgtgacggg cggtgtgtac 120

aagacccggg aacgtattca ccgtagcatg ctgatctacg attactagcg attccagctt 180

catggagtcg agttgcagac tccaatccga actgagaaca gttttatggg attcgcttgg 240

cctcgcggct tcgctgccct ttgtaacctg cccattgtag cacgtgtgta gcccaaatca 300

taaggggcat gatgatttga cgtcatcccc accttcctcc ggtttgtcac cggcagtcaa 360

tctagagtgc ccaactgaat gatggcaact aaatttaagg gttgcgctcg ttgcgggact 420

taacccaaca tctcacgaca cgagctgacg acaaccatgc accacctgtc tctctgccca 480

aaagggaaac catatctctr tggcgatcag aggatgtcaa gatttggtaa ggttcttcgc 540

gttgcttcga attaaaccac atgctccacc gcttgtgcgg gtccccgtca attcctttga 600

gtttcaacct tgcggtcgta ctccccaggc ggagtgctta atgcgttagc tgcagcactg 660

aggggcggaa acccccccaac acttagcact catcgtttac ggcgtggact accagggtat 720

ctaatcctgt ttgatcccca cgctttcgca cctcagcgtc agttacagac cagagagccg 780

ccttcgccca ctggtgttcc tccatatctc tgcgcatttc accgctacac atggaattcc 840

actctcctct tctgcactca agtaaaacag tttccaatga ccctccccgg ttgagccggg 900

ggctttcaca tcagacttat tctaccgcct acgcgcgctt tacgcccaat aattccggat 960

aacgcttgcc acctacgtat taccgcggct gctggcacgt agttagccgt ggctttctgg 1020

ttaagtaccg tcatctctag gccagttact acctaaagtg ttcttcctta acaacagagt 1080

tttacgagcc gaaaccctc ttcactcacg cggcgttgct ccgtcagact tgcgtycatt 1140

gcggaagatt ccctactgct gcctcccgta ggagtctggg ccgtgtctca gtcccagtgt 1200

ggccgatcac cctctcaggt cggctatgca tcgttgcctt ggtgagccac tacctcacca 1260

actagctaat gcaccgcagg cccatccttt agtgacagat aaatccgcct ttcattaaga 1320

ttacttgtgt aatccaactt atccggtatt agctaccgtt tccggtagtt atcccagtct 1380

aaagggtagg ttgcccacgt gttactcacc cgtccgccgc tcgattgtaa ggagcaagct 1440

ccttacgctc gcgctcgact tgcatgtatt aggcacgccg ccagcgttca tcctgagcca 1500

ggatcaa 1507

<210> SEQ ID NO 28
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Carboxylic acid thioesterase peptide motif
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Asp, Asn or Thr
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: Leu, Cys or Gln
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (5)..(9)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: Met, Cys, Asp, Leu, Asn, Thr or Val

<400> SEQUENCE: 28

Gly Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa

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1 5 10

<210> SEQ ID NO 29
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Carboxylic acid thioesterase peptide motif
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Val or Leu
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(3)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Asn, Val, Leu, Cys, Ala, Gly, His, Ile, Thr or Trp
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: Asp or Glu
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: Leu, Ile, Trp, Phe, Thr, Met, Ala, Glu, Asn or Val

<400> SEQUENCE: 29

Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa
1 5

<210> SEQ ID NO 30
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Carboxylic acid thioesterase peptide motif
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (2)..(3)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Pro, Gly, Ala, Phe, Leu, Ser or Val
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (6)..(11)
<223> OTHER INFORMATION: Any naturally-occurring amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: Ile, Leu or Val

<400> SEQUENCE: 30

Asp Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
1 5 10

<210> SEQ ID NO 31
<211> LENGTH: 183

<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 31

Met Ala Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr
1 5 10 15

Arg Met Ser Ala Ser Ala Ala Trp Pro Ala Leu Leu Asn Asp Lys Trp
20 25 30

Gln Asn Lys Thr Ser Val Val Asn Ala Ser Ile Ser Gly Asp Thr Ser
35 40 45

Gln Gln Gly Leu Ala Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro
50 55 60

Arg Trp Val Leu Val Glu Leu Gly Gly Asn Asp Gly Leu Arg Gly Phe
65 70 75 80

Gln Pro Gln Gln Thr Glu Gln Thr Leu Arg Gln Ile Leu Gln Asp Val
85 90 95

Lys Ala Ala Asn Ala Glu Pro Leu Leu Met Gln Ile Arg Leu Pro Ala
100 105 110

Asn Tyr Gly Arg Arg Tyr Asn Glu Ala Phe Ser Ala Ile Tyr Pro Lys
115 120 125

Leu Ala Lys Glu Phe Asp Val Pro Leu Leu Pro Phe Phe Met Glu Glu
130 135 140

Val Tyr Leu Lys Pro Gln Trp Met Gln Asp Asp Gly Ile His Pro Asn
145 150 155 160

Arg Asp Ala Gln Pro Phe Ile Ala Asp Trp Met Ala Lys Gln Leu Gln
165 170 175

Pro Leu Val Asn His Asp Ser
180

<210> SEQ ID NO 32
<211> LENGTH: 552
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 32

atggcggaca cgttattgat tctgggtgat agcctgagcg ccgggtatcg aatgtctgcc 60

agcgcggcct ggcctgcctt gttgaatgat aagtggcaga gtaaaacgtc ggtagttaat 120

gccagcatca gcggcgacac ctcgcaacaa ggactggcgc gccttccggc tctgctgaaa 180

cagcatcagc cgcgttgggt gctggttgaa ctgggcggca atgacggttt gcgtggtttt 240

cagccacagc aaaccgagca aacgctgcgc cagattttgc aggatgtcaa agccgccaac 300

gctgaaccat tgttaatgca aatacgtctg cctgcaaact atggtcgccg ttataatgaa 360

gcctttagcg ccatttaccc caaactcgcc aaagagtttg atgttccgct gctgcccttt 420

tttatggaag aggtctacct caagccacaa tggatgcagg atgacggtat tcatcccaac 480

cgcgacgccc agccgtttat tgccgactgg atggcgaagc agttgcagcc tttagtaaat 540

catgactcat aa 552

<210> SEQ ID NO 33
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic control region of FabA oligonucleotide

<400> SEQUENCE: 33

tttattccga actgatcgga cttgttcagc gtacacgtgt tagctatcct gcgtgcttca 60

ataaaa 66

<210> SEQ ID NO 34
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic control region of FabB oligonucleotide

<400> SEQUENCE: 34

tctttaaatg gctgatcgga cttgttcggc gtacaagtgt acgctattgt gcattcgaaa 60

cttact 66

<210> SEQ ID NO 35
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 35

tcatatgcgc ccattacatc cg 22

<210> SEQ ID NO 36
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 36

tcctaggagg gctaatttag ccctttagtt 30

<210> SEQ ID NO 37
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 37

atagtttagc ggccgcaaat cgagctggat caggatta 38

<210> SEQ ID NO 38
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 38

aggattcaga catcgtgatg taatgaaaca agcaaatcaa gataga 46

<210> SEQ ID NO 39
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

primer

<400> SEQUENCE: 39

cgcggatccg aatcactacg ccactgttcc 30

<210> SEQ ID NO 40
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 40

ttgatttgct tgtttcatta catcacgatg tctgaatcct tg 42

<210> SEQ ID NO 41
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 41

atatgacgtc ggcatccgct tacagaca 28

<210> SEQ ID NO 42
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 42

aattcttaag tcaggagagc gttcaccgac aa 32

<210> SEQ ID NO 43
<211> LENGTH: 71
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 43

taaccggcgt ctgacgactg acttaacgct caggctttat tgtccacttt gtgtaggctg 60

gagctgcttc g 71

<210> SEQ ID NO 44
<211> LENGTH: 75
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 44

catttggggt tgcgatcacg acgaacacgc attttagagg tgaagaattg catatgaata 60

tcctcctttа gttcc 75

<210> SEQ ID NO 45
<211> LENGTH: 20
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 45

cgtccgtggt aatcatttgg 20

<210> SEQ ID NO 46
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 46

tcgcaacctt ttcgttgg 18

<210> SEQ ID NO 47
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 47

catatgtcga tcaacgatca gcgactgac 29

<210> SEQ ID NO 48
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 48

cctaggtcac agcagcccga gcagtc 26

<210> SEQ ID NO 49
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 49

catatgacga tcgaaacgcg 20

<210> SEQ ID NO 50
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 50

cctaggttac agcaatccga gcatct 26

<210> SEQ ID NO 51
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 51

catatgacca gcgatgttca c 21

<210> SEQ ID NO 52
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 52

cctaggtcag atcagaccga actcacg 27

<210> SEQ ID NO 53
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 53

gcgcctcaga tcagcgctgc gaatgatttt caaaaatcgg ctttcaacac tgtaggctgg 60

agctgcttcg 70

<210> SEQ ID NO 54
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 54

ctgccatgct ctacacttcc caaacaacac cagagaagga ccaaaaaatg attccgggga 60

tccgtcgacc 70

<210> SEQ ID NO 55
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 55

gtgctggcga tacgacaaaa ca 22

<210> SEQ ID NO 56
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 56

ccccgccctg ccatgctcta cac 23

<210> SEQ ID NO 57

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<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 57

cacgttattg attctgggta atagcctgag cgccgggtat cg 42

<210> SEQ ID NO 58
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 58

cgatacccgg cgctcaggct attacccaga atcaataacg tg 42

<210> SEQ ID NO 59
<211> LENGTH: 186
<212> TYPE: PRT
<213> ORGANISM: Pectobacterium atrosepticum

<400> SEQUENCE: 59

Met Ala Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr
1 5 10 15

Gln Met Pro Ala Ala Asn Ala Trp Pro Thr Leu Leu Asn Thr Gln Trp
20 25 30

Gln Thr Gln Lys Lys Gly Ile Ala Val Val Asn Ala Ser Ile Ser Gly
35 40 45

Asp Thr Thr Ala Gln Gly Leu Ala Arg Leu Pro Ala Leu Leu Lys Gln
50 55 60

His Gln Pro Arg Trp Val Leu Ile Glu Leu Gly Gly Asn Asp Gly Leu
65 70 75 80

Arg Gly Phe Pro Ala Pro Asn Ile Glu Gln Asp Leu Ala Lys Ile Ile
85 90 95

Thr Leu Val Lys Gln Ala Asn Ala Lys Pro Leu Leu Met Gln Val Arg
100 105 110

Leu Pro Thr Asn Tyr Gly Arg Arg Tyr Thr Glu Ser Phe Ser Asn Ile
115 120 125

Tyr Pro Lys Leu Ala Glu Gln Phe Ala Leu Pro Leu Leu Pro Phe Phe
130 135 140

Met Glu Gln Val Tyr Leu Lys Pro Glu Trp Ile Met Glu Asp Gly Ile
145 150 155 160

His Pro Thr Arg Asp Ala Gln Pro Phe Ile Ala Glu Trp Met Ala Lys
165 170 175

Gln Leu Glu Pro Leu Val Asn His Glu Ser
180 185

<210> SEQ ID NO 60
<211> LENGTH: 561
<212> TYPE: DNA
<213> ORGANISM: Pectobacterium atrosepticum

<400> SEQUENCE: 60

atggctgata cattattaat tctgggtgat agcctcagtg cgggctacca gatgccggcc 60

gctaacgcct ggccaacgct gctgaacacg cagtggcaga cgcagaaaaa gggcatcgcc 120

gtggttaacg ccagcattag cggcgacacc accgcacagg ggctggcgcg acttcctgcc 180

ttactgaaac aacatcagcc gcgttgggtg ttgattgaac tgggcggcaa tgacgggctt 240

cgggggtttc cggcacccaa tatcgagcag gatctggcga aaatcattac gctagtcaaa 300

caggctaacg ctaagcctct gctgatgcag gttcgtttgc caaccaacta tggccgccgc 360

tacaccgagt cattcagcaa catttacccc aaactcgcgg agcagtttgc gcttcctctg 420

ctgcctttct ttatggagca ggtgtatctt aaaccggagt ggatcatgga agatggcatc 480

catccaaccc gtgatgccca accgtttatc gcagaatgga tggcgaagca gctggaaccc 540

ttagttaacc atgagtctta a 561

<210> SEQ ID NO 61
<211> LENGTH: 184
<212> TYPE: PRT
<213> ORGANISM: Photobacterium profundum

<400> SEQUENCE: 61

Met Ala Trp Gly Asn Thr Leu Leu Val Val Gly Asp Ser Leu Ser Ala
1 5 10 15

Gly Tyr Gln Met Arg Ala Glu Gln Ser Trp Pro Val Leu Leu Gln Pro
20 25 30

Ala Leu Lys Gln Gln Gly His Glu Ile Thr Val Val Asn Ala Ser Ile
35 40 45

Ser Gly Asp Thr Thr Gly Asn Gly Leu Ala Arg Leu Pro Thr Leu Leu
50 55 60

Gln Gln His Lys Pro Ala Tyr Val Ile Ile Glu Leu Gly Ala Asn Asp
65 70 75 80

Gly Leu Arg Gly Phe Pro Gln Gly Thr Ile Arg Asn Asn Leu Ser Gln
85 90 95

Met Ile Thr Glu Ile Gln Asn Ala Asp Ala Lys Pro Met Leu Val Gln
100 105 110

Ile Lys Val Pro Pro Asn Tyr Gly Lys Arg Tyr Ser Asp Met Phe Ser
115 120 125

Ser Ile Tyr Pro Gln Leu Ser Lys Glu Leu Ala Thr Pro Leu Leu Pro
130 135 140

Phe Phe Leu Glu Gln Ile Ile Leu Lys Gln Glu Trp Met Met Asn Asp
145 150 155 160

Gly Leu His Pro Lys Ser Asp Ala Gln Pro Trp Ile Ala Glu Tyr Met
165 170 175

Ala Glu Asn Ile Ala Pro Tyr Leu
180

<210> SEQ ID NO 62
<211> LENGTH: 549
<212> TYPE: DNA
<213> ORGANISM: Photobacterium profundum

<400> SEQUENCE: 62

atgggcaaca cattactggt tgtcggtgat agcttgagcg cgggctatca aatgcgggca 60

gaacaaagct ggccggtgtt actgcaaccc gcattaaagc aacaaggtca cgaaatcacc 120

gttgtaaatg ccagtatttc aggcgataca acaggaaacg gcttggctcg attgcctaca 180

ttattacaac aacataaacc agcttacgtc ataattgaac tcggggcgaa tgatggctta 240

cgtggtttcc ctcaaggtac tatacgtaac aatctcagcc aaatgatcac tgaaattcaa 300

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aatgctgatg ccaagccaat gctcgtgcag ataaaagtgc cgcccaatta cggcaaacgc 360

tacagtgata tgttcagttc tatttaccct caactcagta aagagttagc cacaccactg 420

ttacctttct ttttagagca gatcatttta aaacaagaat ggatgatgaa tgacggtttg 480

catcctaaat ctgatgctca gccatggatt gccgaatata tggctgagaa tatcgcgcct 540

tatttataa 549

<210> SEQ ID NO 63
<211> LENGTH: 185
<212> TYPE: PRT
<213> ORGANISM: Photorhabdus luminescens

<400> SEQUENCE: 63

Met Ala Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr
1 5 10 15

His Leu Pro Ile Glu Gln Ser Trp Pro Ala Leu Met Glu Lys Lys Trp
20 25 30

Gln Lys Ser Gly Asn Lys Ile Thr Val Ile Asn Gly Ser Ile Ser Gly
35 40 45

Asn Thr Ala Ala Gln Gly Leu Glu Arg Leu Pro Glu Leu Leu Lys Gln
50 55 60

His Lys Pro Arg Trp Val Leu Ile Glu Leu Gly Ala Asn Asp Gly Leu
65 70 75 80

Arg Gly Phe Pro Pro Gln His Thr Glu Gln Asp Leu Gln Gln Ile Ile
85 90 95

Thr Leu Val Lys Gln Ala Asn Ile Gln Pro Leu Leu Met Gln Ile Arg
100 105 110

Leu Pro Pro Asn Tyr Gly Arg Arg Tyr Thr Glu Ser Phe Ala Lys Ile
115 120 125

Tyr Pro Lys Leu Ala Glu Tyr Asn Gln Ile Pro Leu Leu Pro Phe Tyr
130 135 140

Met Glu Gln Val Ala Ile Lys Pro Glu Trp Val Gln Gln Asp Gly Leu
145 150 155 160

His Pro Asn Leu Ala Ala Gln Pro Phe Ile Ala Asp Trp Met Ser Asp
165 170 175

Thr Leu Ser Ala His Leu Asn Tyr Ser
180 185

<210> SEQ ID NO 64
<211> LENGTH: 558
<212> TYPE: DNA
<213> ORGANISM: Photorhabdus luminescens

<400> SEQUENCE: 64

atggctgata cccttctgat tctcggtgat agccttagtg ccggttacca tctgcctatt 60

gagcagtcat ggcctgcttt gatggaaaaa aagtggcaaa aatccggcaa taaaatcacg 120

gtcatcaacg gcagcatcag cggcaacacc gccgctcagg gccttgagcg gctacctgaa 180

ttacttaaac aacataaacc ccgttgggta ctgatagagc tgggtgccaa cgatggatta 240

cgcggttttc ctccacaaca caccgaacaa gatctacaac agatcattac tttagtgaaa 300

caagctaata ttcagccttt attgatgcag atccgtctac caccaaacta tgggcgccgt 360

tataccgagt cttttgccaa gatttacccc aaactggcag aatataatca aattcccctg 420

ctcccgtttt atatggagca agtcgccatt aaaccggagt gggtgcaaca agatgggtta 480

catcctaatc tggcagccca accatttatc gccgattgga tgtctgacac actatcagca 540

catcttaatt attcttaa 558

<210> SEQ ID NO 65
<211> LENGTH: 182
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas putida

<400> SEQUENCE: 65

Met Ala Gly Thr Leu Leu Val Val Gly Asp Ser Ile Ser Ala Gly Phe
1 5 10 15

Gly Leu Asp Ser Arg Gln Gly Trp Val Ser Leu Leu Gln Ala Arg Leu
20 25 30

Arg Asp Glu Gly Phe Asp Asp Lys Val Val Asn Ala Ser Ile Ser Gly
35 40 45

Asp Thr Ser Ala Gly Gly Gln Ala Arg Leu Pro Ala Leu Leu Ala Ala
50 55 60

His Lys Pro Ser Leu Val Val Leu Glu Leu Gly Gly Asn Asp Gly Leu
65 70 75 80

Arg Gly Gln Pro Pro Ala Gln Leu Gln Gln Asn Leu Ala Ser Met Ile
85 90 95

Glu Arg Ser Arg Gln Ala Gly Ala Lys Val Leu Leu Leu Gly Met Arg
100 105 110

Leu Pro Pro Asn Tyr Gly Val Arg Tyr Thr Thr Ala Phe Ala Lys Val
115 120 125

Tyr Glu Gln Leu Ala Ala Asp Lys Gln Val Pro Leu Val Pro Phe Phe
130 135 140

Leu Glu Gly Val Gly Gly Val Pro Glu Leu Met Gln Ala Asp Gly Ile
145 150 155 160

His Pro Ala Gln Gly Ala Gln Gln Arg Leu Leu Glu Asn Ala Trp Pro
165 170 175

Ala Ile Lys Pro Leu Leu
180

<210> SEQ ID NO 66
<211> LENGTH: 549
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas putida

<400> SEQUENCE: 66

atggcaggaa cactgctggt tgttggcgat agtatcagcg ccggttttgg cctggatagc 60

cgtcagggct gggtgtctct cttgcaggcc cgtctcaggg acgaaggttt tgacgacaaa 120

gtggtcaatg cttcgatcag tggcgatacc agcgcaggtg gccaggcgcg gctgccggcg 180

ctgcttgcag cacataaacc gagcctggtg gtgctggagc tgggcggcaa cgatggcctg 240

cgcgggcagc cgcctgcaca attgcaacaa aatcttgcct cgatgatcga gcgttcgcgt 300

caggcagggg ccaaggtgct gctattgggc atgcgcctgc cgcccaatta tggtgtgcgt 360

tacaccaccg cctttgccaa ggtgtatgaa cagctggcag cggacaaaca ggttcccttg 420

gtgccgtttt tcctcgaagg ggtaggggcc gtacctgaac tgatgcaggc tgatggcatc 480

catccggccc agggggctca gcagcgcctg ctggaaaatg cctggccagc gataaaaccc 540

ttgctgtga 549

<210> SEQ ID NO 67
<211> LENGTH: 182
<212> TYPE: PRT

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<213> ORGANISM: Vibrio harveyi

<400> SEQUENCE: 67

Met Ser Glu Lys Leu Leu Val Leu Gly Asp Ser Leu Ser Ala Gly Tyr
1 5 10 15

Gln Met Pro Ile Glu Glu Ser Trp Pro Ser Leu Leu Pro Gly Ala Leu
20 25 30

Leu Glu His Gly Gln Asp Val Lys Val Val Asn Gly Ser Ile Ser Gly
35 40 45

Asp Thr Thr Gly Asn Gly Leu Ala Arg Leu Pro Ser Leu Leu Glu Gln
50 55 60

His Thr Pro Asp Leu Val Leu Ile Glu Leu Gly Ala Asn Asp Gly Leu
65 70 75 80

Arg Gly Phe Pro Pro Lys Leu Ile Thr Leu Asn Leu Ser Lys Met Ile
85 90 95

Thr Met Ile Lys Asp Ser Gly Ala Asp Val Val Met Met Gln Ile Arg
100 105 110

Val Pro Pro Asn Tyr Gly Lys Arg Tyr Ser Asp Met Phe Tyr Asp Ile
115 120 125

Tyr Pro Lys Leu Ala Glu His Gln Gln Val Ala Leu Met Pro Phe Phe
130 135 140

Leu Glu His Val Ile Ile Lys Pro Glu Trp Met Met Asp Asp Gly Leu
145 150 155 160

His Pro Lys Pro Glu Ala Gln Pro Tyr Ile Ala Asp Phe Val Ala Gln
165 170 175

Glu Leu Val Lys His Leu
180

<210> SEQ ID NO 68
<211> LENGTH: 549
<212> TYPE: DNA
<213> ORGANISM: Vibrio harveyi

<400> SEQUENCE: 68

atgagcgaaa agctacttgt tttgggcgac agcctgagcg ctggttatca aatgcctata 60

gaggagagtt ggcctagctt actcccaggc gcgttattag aacatggcca agatgtaaaa 120

gttgtaaacg gtagcatctc tggtgacacc acaggcaatg gccttgcacg gttaccttct 180

ctccttgagc aacacacgcc cgatttggta ctgattgagc ttggcgctaa cgatggccta 240

cgcggtttcc cacctaaact tattacgtta aacctatcga aaatgattac catgatcaaa 300

gattctggtg cggatgtcgt catgatgcaa atccgcgtcc caccaaatta tggtaagcgt 360

tacagcgata tgttctacga catctaccct aaactggcag aacatcagca agtagcgcta 420

atgccgttct tcttagagca tgtcatcatt aaaccagaat ggatgatgga cgatggcttg 480

cacccaaaac cggaagctca accctacatt gctgactttg tcgctcaaga attggttaaa 540

catctctaa 549

<210> SEQ ID NO 69
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 69

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aaaaacagca acaatgtgag ctttgttgta attatattgt aaacatattg attccgggga 60

tccgtcgacc 70

<210> SEQ ID NO 70
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 70

aaacggagcc tttcgggctc cgttattcat ttacgcggct tcaactttcc tgtaggctgg 60

agctgcttc 69

<210> SEQ ID NO 71
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 71

cgggcaggtg ctatgaccag gac 23

<210> SEQ ID NO 72
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 72

cgcggcgttg accggcagcc tgg 23

<210> SEQ ID NO 73
<211> LENGTH: 182
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 73

Ala Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg
1 5 10 15

Met Ser Ala Ser Ala Ala Trp Pro Ala Leu Leu Asn Asp Lys Trp Gln
20 25 30

Ser Lys Thr Ser Val Val Asn Ala Ser Ile Ser Gly Asp Thr Ser Gln
35 40 45

Gln Gly Leu Ala Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro Arg
50 55 60

Trp Val Leu Val Glu Leu Gly Gly Asn Asp Gly Leu Arg Gly Phe Gln
65 70 75 80

Pro Gln Gln Thr Glu Gln Thr Leu Arg Gln Ile Leu Gln Asp Val Lys
85 90 95

Ala Ala Asn Ala Glu Pro Leu Leu Met Gln Ile Arg Leu Pro Ala Asn
100 105 110

Tyr Gly Arg Arg Tyr Asn Glu Ala Phe Ser Ala Ile Tyr Pro Lys Leu
115 120 125

Ala Lys Glu Phe Asp Val Pro Leu Leu Pro Phe Phe Met Glu Glu Val
130 135 140

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Tyr Leu Lys Pro Gln Trp Met Gln Asp Asp Gly Ile His Pro Asn Arg
145                 150                 155                 160

Asp Ala Gln Pro Phe Ile Ala Asp Trp Met Ala Lys Gln Leu Gln Pro
                165                 170                 175

Leu Val Asn His Asp Ser
            180


<210> SEQ ID NO 74
<211> LENGTH: 190
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      1J00_A polypeptide
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: Chemically modified-Ser

<400> SEQUENCE: 74

Ala Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg
1               5                   10                  15

Met Ser Ala Ser Ala Ala Trp Pro Ala Leu Leu Asn Asp Lys Trp Gln
            20                  25                  30

Ser Lys Thr Ser Val Val Asn Ala Ser Ile Ser Gly Asp Thr Ser Gln
        35                  40                  45

Gln Gly Leu Ala Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro Arg
    50                  55                  60

Trp Val Leu Val Glu Leu Gly Gly Asn Asp Gly Leu Arg Gly Phe Gln
65                  70                  75                  80

Pro Gln Gln Thr Glu Gln Thr Leu Arg Gln Ile Leu Gln Asp Val Lys
                85                  90                  95

Ala Ala Asn Ala Glu Pro Leu Leu Met Gln Ile Arg Leu Pro Ala Asn
            100                 105                 110

Tyr Gly Arg Arg Tyr Asn Glu Ala Phe Ser Ala Ile Tyr Pro Lys Leu
        115                 120                 125

Ala Lys Glu Phe Asp Val Pro Leu Leu Pro Phe Phe Met Glu Glu Val
    130                 135                 140

Tyr Leu Lys Pro Gln Trp Met Gln Asp Asp Gly Ile His Pro Asn Arg
145                 150                 155                 160

Asp Ala Gln Pro Phe Ile Ala Asp Trp Met Ala Lys Gln Leu Gln Pro
                165                 170                 175

Leu Val Asn His Asp Ser Leu Glu His His His His His His
            180                 185                 190


<210> SEQ ID NO 75
<211> LENGTH: 190
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      1JRL_A polypeptide

<400> SEQUENCE: 75

Ala Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg
1               5                   10                  15

Met Ser Ala Ser Ala Ala Trp Pro Ala Leu Leu Asn Asp Lys Trp Gln
            20                  25                  30

Ser Lys Thr Ser Val Val Asn Ala Ser Ile Ser Gly Asp Thr Ser Gln
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        35                  40                  45

Gln Gly Leu Ala Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro Arg
    50                  55                  60

Trp Val Leu Val Glu Leu Gly Gly Asn Asp Gly Leu Arg Gly Phe Gln
65                  70                  75                  80

Pro Gln Gln Thr Glu Gln Thr Leu Arg Gln Ile Leu Gln Asp Val Lys
                85                  90                  95

Ala Ala Asn Ala Glu Pro Leu Leu Met Gln Ile Arg Pro Pro Ala Asn
            100                 105                 110

Tyr Gly Arg Arg Tyr Asn Glu Ala Phe Ser Ala Ile Tyr Pro Lys Leu
        115                 120                 125

Ala Lys Glu Phe Asp Val Pro Leu Leu Pro Phe Phe Met Glu Glu Val
    130                 135                 140

Tyr Leu Lys Pro Gln Trp Met Gln Asp Asp Gly Ile His Pro Asn Arg
145                 150                 155                 160

Asp Ala Gln Pro Phe Ile Ala Asp Trp Met Ala Lys Gln Leu Gln Pro
                165                 170                 175

Leu Val Asn His Asp Ser Leu Glu His His His His His His
            180                 185                 190


<210> SEQ ID NO 76
<211> LENGTH: 208
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 76

Met Met Asn Phe Asn Asn Val Phe Arg Trp His Leu Pro Phe Leu Phe
1               5                   10                  15

Leu Val Leu Leu Thr Phe Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile
            20                  25                  30

Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ser Ala Ser Ala Ala
        35                  40                  45

Trp Pro Ala Leu Leu Asn Asp Lys Trp Gln Ser Lys Thr Ser Val Val
    50                  55                  60

Asn Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu
65                  70                  75                  80

Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu Val Glu Leu
                85                  90                  95

Gly Gly Asn Asp Gly Leu Arg Gly Phe Gln Pro Gln Gln Thr Glu Gln
            100                 105                 110

Thr Leu Arg Gln Ile Leu Gln Asp Val Lys Ala Ala Asn Ala Glu Pro
        115                 120                 125

Leu Leu Met Gln Ile Arg Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn
    130                 135                 140

Glu Ala Phe Ser Ala Ile Tyr Pro Lys Leu Ala Lys Glu Phe Asp Val
145                 150                 155                 160

Pro Leu Leu Pro Phe Leu Met Glu Glu Val Tyr Leu Lys Pro Gln Trp
                165                 170                 175

Met Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile
            180                 185                 190

Ala Asp Trp Met Ala Lys Gln Leu Gln Pro Leu Val Asn His Asp Ser
        195                 200                 205


<210> SEQ ID NO 77
<211> LENGTH: 208
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<212> TYPE: PRT
<213> ORGANISM: Shigella boydii

<400> SEQUENCE: 77

Met Met Asn Phe Asn Asn Val Phe Arg Trp His Leu Pro Phe Leu Phe
1 5 10 15

Leu Val Leu Leu Thr Phe Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile
20 25 30

Leu Gly Asn Ser Leu Ser Ala Gly Tyr Arg Met Ser Ala Ser Ala Ala
35 40 45

Trp Pro Ala Leu Leu Asn Asp Lys Trp Gln Ser Lys Thr Ser Val Val
50 55 60

Asn Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu
65 70 75 80

Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu Val Glu Leu
85 90 95

Gly Gly Asn Asp Gly Leu Arg Gly Phe Gln Pro Gln Gln Thr Glu Gln
100 105 110

Thr Leu Arg Gln Ile Leu Gln Asp Val Lys Ala Ala Asn Ala Glu Pro
115 120 125

Leu Leu Met Gln Ile Arg Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn
130 135 140

Glu Ala Phe Ser Ala Ile Tyr Pro Lys Leu Ala Lys Glu Phe Asp Val
145 150 155 160

Pro Leu Leu Pro Phe Phe Met Glu Glu Val Tyr Leu Lys Pro Gln Trp
165 170 175

Met Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile
180 185 190

Ala Asp Trp Met Ala Lys Gln Leu Gln Pro Leu Val Asn His Asp Ser
195 200 205

<210> SEQ ID NO 78
<211> LENGTH: 207
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 78

Met Asn Phe Asn Asn Val Phe Arg Trp His Leu Pro Phe Leu Phe Leu
1 5 10 15

Val Leu Leu Thr Phe Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile Leu
20 25 30

Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ser Ala Ser Ala Ala Trp
35 40 45

Pro Ala Leu Leu Asn Asp Lys Trp Gln Ser Lys Thr Ser Val Val Asn
50 55 60

Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu Pro
65 70 75 80

Ala Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu Val Glu Leu Gly
85 90 95

Gly Asn Asp Gly Leu Arg Gly Phe Gln Pro Gln Gln Thr Glu Gln Thr
100 105 110

Leu Arg Gln Ile Leu Gln Asp Val Lys Ala Ala Asn Ala Glu Pro Leu
115 120 125

Leu Met Gln Ile Arg Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn Glu
130 135 140

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Ala Phe Ser Ala Ile Tyr Pro Lys Leu Ala Lys Glu Phe Asp Val Pro
145                 150                 155                 160

Leu Leu Pro Phe Leu Met Glu Glu Val Tyr Leu Lys Pro Gln Trp Met
                165                 170                 175

Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile Ala
            180                 185                 190

Asp Trp Met Ala Lys Gln Leu Gln Pro Leu Val Asn His Asp Ser
        195                 200                 205


<210> SEQ ID NO 79
<211> LENGTH: 207
<212> TYPE: PRT
<213> ORGANISM: Escherichia albertii

<400> SEQUENCE: 79

Met Asn Phe Asn Asn Val Phe Arg Trp His Leu Pro Phe Leu Phe Leu
1               5                   10                  15

Val Leu Leu Thr Phe Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile Leu
            20                  25                  30

Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ser Ala Ser Ala Ala Trp
        35                  40                  45

Pro Ala Leu Leu Asn Asp Lys Trp Gln Ser Lys Thr Ser Val Val Asn
    50                  55                  60

Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu Pro
65                  70                  75                  80

Ala Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu Val Glu Leu Gly
                85                  90                  95

Gly Asn Asp Gly Leu Arg Gly Phe Gln Pro Gln Gln Thr Glu Gln Thr
            100                 105                 110

Leu Arg Gln Ile Leu Gln Asp Val Lys Ala Ala Asn Ala Glu Pro Leu
        115                 120                 125

Leu Met Gln Ile Arg Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn Glu
    130                 135                 140

Ala Phe Ser Ala Ile Tyr Pro Lys Leu Ala Lys Glu Phe Asp Ile Pro
145                 150                 155                 160

Leu Leu Pro Phe Phe Met Glu Glu Val Tyr Leu Lys Pro Gln Trp Met
                165                 170                 175

Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile Ala
            180                 185                 190

Asp Trp Met Ala Lys Gln Leu Gln Pro Leu Val Asn His Asp Ser
        195                 200                 205


<210> SEQ ID NO 80
<211> LENGTH: 197
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 80

Met Pro Phe Leu Phe Leu Val Leu Leu Thr Phe Arg Ala Ala Ala Ala
1               5                   10                  15

Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met
            20                  25                  30

Ser Ala Ser Ala Ala Trp Pro Ala Leu Leu Asn Asp Lys Trp Gln Ser
        35                  40                  45

Lys Thr Ser Val Val Asn Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln
    50                  55                  60
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Gly Leu Ala Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp
65                  70                  75                  80

Val Leu Val Glu Leu Gly Gly Asn Asp Gly Leu Arg Gly Phe Gln Pro
                85                  90                  95

Gln Gln Thr Glu Gln Thr Leu Arg Gln Ile Leu Gln Asp Val Lys Ala
            100                 105                 110

Ala Asn Ala Glu Pro Leu Leu Met Gln Ile Arg Leu Pro Ala Asn Tyr
        115                 120                 125

Gly Arg Arg Tyr Asn Glu Ala Phe Ser Ala Ile Tyr Pro Lys Leu Ala
    130                 135                 140

Lys Glu Phe Asp Val Pro Leu Leu Pro Phe Leu Met Glu Glu Val Tyr
145                 150                 155                 160

Leu Lys Pro Gln Trp Met Gln Asp Asp Gly Ile His Pro Asn Arg Asp
                165                 170                 175

Ala Gln Pro Phe Ile Ala Asp Trp Met Ala Lys Gln Leu Gln Pro Leu
            180                 185                 190

Val Asn His Asp Ser
        195


<210> SEQ ID NO 81
<211> LENGTH: 208
<212> TYPE: PRT
<213> ORGANISM: Shigella dysenteriae

<400> SEQUENCE: 81

Met Met Asn Phe Asn Asn Val Phe Arg Trp His Leu Pro Phe Leu Phe
1               5                   10                  15

Leu Val Leu Leu Thr Phe Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile
            20                  25                  30

Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ser Ala Ser Ala Ala
        35                  40                  45

Trp Pro Ala Leu Leu Asn Asp Lys Trp Gln Ser Lys Thr Ser Val Val
    50                  55                  60

Asn Ala Ser Ile Ser Ser Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu
65                  70                  75                  80

Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu Val Glu Leu
                85                  90                  95

Gly Gly Asn Asp Gly Leu Arg Gly Phe Gln Pro Gln Gln Thr Glu Gln
            100                 105                 110

Thr Leu Arg Gln Ile Leu Gln Asp Val Lys Ala Asp Asn Ala Glu Pro
        115                 120                 125

Leu Leu Met Gln Ile Arg Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn
    130                 135                 140

Glu Ala Phe Ser Ala Ile Tyr Pro Lys Leu Ala Lys Glu Phe Asp Val
145                 150                 155                 160

Pro Leu Leu Pro Phe Phe Met Glu Glu Val Tyr Leu Lys Pro Gln Trp
                165                 170                 175

Met Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile
            180                 185                 190

Ala Asp Trp Met Ala Lys Gln Leu Gln Pro Leu Val Asn His Asp Ser
        195                 200                 205


<210> SEQ ID NO 82
<211> LENGTH: 197
<212> TYPE: PRT
<213> ORGANISM: Citrobacter koseri
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<400> SEQUENCE: 82

Met Pro Phe Leu Phe Leu Val Leu Leu Thr Phe Arg Ala Ala Ala Ala
1 5 10 15

Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met
20 25 30

Ser Ala Ser Ala Ala Trp Pro Ala Leu Leu Asn Asp Lys Trp Gln Asp
35 40 45

Lys Thr Pro Val Ile Asn Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln
50 55 60

Gly Leu Ala Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp
65 70 75 80

Val Leu Val Glu Leu Gly Gly Asn Asp Gly Leu Arg Gly Phe Gln Pro
85 90 95

Gln Gln Thr Glu Gln Thr Leu Arg Lys Ile Leu Leu Asp Val Lys Ala
100 105 110

Ala Asn Ala Glu Pro Leu Leu Met Gln Ile Arg Leu Pro Ala Asn Tyr
115 120 125

Gly Arg Arg Tyr Asn Glu Thr Phe Ser Ala Ile Tyr Pro Arg Leu Ala
130 135 140

Lys Glu Phe Asp Ile Pro Leu Leu Pro Phe Phe Met Glu Glu Val Tyr
145 150 155 160

Leu Lys Pro Gln Trp Met Gln Asp Asp Gly Ile His Pro Asn Arg Asp
165 170 175

Ala Gln Pro Phe Ile Ala Asp Trp Met Ala Gln Gln Leu Thr Pro Leu
180 185 190

Val Asn His Asp Ser
195

<210> SEQ ID NO 83
<211> LENGTH: 218
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown: Marine metagenome polypeptide

<400> SEQUENCE: 83

Val Leu Pro Leu Thr Asp Gly Leu Leu Lys Met Met Asn Phe Asn Asn
1 5 10 15

Val Phe Arg Trp His Leu Pro Ile Leu Phe Leu Ile Leu Leu Phe Thr Cys
20 25 30

Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser
35 40 45

Ala Gly Tyr Arg Met Ser Ala Ser Ala Ala Trp Pro Ala Leu Leu Asn
50 55 60

Asp Lys Trp Gln Ser Lys Thr Thr Val Val Asn Ala Ser Ile Ser Gly
65 70 75 80

Asp Thr Ser Gln Gln Ala Leu Ala Arg Leu Pro Ala Leu Leu Lys Gln
85 90 95

His Gln Pro Arg Trp Val Leu Val Glu Leu Gly Gly Asn Asp Gly Leu
100 105 110

Arg Gly Phe Ala Pro Gln Gln Thr Glu Gln Thr Leu Arg Thr Ile Val
115 120 125

Gln Asp Val Lys Thr Ala Asn Ala Glu Pro Leu Leu Met Gln Ile Arg
130 135 140

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Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn Glu Thr Phe Ser Ala Leu
145                 150                 155                 160

Tyr Pro Lys Leu Ala Lys Glu Phe Asp Ile Pro Leu Leu Pro Phe Phe
                165                 170                 175

Met Glu Glu Val Tyr Leu Lys Pro Gln Trp Met Gln Asp Asp Gly Ile
            180                 185                 190

His Pro Asn Arg Asp Ala Gln Pro Phe Ile Ala Asp Trp Met Ala Lys
        195                 200                 205

Gln Leu Ser Pro Leu Val Lys His Glu Ser
    210                 215


<210> SEQ ID NO 84
<211> LENGTH: 295
<212> TYPE: PRT
<213> ORGANISM: Enterobacter cloacae

<400> SEQUENCE: 84

Leu Lys Asp Lys Pro Asp Met Pro Gly Ser Gln Arg Gly Ala Gly Leu
1               5                   10                  15

Phe Ile Lys Arg Val Glu Gly Leu Ala Asp Gln Val His Phe Pro Thr
            20                  25                  30

Ala Ala Ile Val Gln Thr Gly Glu Asn Gly Gln Gln Arg Gly Leu Thr
        35                  40                  45

Gly Thr Gly Phe Thr Asn Gln Gly Asp Gly Phe Gly Thr Phe Asp Asn
    50                  55                  60

Glu Phe Asn Ser Gly Glu Asp Gly Lys Leu Val Phe Pro Leu Thr Asp
65                  70                  75                  80

Arg Leu Leu Lys Thr Met Asn Phe Asn Asn Val Phe Arg Trp His Leu
                85                  90                  95

Pro Phe Leu Phe Leu Met Leu Met Thr Phe Arg Ala Ala Ala Ala Asp
            100                 105                 110

Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ala
        115                 120                 125

Ala Ser Ala Ala Trp Pro Ala Leu Leu Asn Asp Lys Trp Gln Ser Arg
    130                 135                 140

Ala Ser Val Val Asn Gly Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly
145                 150                 155                 160

Leu Ser Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp Val
                165                 170                 175

Leu Val Glu Leu Gly Gly Asn Asp Gly Leu Arg Gly Phe Gln Pro Gln
            180                 185                 190

Gln Thr Glu Gln Thr Leu Arg Thr Ile Leu Gln Thr Ile Lys Ala Ala
        195                 200                 205

Asp Ala Gln Pro Leu Leu Met Gln Ile Arg Leu Pro Ala Asn Tyr Gly
    210                 215                 220

Arg Arg Tyr Asn Glu Ala Phe Ser Ala Ile Tyr Pro Lys Leu Ala Lys
225                 230                 235                 240

Glu Phe Asp Ile Pro Leu Leu Pro Phe Phe Met Glu Glu Val Tyr Leu
                245                 250                 255

Lys Pro Gln Trp Met Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala
            260                 265                 270

Gln Pro Phe Ile Ala Asp Trp Met Ala Thr Arg Leu Ala Pro Leu Val
        275                 280                 285

Asn His Asp Ser Ser Asn Ser
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290 295

<210> SEQ ID NO 85
<211> LENGTH: 197
<212> TYPE: PRT
<213> ORGANISM: Enterobacter cancerogenus

<400> SEQUENCE: 85

Met Pro Phe Leu Phe Leu Ile Leu Leu Thr Phe Arg Ala Ala Ala Ala
1 5 10 15

Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met
20 25 30

Ala Ala Ser Ala Ala Trp Pro Ala Leu Leu Asn Asp Lys Trp Gln Ser
35 40 45

Gln Thr Thr Val Val Asn Gly Ser Ile Ser Gly Asp Thr Ser Gln Gln
50 55 60

Gly Leu Ser Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp
65 70 75 80

Val Leu Val Glu Leu Gly Gly Asn Asp Gly Leu Arg Gly Phe Gln Pro
85 90 95

Gln Gln Thr Glu His Thr Leu Arg Thr Ile Leu Gln Glu Ile Lys Ala
100 105 110

Ala Asn Ala Gln Pro Leu Leu Met Gln Ile Arg Leu Pro Ala Asn Tyr
115 120 125

Gly Arg Arg Tyr Asn Glu Ala Phe Ser Ala Ile Tyr Pro Lys Leu Ala
130 135 140

Lys Glu Phe Asp Ile Pro Leu Leu Pro Phe Phe Met Glu Glu Val Tyr
145 150 155 160

Leu Lys Pro Gln Trp Met Gln Asp Asp Gly Ile His Pro Asn Arg Asp
165 170 175

Ala Gln Pro Phe Ile Ala Asp Trp Met Ala Thr Arg Leu Ala Pro Leu
180 185 190

Val Lys His Asp Ser
195

<210> SEQ ID NO 86
<211> LENGTH: 467
<212> TYPE: PRT
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 86

Gly Leu Ser Pro Ser Asp Arg Leu Ser Thr Pro Gly Pro Ala Arg Arg
1 5 10 15

Pro Arg Arg Gly Leu Thr Pro Ala Arg Arg Ser Ala Ala Thr Ala Ser
20 25 30

Ala Ile Arg Ala Arg Thr Ser Gly Arg Ser Cys Phe Leu Pro Gln Leu
35 40 45

Ala Ile Arg Gln Ala Gln Thr Ala Ile Ala Ala Arg Arg Gln Gln Arg
50 55 60

Ile Val Ser Asp Glu Asp Gln Gly Gly Ala Val Phe Ala Ile Lys Arg
65 70 75 80

Glu Gln Gln Ile Gly Asn Phe Val Pro Gly Leu Ala Ile Glu Val Ala
85 90 95

Gly Gly Leu Ile Gly Glu Gln Asn Gly Arg Ala Pro Val Lys Gly Pro
100 105 110

Gly Gln Arg His Pro Leu Leu Phe Ala Ala Gly Glu Leu Arg Arg Gln

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        115                 120                 125

Val Val Gln Ala Phe Ala Lys Ser Gln Leu Leu Lys Gln Arg Ala Gly
    130                 135                 140

Ile Ala Pro Ala Leu Ala Ile Ala Gly Ala Ala Gln Gln Arg Arg Gln
145                 150                 155                 160

Leu Asp Val Leu Gln Gly Val Glu Arg Arg Asp Gln His Lys Arg Leu
                165                 170                 175

Lys Asn Lys Thr Asn Val Leu Arg Pro Gln Arg Arg Pro Arg Leu Phe
            180                 185                 190

Ile His Pro Val Gln Arg Phe Ala Gln His Arg Tyr Phe Pro Ala Ala
        195                 200                 205

Ala Ile Val Glu Ala Gly Glu Asp Arg Gln Gln Gly Arg Phe Thr Gly
    210                 215                 220

Thr Arg Leu Ala Asp Gln Gly Asp Gly Leu Pro Arg Phe Asp Asn Gln
225                 230                 235                 240

Leu Asn Ser Gly Lys Asp Gly Glu Leu Met Leu Pro Leu Thr Asp Gly
                245                 250                 255

Leu Leu Lys Met Met Asn Phe Lys Tyr Val Phe Arg Trp His Val Pro
            260                 265                 270

Phe Leu Leu Leu Phe Leu Phe Thr Cys Arg Ala Met Ala Ala Asp Thr
        275                 280                 285

Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ala Ala
    290                 295                 300

Asn Ala Ala Trp Pro Ala Leu Leu Asn Glu Gln Trp Gln Ala Lys Thr
305                 310                 315                 320

Pro Val Val Asn Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu
                325                 330                 335

Ala Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu
            340                 345                 350

Val Glu Leu Gly Gly Asn Asp Gly Leu Arg Gly Phe Pro Pro Gln Gln
        355                 360                 365

Thr Glu Gln Thr Leu Arg Thr Ile Ile Lys Asp Ile Lys Ala Ala Asn
    370                 375                 380

Ala Glu Pro Leu Leu Met Gln Ile His Leu Pro Ala Asn Tyr Gly Arg
385                 390                 395                 400

Arg Tyr Asn Glu Ala Phe Gly Ala Ile Tyr Pro Ala Leu Ala Lys Glu
                405                 410                 415

Phe Ala Ile Pro Leu Leu Pro Phe Phe Met Glu Glu Val Tyr Leu Lys
            420                 425                 430

Pro Gln Trp Met Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln
        435                 440                 445

Pro Phe Ile Ala Asp Trp Met Ala Lys Arg Leu Ala Pro Leu Val Asn
    450                 455                 460

His Asp Ser
465


<210> SEQ ID NO 87
<211> LENGTH: 208
<212> TYPE: PRT
<213> ORGANISM: Enterobacter sp.

<400> SEQUENCE: 87

Met Met Asn Cys Asn Asn Val Phe Arg Trp His Leu Pro Phe Leu Phe
1               5                   10                  15
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Leu Ile Leu Met Thr Phe Arg Ala Ala Ala Asp Thr Leu Leu Val
            20                  25                  30

Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ala Ala Thr Ala Ala
        35                  40                  45

Trp Pro Ala Leu Leu Asn Asp Lys Trp Gln Thr Lys Thr Pro Val Leu
    50                  55                  60

Asn Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu
65                  70                  75                  80

Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu Val Glu Leu
                85                  90                  95

Gly Gly Asn Asp Gly Leu Arg Gly Phe Gln Pro Gln Gln Thr Glu Gln
            100                 105                 110

Thr Leu Arg Lys Ile Ile Gln Asp Ile Gln Ala Ala Asn Ala Gln Pro
        115                 120                 125

Leu Leu Met Gln Ile Arg Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn
    130                 135                 140

Glu Ser Phe Ser Ala Ile Tyr Pro Lys Leu Ala Lys Glu Phe Asp Ile
145                 150                 155                 160

Pro Leu Leu Pro Phe Phe Met Glu Glu Val Tyr Leu Lys Pro Gln Trp
                165                 170                 175

Met Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile
            180                 185                 190

Ala Asp Trp Met Ala Thr Arg Leu Ala Pro Leu Val Lys His Asp Ser
        195                 200                 205


<210> SEQ ID NO 88
<211> LENGTH: 197
<212> TYPE: PRT
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 88

Met Pro Phe Leu Leu Leu Phe Leu Phe Thr Cys Arg Ala Met Ala Ala
1               5                   10                  15

Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met
            20                  25                  30

Ala Ala Asn Ala Ala Trp Pro Ala Leu Leu Asn Glu Gln Trp Gln Ala
        35                  40                  45

Lys Thr Pro Val Val Asn Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln
    50                  55                  60

Gly Leu Ala Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp
65                  70                  75                  80

Val Leu Val Glu Leu Gly Gly Asn Asp Gly Leu Arg Gly Phe Pro Pro
                85                  90                  95

Gln Gln Thr Glu Gln Thr Leu Arg Thr Ile Ile Lys Asp Ile Lys Ala
            100                 105                 110

Ala Asn Ala Glu Pro Leu Leu Met Gln Ile His Leu Pro Ala Asn Tyr
        115                 120                 125

Gly Arg Arg Tyr Asn Glu Ala Phe Gly Ala Ile Tyr Pro Ala Leu Ala
    130                 135                 140

Lys Glu Phe Ala Ile Pro Leu Leu Pro Phe Phe Met Glu Glu Val Tyr
145                 150                 155                 160

Leu Lys Pro Gln Trp Met Gln Asp Asp Gly Ile His Pro Asn Arg Asp
                165                 170                 175

Ala Gln Pro Phe Ile Ala Asp Trp Met Ala Lys Arg Leu Ala Pro Leu
            180                 185                 190
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Val Asn His Asp Ser
        195


<210> SEQ ID NO 89
<211> LENGTH: 207
<212> TYPE: PRT
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 89

Met Asn Phe Lys Tyr Val Phe Arg Trp His Val Pro Phe Leu Phe Leu
1               5                   10                  15

Phe Leu Phe Thr Cys Arg Ala Met Ala Ala Asp Thr Leu Leu Ile Leu
            20                  25                  30

Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ala Ala Asn Ala Ala Trp
        35                  40                  45

Pro Ala Leu Leu Asn Glu Lys Trp Gln Ala Lys Thr Pro Val Val Asn
    50                  55                  60

Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu Pro
65                  70                  75                  80

Ala Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu Val Glu Leu Gly
                85                  90                  95

Gly Asn Asp Gly Leu Arg Gly Phe Pro Pro Gln Gln Thr Glu Gln Thr
            100                 105                 110

Leu Arg Thr Ile Ile Lys Asp Ile Lys Ala Ala Asn Ala Glu Pro Leu
        115                 120                 125

Leu Met Gln Ile His Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn Glu
    130                 135                 140

Ala Phe Gly Ala Ile Tyr Pro Ala Leu Ala Lys Glu Phe Asp Ile Pro
145                 150                 155                 160

Leu Leu Pro Phe Phe Met Glu Glu Val Tyr Leu Lys Pro Gln Trp Met
                165                 170                 175

Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile Ala
            180                 185                 190

Asp Trp Met Ala Asn Arg Leu Ala Pro Leu Val Asn His Asp Ser
        195                 200                 205


<210> SEQ ID NO 90
<211> LENGTH: 204
<212> TYPE: PRT
<213> ORGANISM: Salmonella enterica

<400> SEQUENCE: 90

Met Asn Phe Asn Thr Val Phe Arg Trp His Leu Pro Phe Leu Phe Leu
1               5                   10                  15

Ile Leu Leu Thr Phe Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile Leu
            20                  25                  30

Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Thr Ala Ser Ala Ala Trp
        35                  40                  45

Pro Ser Leu Leu Asn Asp Lys Trp Gln Asn Lys Thr Ser Val Val Asn
    50                  55                  60

Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu Pro
65                  70                  75                  80

Ala Leu Leu Gln Gln His His Pro Arg Trp Val Val Val Glu Leu Gly
                85                  90                  95

Gly Asn Asp Gly Leu Arg Gly Phe Ala Pro Ala Gln Thr Glu Gln Thr
            100                 105                 110
```

```
Leu Arg Lys Ile Ile Gln Thr Val Lys Ala Ala Asp Ala Gln Pro Leu
        115                 120                 125

Leu Met Gln Ile His Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn Glu
    130                 135                 140

Ser Phe Ser Ala Ile Tyr Pro Lys Leu Ala Lys Glu Phe Asp Ile Pro
145                 150                 155                 160

Leu Leu Pro Phe Phe Met Glu Glu Val Tyr Leu Lys Pro Gln Trp Met
                165                 170                 175

Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile Ala
            180                 185                 190

Asp Trp Met Ala Lys Gln Leu Thr Pro Phe Leu Ser
        195                 200


<210> SEQ ID NO 91
<211> LENGTH: 204
<212> TYPE: PRT
<213> ORGANISM: Salmonella typhimurium

<400> SEQUENCE: 91

Met Asn Phe Asn Thr Val Phe Arg Trp His Leu Pro Phe Leu Phe Leu
1               5                   10                  15

Ile Leu Leu Thr Phe Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile Leu
            20                  25                  30

Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ala Ala Ser Ala Ala Trp
        35                  40                  45

Pro Ser Leu Leu Asn Asp Lys Trp Gln Asn Lys Thr Ser Val Val Asn
    50                  55                  60

Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu Pro
65                  70                  75                  80

Ala Leu Leu Gln Gln His His Pro Arg Trp Val Val Val Glu Leu Gly
                85                  90                  95

Gly Asn Asp Gly Leu Arg Gly Phe Ala Pro Ala Gln Thr Glu Gln Thr
            100                 105                 110

Leu Arg Lys Ile Ile Gln Thr Val Lys Ala Ala Asp Ala Gln Pro Leu
        115                 120                 125

Leu Met Gln Ile His Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn Glu
    130                 135                 140

Ser Phe Ser Ala Ile Tyr Pro Lys Leu Ala Lys Glu Phe Asp Ile Pro
145                 150                 155                 160

Leu Leu Pro Phe Phe Met Glu Glu Val Tyr Leu Lys Pro Gln Trp Met
                165                 170                 175

Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile Ala
            180                 185                 190

Asp Trp Met Ala Lys Gln Leu Thr Pro Phe Leu Ser
        195                 200


<210> SEQ ID NO 92
<211> LENGTH: 204
<212> TYPE: PRT
<213> ORGANISM: Salmonella enterica

<400> SEQUENCE: 92

Met Asn Phe Asn Thr Val Phe Arg Trp His Leu Pro Phe Leu Phe Leu
1               5                   10                  15

Ile Leu Leu Thr Phe Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile Leu
            20                  25                  30
```

```
Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ala Ala Ser Ala Ala Trp
        35                  40                  45

Pro Ser Leu Leu Asn Asp Lys Trp Gln Asn Lys Thr Ser Val Val Asn
    50                  55                  60

Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu Pro
65                  70                  75                  80

Ala Leu Leu Gln Gln His His Pro Arg Trp Val Val Val Glu Leu Gly
                85                  90                  95

Gly Asn Asp Gly Leu Arg Gly Phe Ala Pro Ala Gln Thr Glu Gln Thr
            100                 105                 110

Leu Arg Lys Ile Ile Gln Thr Val Lys Ala Ala Asp Ala Gln Pro Leu
        115                 120                 125

Leu Met Gln Ile His Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn Glu
    130                 135                 140

Ser Phe Ser Ala Ile Tyr Pro Lys Leu Ala Lys Glu Phe Asp Ile Pro
145                 150                 155                 160

Leu Leu Pro Phe Phe Met Glu Glu Ile Tyr Leu Lys Pro Gln Trp Met
                165                 170                 175

Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile Ala
            180                 185                 190

Asp Trp Met Ala Lys Gln Leu Thr Pro Phe Leu Ser
        195                 200


<210> SEQ ID NO 93
<211> LENGTH: 215
<212> TYPE: PRT
<213> ORGANISM: Salmonella enterica

<400> SEQUENCE: 93

Met Leu Thr Leu Thr Asp Gly Leu Pro Glu Thr Met Asn Phe Asn Thr
1               5                   10                  15

Val Phe Arg Trp His Leu Pro Phe Leu Phe Leu Ile Leu Leu Thr Phe
            20                  25                  30

Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser
        35                  40                  45

Ala Gly Tyr Arg Met Ala Ala Ser Ala Ala Trp Pro Ser Leu Leu Asn
    50                  55                  60

Asp Lys Trp Gln Asn Lys Thr Ser Val Val Asn Ala Ser Ile Ser Gly
65                  70                  75                  80

Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu Pro Ala Leu Leu Gln Gln
                85                  90                  95

His His Pro Arg Trp Val Val Val Glu Leu Gly Gly Asn Asp Gly Leu
            100                 105                 110

Arg Gly Phe Ala Pro Ala Gln Thr Glu Gln Thr Leu Arg Lys Ile Ile
        115                 120                 125

Gln Thr Val Lys Ala Ala Asp Ala Gln Pro Leu Leu Met Gln Ile His
    130                 135                 140

Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn Glu Ser Phe Ser Ala Ile
145                 150                 155                 160

Tyr Pro Lys Leu Ala Lys Lys Phe Asp Ile Pro Leu Leu Pro Phe Phe
                165                 170                 175

Met Glu Glu Val Tyr Leu Lys Pro Gln Trp Met Gln Asp Asp Gly Ile
            180                 185                 190

His Pro Asn Arg Asp Ala Gln Pro Phe Ile Ala Asp Trp Met Ala Lys
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        195                 200                 205

Gln Leu Thr Pro Phe Leu Ser
    210                 215


<210> SEQ ID NO 94
<211> LENGTH: 204
<212> TYPE: PRT
<213> ORGANISM: Salmonella enterica

<400> SEQUENCE: 94

Met Asn Phe Asn Thr Val Phe Arg Trp His Leu Pro Phe Leu Phe Leu
1               5                   10                  15

Ile Leu Leu Thr Phe Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile Leu
            20                  25                  30

Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ala Ala Ser Ala Ala Trp
        35                  40                  45

Pro Ser Leu Leu Asn Asp Lys Trp Gln Asn Lys Thr Ser Val Val Asn
    50                  55                  60

Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu Pro
65                  70                  75                  80

Ala Leu Leu Gln Gln His His Pro Arg Trp Val Val Val Glu Leu Gly
                85                  90                  95

Gly Asn Asp Gly Leu Arg Gly Phe Ala Pro Ala Gln Thr Glu Gln Thr
            100                 105                 110

Leu Arg Lys Ile Ile Gln Thr Val Lys Ala Ala Asp Ala Gln Pro Leu
        115                 120                 125

Leu Met Gln Ile His Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn Glu
    130                 135                 140

Ser Phe Ser Ala Ile Tyr Pro Lys Leu Ala Lys Glu Phe Asp Ile Pro
145                 150                 155                 160

Leu Leu Pro Phe Phe Met Lys Glu Val Tyr Leu Lys Pro Gln Trp Met
                165                 170                 175

Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile Ala
            180                 185                 190

Asp Trp Met Ala Lys Gln Leu Thr Pro Phe Leu Ser
        195                 200


<210> SEQ ID NO 95
<211> LENGTH: 204
<212> TYPE: PRT
<213> ORGANISM: Salmonella enterica

<400> SEQUENCE: 95

Met Asn Phe Asn Thr Val Phe Arg Trp His Leu Pro Phe Leu Phe Leu
1               5                   10                  15

Ile Leu Leu Thr Phe Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile Leu
            20                  25                  30

Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ala Ala Ser Ala Ala Trp
        35                  40                  45

Pro Ser Leu Leu Asn Asp Lys Trp Gln Asn Lys Thr Ser Val Val Asn
    50                  55                  60

Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu Pro
65                  70                  75                  80

Thr Leu Leu Gln Gln His His Pro Arg Trp Val Val Val Glu Leu Gly
                85                  90                  95

Gly Asn Asp Gly Leu Arg Gly Phe Ala Pro Ala Gln Thr Glu Gln Thr
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            100                 105                 110

Leu Arg Lys Ile Ile Gln Thr Val Lys Ala Ala Asp Ala Gln Pro Leu
        115                 120                 125

Leu Met Gln Ile His Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn Glu
    130                 135                 140

Ser Phe Ser Ala Ile Tyr Pro Lys Leu Ala Lys Glu Phe Asp Ile Pro
145                 150                 155                 160

Leu Leu Pro Phe Phe Met Glu Glu Val Tyr Leu Lys Pro Gln Trp Met
                165                 170                 175

Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile Ala
            180                 185                 190

Asp Trp Met Ala Lys Gln Leu Thr Pro Phe Leu Ser
        195                 200


<210> SEQ ID NO 96
<211> LENGTH: 204
<212> TYPE: PRT
<213> ORGANISM: Salmonella enterica

<400> SEQUENCE: 96

Met Asn Phe Asn Thr Val Phe Arg Trp His Leu Pro Phe Leu Phe Leu
1               5                   10                  15

Ile Leu Leu Thr Phe Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile Leu
            20                  25                  30

Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ala Ala Ser Ala Ala Trp
        35                  40                  45

Pro Ser Leu Leu Asn Asp Lys Trp Gln Asn Lys Thr Ser Val Val Asn
    50                  55                  60

Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu Pro
65                  70                  75                  80

Ala Leu Leu Gln Gln His His Pro Arg Trp Val Val Val Glu Leu Gly
                85                  90                  95

Gly Asn Asp Gly Leu Arg Gly Phe Ala Pro Ala Gln Thr Glu Gln Thr
            100                 105                 110

Leu Arg Lys Ile Ile Gln Thr Val Lys Ala Ala Asp Ala Gln Pro Leu
        115                 120                 125

Leu Met Gln Ile His Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn Glu
    130                 135                 140

Ser Phe Ser Ala Ile Tyr Leu Lys Leu Ala Lys Glu Phe Asp Ile Pro
145                 150                 155                 160

Leu Leu Pro Phe Phe Met Glu Glu Val Tyr Leu Lys Pro Gln Trp Met
                165                 170                 175

Gln Asp Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile Ala
            180                 185                 190

Asp Trp Met Ala Lys Gln Leu Thr Pro Phe Leu Ser
        195                 200


<210> SEQ ID NO 97
<211> LENGTH: 204
<212> TYPE: PRT
<213> ORGANISM: Salmonella enterica

<400> SEQUENCE: 97

Met Asn Phe Asn Thr Val Phe Arg Trp His Leu Pro Phe Leu Phe Leu
1               5                   10                  15

Ile Leu Leu Thr Phe Arg Ala Ala Ala Ala Asp Thr Leu Leu Ile Leu
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            20                  25                  30

Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ala Ala Ser Ala Ala Trp
        35                  40                  45

Pro Ser Leu Leu Asn Asp Lys Trp Gln Asn Lys Thr Ser Val Val Asn
    50                  55                  60

Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu Pro
65                  70                  75                  80

Ala Leu Leu Gln Gln His His Pro Arg Trp Val Val Val Glu Leu Gly
                85                  90                  95

Gly Asn Asp Gly Leu Arg Gly Phe Ala Pro Ala Gln Thr Glu Gln Thr
            100                 105                 110

Leu Arg Lys Ile Ile Gln Thr Val Lys Ala Ala Asp Ala Gln Pro Leu
        115                 120                 125

Leu Met Gln Ile His Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn Glu
    130                 135                 140

Ser Phe Ser Ala Ile Tyr Pro Lys Leu Ala Lys Glu Phe Asp Ile Pro
145                 150                 155                 160

Leu Leu Pro Phe Phe Met Glu Glu Val Tyr Leu Lys Pro Gln Trp Met
                165                 170                 175

Gln Asp Asp Gly Ile His Pro Asn His Asp Ala Gln Pro Phe Ile Ala
            180                 185                 190

Asp Trp Met Ala Lys Gln Leu Thr Pro Phe Leu Ser
        195                 200


<210> SEQ ID NO 98
<211> LENGTH: 194
<212> TYPE: PRT
<213> ORGANISM: Salmonella enterica

<400> SEQUENCE: 98

Met Pro Phe Leu Phe Leu Phe Leu Leu Thr Phe Arg Val Ala Ala Ala
1               5                   10                  15

Asp Thr Leu Leu Val Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met
            20                  25                  30

Ala Ala Asn Ala Ala Trp Pro Ser Leu Leu Asn Asp Lys Trp Gln Asn
        35                  40                  45

Gln Thr Pro Val Val Asn Ala Ser Ile Ser Gly Asp Thr Ser Leu Gln
    50                  55                  60

Gly Leu Thr Arg Leu Pro Ala Leu Leu Gln Gln His Gln Pro Arg Trp
65                  70                  75                  80

Val Leu Val Glu Leu Gly Gly Asn Asp Gly Leu Arg Gly Phe Ala Pro
                85                  90                  95

Ala Gln Thr Glu Gln Thr Leu Arg Lys Ile Ile Gln Ala Val Lys Ala
            100                 105                 110

Ala Asn Ala Gln Pro Leu Leu Met Gln Ile His Leu Pro Ala Asn Tyr
        115                 120                 125

Gly Arg Arg Tyr Asn Glu Ser Phe Ser Ala Ile Tyr Pro Lys Leu Ala
    130                 135                 140

Lys Glu Phe Asp Ile Pro Leu Leu Pro Phe Phe Met Glu Glu Val Tyr
145                 150                 155                 160

Leu Lys Pro Gln Trp Met Gln Asp Asp Gly Ile His Pro Asn Arg Asp
                165                 170                 175

Ala Gln Pro Phe Ile Ala Asp Trp Met Ala Lys Gln Leu Thr Pro Phe
            180                 185                 190
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Leu Ser

<210> SEQ ID NO 99
<211> LENGTH: 272
<212> TYPE: PRT
<213> ORGANISM: Klebsiella sp.

<400> SEQUENCE: 99

Met Gln Arg Phe Ala Gln His Arg Tyr Phe Pro Ala Ala Ala Ile Val
1 5 10 15

Gln Ala Gly Glu Asp Arg Gln Gln Gly Arg Phe Thr Gly Ala Arg Leu
20 25 30

Ala Asp Gln Gly Asp Gly Leu Pro Arg Phe Asp Asn Gln Leu Asn Ser
35 40 45

Gly Lys Asp Gly Glu Leu Met Leu Pro Leu Thr Asp Gly Leu Leu Lys
50 55 60

Met Met Asn Phe Lys Tyr Val Phe Arg Trp His Val Pro Phe Leu Phe
65 70 75 80

Leu Phe Leu Phe Thr Cys Arg Ala Met Ala Ala Asp Thr Leu Leu Ile
85 90 95

Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ala Ala Asn Ala Ala
100 105 110

Trp Pro Ala Leu Leu Asn Glu Lys Trp Gln Ala Lys Thr Pro Val Val
115 120 125

Asn Ala Ser Ile Ser Gly Asp Thr Ser Gln Gln Gly Leu Ala Arg Leu
130 135 140

Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu Val Glu Leu
145 150 155 160

Gly Gly Asn Asp Gly Leu Arg Gly Phe Pro Pro Gln Gln Thr Glu Gln
165 170 175

Thr Leu Arg Thr Ile Ile Gln Thr Ile Lys Ala Ala Asn Ala Glu Pro
180 185 190

Leu Leu Met Gln Ile His Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn
195 200 205

Glu Ala Phe Gly Ala Ile Tyr Pro Ala Leu Ala Lys Glu Phe Ala Ile
210 215 220

Pro Leu Leu Pro Phe Phe Met Glu Glu Val Tyr Leu Lys Pro Gln Arg
225 230 235 240

Met Glu Glu Asp Gly Ile His Pro Asn Arg Asp Ala Gln Pro Asn Ile
245 250 255

Ala Ala Trp Met Glu Asn Arg Leu Ala Pro Leu Asp Lys His Val Ser
260 265 270

<210> SEQ ID NO 100
<211> LENGTH: 219
<212> TYPE: PRT
<213> ORGANISM: Cronobacter sakazakii

<400> SEQUENCE: 100

Met Phe Pro Leu Thr Asp Gly Phe Ile Lys Met Met Asn Phe Lys Asn
1 5 10 15

Val Phe Arg Trp His Phe Pro Phe Leu Leu Leu Ala Leu Leu Ser Phe
20 25 30

Arg Ala Ala Ala Ala Asp Thr Leu Leu Val Leu Gly Asp Ser Leu Ser
35 40 45

Ala Gly Tyr Arg Met Ala Ala Asp Ala Ala Trp Pro Ala Leu Leu Asn

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    50                  55                  60

Asp Lys Trp Gln Gln Arg Asp Val Arg Val Val Asn Ala Ser Ile Ser
65                  70                  75                  80

Gly Asp Thr Ala Gln Gln Gly Leu Ser Arg Leu Pro Ala Leu Leu Lys
                85                  90                  95

Gln His Gln Pro Arg Trp Val Leu Ile Glu Leu Gly Gly Asn Asp Gly
            100                 105                 110

Leu Arg Gly Phe Pro Pro Asp Thr Leu Ser Ala Thr Leu Arg Lys Ile
        115                 120                 125

Ile Glu Gln Val Lys Thr Ala Gly Ala Glu Pro Leu Leu Met Gln Ile
    130                 135                 140

Arg Leu Pro Ala Asn Tyr Gly Arg Arg Tyr Asn Gln Ala Phe Glu Ala
145                 150                 155                 160

Ile Tyr Pro Glu Leu Ala Gln Ser Phe Ser Ile Pro Leu Leu Pro Phe
                165                 170                 175

Phe Met Glu Glu Val Tyr Leu Lys Pro Gln Trp Met Gln Asp Asp Gly
            180                 185                 190

Ile His Pro Asn Arg Asp Ala Gln Pro Phe Ile Ala Asp Trp Met Ala
        195                 200                 205

Gln Arg Leu Ala Pro Leu Val Lys His Asp Ser
    210                 215


<210> SEQ ID NO 101
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Pectobacterium atrosepticum

<400> SEQUENCE: 101

Met Met Asn Phe Lys Asn Val Phe Tyr Val Arg Ser Phe Ala Trp Arg
1               5                   10                  15

Ser Thr Arg Trp Ala Gly Leu Arg Lys His Val Phe Val Leu Leu Leu
            20                  25                  30

Leu Gly Leu Cys Ser Val Arg Ala Phe Ala Ala Asp Thr Leu Leu Ile
        35                  40                  45

Leu Gly Asp Ser Leu Ser Ala Gly Tyr Gln Met Pro Ala Ala Asn Ala
    50                  55                  60

Trp Pro Thr Leu Leu Asn Thr Gln Trp Gln Thr Gln Lys Lys Gly Ile
65                  70                  75                  80

Ala Val Val Asn Ala Ser Ile Ser Gly Asp Thr Thr Ala Gln Gly Leu
                85                  90                  95

Ala Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu
            100                 105                 110

Ile Glu Leu Gly Gly Asn Asp Gly Leu Arg Gly Phe Pro Ala Pro Asn
        115                 120                 125

Ile Glu Gln Asp Leu Ala Lys Ile Ile Thr Leu Val Lys Gln Ala Asn
    130                 135                 140

Ala Lys Pro Leu Leu Met Gln Val Arg Leu Pro Thr Asn Tyr Gly Arg
145                 150                 155                 160

Arg Tyr Thr Glu Ser Phe Ser Asn Ile Tyr Pro Lys Leu Ala Glu Gln
                165                 170                 175

Phe Ala Leu Pro Leu Leu Pro Phe Phe Met Glu Gln Val Tyr Leu Lys
            180                 185                 190

Pro Glu Trp Ile Met Glu Asp Gly Ile His Pro Thr Arg Asp Ala Gln
        195                 200                 205
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Pro Phe Ile Ala Glu Trp Met Ala Lys Gln Leu Glu Pro Leu Val Asn
    210                 215                 220

His Glu Ser
225


<210> SEQ ID NO 102
<211> LENGTH: 200
<212> TYPE: PRT
<213> ORGANISM: Erwinia tasmaniensis

<400> SEQUENCE: 102

Met Ala Phe Met Thr Leu Arg Ala Ala Ala Ala Asp Thr Leu Leu Val
1               5                   10                  15

Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Met Ser Ala Ser Ala Ala
            20                  25                  30

Trp Pro Ala Leu Leu Asn Glu Lys Trp Gln Lys Ser Pro Ala Ile Ile
        35                  40                  45

Asn Gly Ser Ile Ser Gly Asp Thr Thr Ala Gln Gly Leu Ala Arg Leu
    50                  55                  60

Ser Ala Leu Leu Glu Gln His Gln Pro Arg Trp Val Leu Ile Glu Leu
65                  70                  75                  80

Gly Gly Asn Asp Gly Leu Arg Gly Phe Pro Pro Gln Gln Val Glu Gln
                85                  90                  95

Asp Leu Asn Gln Ala Ile Ala Gln Ile Gln Ala Ala Lys Ala Gln Pro
            100                 105                 110

Leu Leu Met Gln Val Arg Leu Pro Ala Asn Tyr Gly Lys Arg Tyr Thr
        115                 120                 125

Asp Ser Phe Ala Ala Ile Tyr Pro Arg Leu Ala Ser Gln His Ala Ile
    130                 135                 140

Pro Leu Val Pro Phe Phe Met Glu Gln Val Tyr Leu Lys Pro Glu Trp
145                 150                 155                 160

Met Gln Asp Asp Gly Ile His Pro Asn Pro Ser Ala Gln Pro Phe Ile
                165                 170                 175

Ala Asp Leu Met Ala Lys Gln Leu Ala Pro Leu Val Lys His Glu Ala
            180                 185                 190

Ser Arg Ser Val Gly Asn Asp Gly
        195                 200


<210> SEQ ID NO 103
<211> LENGTH: 190
<212> TYPE: PRT
<213> ORGANISM: Yersinia pestis

<400> SEQUENCE: 103

Met Arg Ala Ala Ala Thr Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu
1               5                   10                  15

Ser Ala Gly Tyr Arg Leu Pro Ile Ala Gln Ala Trp Pro Ser Leu Leu
            20                  25                  30

Asp Lys Lys Trp Gln Ala Thr Pro Ser Leu Pro Lys Val Val Asn Ala
        35                  40                  45

Ser Ile Ser Gly Asp Thr Ala Ala Gln Gly Leu Ala Arg Leu Pro Ala
    50                  55                  60

Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu Ile Glu Leu Gly Ala
65                  70                  75                  80

Asn Asp Ala Leu Arg Gly Phe Pro Thr Gln Asp Ile Gln Arg Asp Leu
                85                  90                  95
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```
Ser Glu Ile Ile Asn Gln Ile Thr Ala Ala Lys Ala Gln Pro Leu Leu
            100                 105                 110

Met Gln Ile Arg Ile Pro Pro Asn Tyr Gly Arg Arg Tyr Thr Asp Ala
        115                 120                 125

Phe Thr Ala Ile Tyr Pro Gln Leu Ala Gln Gln Phe Asp Ile Pro Leu
    130                 135                 140

Leu Pro Phe Phe Met Glu Gln Val Ala Val Lys Pro Glu Trp Met Gln
145                 150                 155                 160

Asp Asp Gly Leu His Pro Asn Gly Asp Ala Gln Pro Phe Ile Ala Asp
                165                 170                 175

Trp Met Ala Gln Gln Leu Lys Pro Leu Val Val Asp Pro Lys
            180                 185                 190


<210> SEQ ID NO 104
<211> LENGTH: 212
<212> TYPE: PRT
<213> ORGANISM: Yersinia pestis

<400> SEQUENCE: 104

Met Met Asn Phe Lys Asn Val Phe Arg Trp His Leu Pro Phe Leu Leu
1               5                   10                  15

Leu Leu Gly Leu Phe Ser Leu Arg Ala Ala Ala Thr Asp Thr Leu Leu
            20                  25                  30

Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Leu Pro Ile Ala Gln
        35                  40                  45

Ala Trp Pro Ser Leu Leu Asp Lys Lys Trp Gln Ala Thr Pro Ser Leu
    50                  55                  60

Pro Lys Val Val Asn Ala Ser Ile Ser Gly Asp Thr Ala Ala Gln Gly
65                  70                  75                  80

Leu Ala Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp Val
                85                  90                  95

Leu Ile Glu Leu Gly Ala Asn Asp Ala Leu Arg Gly Phe Pro Thr Gln
            100                 105                 110

Asp Ile Gln Arg Asp Leu Ser Glu Ile Ile Asn Gln Ile Thr Ala Ala
        115                 120                 125

Lys Ala Gln Pro Leu Leu Met Gln Ile Arg Ile Pro Pro Asn Tyr Gly
    130                 135                 140

Arg Arg Tyr Thr Asp Ala Phe Thr Ala Ile Tyr Pro Gln Leu Ala Gln
145                 150                 155                 160

Gln Phe Asp Ile Pro Leu Leu Pro Phe Phe Met Glu Gln Val Ala Val
                165                 170                 175

Lys Pro Glu Trp Met Gln Asp Asp Gly Leu His Pro Asn Gly Asp Ala
            180                 185                 190

Gln Pro Phe Ile Ala Asp Trp Met Ala Gln Gln Leu Lys Pro Leu Val
        195                 200                 205

Val Asp Pro Lys
    210


<210> SEQ ID NO 105
<211> LENGTH: 222
<212> TYPE: PRT
<213> ORGANISM: Yersinia pestis

<400> SEQUENCE: 105

Met Leu Thr Leu Thr Asp Val Leu Ile Lys Met Met Asn Phe Lys Asn
1               5                   10                  15
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```
Val Phe Arg Trp His Leu Pro Phe Leu Leu Leu Leu Gly Leu Phe Ser
            20                  25                  30

Leu Arg Ala Ala Ala Thr Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu
        35                  40                  45

Ser Ala Gly Tyr Arg Leu Pro Ile Ala Gln Ala Trp Pro Ser Leu Leu
    50                  55                  60

Asp Lys Lys Trp Gln Ala Thr Pro Ser Leu Pro Lys Val Val Asn Ala
65                  70                  75                  80

Ser Ile Ser Gly Asp Thr Ala Ala Gln Gly Leu Ala Arg Leu Pro Ala
                85                  90                  95

Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu Ile Glu Leu Gly Ala
            100                 105                 110

Asn Asp Ala Leu Arg Gly Phe Pro Thr Gln Asp Ile Gln Arg Asp Leu
        115                 120                 125

Ser Glu Ile Ile Asn Gln Ile Thr Ala Ala Lys Ala Gln Pro Leu Leu
    130                 135                 140

Met Gln Ile Arg Ile Pro Pro Asn Tyr Gly Arg Arg Tyr Thr Asp Ala
145                 150                 155                 160

Phe Thr Ala Ile Tyr Pro Gln Leu Ala Gln Gln Phe Asp Ile Pro Leu
                165                 170                 175

Leu Pro Phe Phe Met Glu Gln Val Ala Val Lys Pro Glu Trp Met Gln
            180                 185                 190

Asp Asp Gly Leu His Pro Asn Gly Asp Ala Gln Pro Phe Ile Ala Asp
        195                 200                 205

Trp Met Ala Gln Gln Leu Lys Pro Leu Val Val Asp Pro Lys
    210                 215                 220


<210> SEQ ID NO 106
<211> LENGTH: 211
<212> TYPE: PRT
<213> ORGANISM: Yersinia pseudotuberculosis

<400> SEQUENCE: 106

Met Asn Phe Lys Asn Val Phe Arg Trp His Leu Pro Phe Leu Leu Leu
1               5                   10                  15

Leu Gly Leu Phe Ser Leu Arg Ala Ala Ala Thr Asp Thr Leu Leu Ile
            20                  25                  30

Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Leu Pro Ile Ala Gln Ala
        35                  40                  45

Trp Pro Ser Leu Leu Asp Lys Lys Trp Gln Ala Thr Pro Ser Leu Pro
    50                  55                  60

Lys Val Val Asn Ala Ser Ile Ser Gly Asp Thr Ala Ala Gln Gly Leu
65                  70                  75                  80

Ala Arg Leu Pro Ala Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu
                85                  90                  95

Ile Glu Leu Gly Ala Asn Asp Ala Leu Arg Gly Phe Pro Thr Gln Asp
            100                 105                 110

Ile Gln Arg Asp Leu Ser Glu Ile Ile Asn Gln Ile Thr Ala Ala Lys
        115                 120                 125

Ala Gln Pro Leu Leu Met Gln Ile Arg Ile Pro Pro Asn Tyr Gly Arg
    130                 135                 140

Arg Tyr Thr Asp Ala Phe Thr Ala Ile Tyr Pro Gln Leu Ala Gln Gln
145                 150                 155                 160

Phe Asp Ile Pro Leu Leu Pro Phe Phe Met Glu Gln Val Ala Val Lys
                165                 170                 175
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```
Pro Glu Trp Met Gln Asp Asp Gly Leu His Pro Asn Gly Asp Ala Gln
            180                 185                 190

Pro Phe Ile Ala Asp Trp Met Ala Gln Gln Leu Lys Pro Leu Val Val
        195                 200                 205

Asp Pro Lys
    210
```

<210> SEQ ID NO 107
<211> LENGTH: 196
<212> TYPE: PRT
<213> ORGANISM: Serratia proteamaculans

<400> SEQUENCE: 107

```
Met Gly Leu Phe Ser Leu Arg Ala Val Ala Ala Asp Thr Leu Leu Ile
1               5                   10                  15

Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Leu Pro Val Ala Gln Ala
            20                  25                  30

Trp Pro Thr Leu Leu Ala Asp Gln Trp Gln Lys Lys Pro Gly Asp Pro
        35                  40                  45

Gln Leu Val Asn Ala Ser Ile Ser Gly Asp Thr Ala Ala Gln Gly Leu
    50                  55                  60

Ala Arg Leu Pro Glu Leu Leu Lys Gln His Gln Pro Arg Trp Val Leu
65                  70                  75                  80

Ile Glu Leu Gly Ala Asn Asp Gly Leu Arg Gly Phe Pro Ala Gln Asp
                85                  90                  95

Leu Gln Arg Asp Leu Ser Gln Ile Ile Thr Leu Val Gln Gln Ala Gly
            100                 105                 110

Ala Gln Pro Leu Leu Met Gln Ile Arg Ile Pro Pro Asn Tyr Gly Arg
        115                 120                 125

Arg Tyr Thr Glu Ala Phe Ser Ala Ile Tyr Pro Gln Leu Ala Lys Gln
    130                 135                 140

Phe Asp Ile Pro Leu Leu Pro Phe Tyr Met Glu Gln Val Val Val Lys
145                 150                 155                 160

Ala Glu Trp Met Gln Asp Asp Gly Leu His Pro Asn Lys Asp Ala Gln
                165                 170                 175

Pro Phe Ile Ala Thr Trp Met Ala Glu Arg Leu Glu Pro Leu Val Lys
            180                 185                 190

His Glu Ser Asn
        195
```

<210> SEQ ID NO 108
<211> LENGTH: 216
<212> TYPE: PRT
<213> ORGANISM: Yersinia pestis

<400> SEQUENCE: 108

```
Met Leu Ile Lys Met Met Asn Phe Lys Asn Val Phe Arg Trp His Leu
1               5                   10                  15

Pro Phe Leu Leu Leu Leu Gly Leu Phe Ser Leu Arg Ala Ala Ala Thr
            20                  25                  30

Asp Thr Leu Leu Ile Leu Gly Asp Ser Leu Ser Ala Gly Tyr Arg Leu
        35                  40                  45

Pro Ile Ala Gln Ala Trp Pro Ser Leu Leu Asp Lys Lys Trp Gln Ala
    50                  55                  60

Thr Pro Ser Leu Pro Lys Val Val Asn Ala Ser Ile Ser Gly Asp Thr
65                  70                  75                  80
```

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```
Ala Ala Gln Gly Leu Ala Arg Leu Pro Ala Leu Leu Lys Gln His Gln
                85                  90                  95

Pro Arg Trp Val Leu Ile Glu Leu Gly Ala Asn Asp Ala Leu Arg Gly
            100                 105                 110

Phe Pro Thr Gln Asp Ile Gln Arg Asp Leu Ser Glu Ile Ile Asn Gln
        115                 120                 125

Ile Thr Ala Ala Lys Ala Gln Pro Leu Leu Met Gln Ile Arg Ile Pro
    130                 135                 140

Pro Asn Tyr Gly Arg Arg Tyr Thr Asp Ala Phe Thr Ala Ile Tyr Pro
145                 150                 155                 160

Gln Leu Ala Gln Gln Phe Asp Ile Pro Leu Leu Pro Phe Phe Met Glu
                165                 170                 175

Gln Val Ala Val Lys Pro Glu Trp Met Gln Asp Asp Gly Leu His Pro
            180                 185                 190

Asn Gly Asp Ala Gln Pro Phe Ile Ala Asp Trp Met Ala Gln Gln Leu
        195                 200                 205

Lys Pro Leu Val Val Asp Ser Lys
    210                 215
```

The invention claimed is:

1. An engineered thioesterase enzyme which converts a C10, C12, or C14 acyl-ACP substrate to a fatty acid derivative with a greater activity as compared to a wild-type thioesterase enzyme, wherein the engineered thioesterase enzyme comprises an amino acid sequence that is at least 90% identical to SEQ ID NO: 73 and has a substitution at an amino acid position selected from the group consisting of position 78, 80, 101, 108, 111, 117, 118, 122, 145, 152, and 178.

2. The engineered thioesterase enzyme of claim **1**, wherein the amino acid sequence has a feature selected from the group consisting of: (a) the amino acid residue at position 78 is methionine; (b) the amino acid residue at position 80 is tryptophan; (c) the amino acid residue at position 101 is leucine, alanine, or valine; (d) the amino acid residue at position 108 is tryptophan; (e) the amino acid residue at position 111 is tyrosine or tryptophan; (f) the amino acid residue at position 117 is arginine; (g) the amino acid residue at position 122 is arginine; (h) the amino acid residue at position 145 is alanine, cysteine, aspartic acid, glutamic acid, isoleucine, leucine, methionine, glutamine, arginine, serine, or threonine; (i) the amino acid residue at position 152 is arginine; and (j) the amino acid residue at position 178 is threonine or tryptophan.

3. The engineered thioesterase enzyme of claim **1**, wherein the amino acid residue at position 101 is leucine, the amino acid residue at position 111 is tyrosine, the amino acid residue at position 145 is cysteine, or the amino acid residue at position 178 is threonine.

4. The engineered thioesterase enzyme of claim **1**, wherein the amino acid residue at position 111 is tyrosine or the amino acid residue at position 145 is cysteine.

5. The engineered thioesterase enzyme of claim **1**, wherein the amino acid residue at 78 is methionine, the amino acid residue at position 108 is tryptophan, or the amino acid residue at position 145 is cysteine.

6. The engineered thioesterase enzyme of claim **1**, wherein the amino acid residue at 78 is methionine, the amino acid residue at position 108 is tryptophan, or the amino acid residue at position 145 is leucine.

7. An engineered thioesterase enzyme which converts an acyl-ACP substrate to a fatty acid derivative with a greater yield or an increased percentage of short-chain fatty acid derivatives as compared to a wild-type thioesterase enzyme, wherein the engineered thioesterase enzyme comprises an amino acid sequence that is at least 90% identical to SEQ ID NO: 73 and has a substitution at an amino acid position selected from the group consisting of position 78, 80, 101, 108, 111, 117, 118, 122, 145, 152 and 178.

8. The engineered thioesterase enzyme of claim **7**, wherein the amino acid sequence has a feature selected from the group consisting of: (a) the amino acid residue at position 78 is methionine; (b) the amino acid residue at position 80 is tryptophan; (c) the amino acid residue at position 101 is leucine, alanine or valine; (d) the amino acid residue at position 108 is tryptophan; (e) the amino acid residue at position 111 is tyrosine or tryptophan; (f) the amino acid residue at position 117 is arginine; (g) the amino acid residue at position 122 is arginine; (h) the amino acid residue at position 145 is alanine, cysteine, aspartic acid, glutamic acid, isoleucine, leucine, methionine, glutamine, arginine, serine or threonine; (i) the amino acid residue at position 152 is arginine; and (j) the amino acid residue at position 178 is threonine or tryptophan.

9. The engineered thioesterase enzyme of claim **7**, wherein the amino acid residue at position 145 is cysteine.

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